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(54) Title: COMPOSITIONS AND METHODS FOR DELIVERY OF AAV

(57) Abstract: The invention provides compositions and methods for the preparation, manufacture, formulation and therapeutic use of adeno-associated virus (AAV) particles for the prevention and/or treatment of diseases.

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COMPOSITIONS AND METHODS FOR DELIVERY OF AAV

REFERENCE TO RELEVANT APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application NO. 62/540,776, entitled "Compositions and methods for delivery of AAV across the blood brain barrier", filed August 3, 2017, U.S. Provisional Patent Application NO. 62/565,264, entitled "Compositions and methods for delivery of AAV" filed September 29, 2017, and U.S. Provisional Patent Application NO. 62/572,706, entitled "Compositions and methods for delivery of AAV", filed October 16, 2017; the contents of each of which are herein incorporated by reference in their entirety.

REFERENCE TO THE SEQUENCE LISTING

[0002] The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled 20571050PCTSL.txt, created on August 3, 2018, which is 6,728,739 bytes in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0003] The present invention relates to compositions, methods and processes for the design, preparation, manufacture, use and/or formulation of adeno-associated virus capsids for improved biodistribution.

BACKGROUND OF THE INVENTION

[0004] Adeno-associated viral (AAV) vectors are a promising candidate for therapeutic gene delivery and have proven safe and efficacious in clinical trial.

[0005] Delivery of AAV to some systems in the body has proven to be particularly challenging, requiring invasive surgeries for sufficient levels of gene transfer. For some body systems, intravenous delivery has historically resulted in limited gene transfer, in part due to inefficient transduction into cells. There remains a need in the art for AAV vectors that may be administered by intravenous delivery and yet are able to efficiently target regions critical for treating a multitude of diseases.

[0006] One example of a system where delivery is challenging is the central nervous system. Delivery of AAV to regions of the central nervous system (CNS) has proven to be particularly challenging, requiring invasive surgeries for sufficient levels of gene transfer (See e.g., Bevan et al. Mol Ther. 2011 Nov; 19(11): 1971–1980). Intravenous delivery has

historically resulted in limited gene transfer to the CNS, in part due to the presence of the blood brain barrier (BBB). There remains a need in the art for AAV vectors that may be administered by intravenous delivery and yet are able to efficiently cross the blood brain barrier and target regions of the CNS critical for treating a multitude of CNS diseases.

[0007] Another example of a system where delivery is challenging is the cardiovascular system. Delivery of AAV to the cardiovascular system has proven to be particularly challenging, requiring invasive surgeries for sufficient levels of gene transfer. Intravenous delivery has historically resulted in limited gene transfer to the cardiovascular system, in part due to inefficient transduction into cardiomyocytes. There remains a need in the art for AAV vectors that may be administered by intravenous delivery and yet are able to efficiently target regions of the cardiovascular system critical for treating a multitude of diseases.

[0008] The present invention addresses this need by providing novel AAV particles with engineered capsid proteins that allow for efficient transduction of CNS tissues following intravenous delivery. Further, the viral genomes of these AAV particles may be altered to suit the needs of any number of CNS diseases, providing platform capsids for crossing the blood brain barrier and targeting of CNS tissues.

SUMMARY OF THE INVENTION

[0009] The invention provides an adeno-associated viral (AAV) particle comprising a capsid and a viral genome.

[0010] The AAV particle may comprise a capsid or a peptide insert such as, but not limited to, VOY101, VOY201, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5 (G2B5), PHP.S, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b,

AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1,

AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11,

AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, and/or AAVF9/HSC9 and variants thereof. In one aspect, the capsid of the AAV particle is VOY101. In one aspect, the capsid of the AAV particle is VOY201. In one aspect, the AAV particle comprises a peptide insert and the peptide insert is AAVPHP.N. In one aspect, the AAV particle comprises a peptide insert and the peptide insert is AAVPHP.B. In one aspect, the AAV particle comprises a peptide insert and the peptide insert is AAVPHP.A. In one aspect, the AAV particle comprises a peptide insert and the peptide insert is AAVPHP.S.

[0011] In one aspect, the AAV particle comprises a viral genome which comprises a nucleic acid sequence position between two inverted terminal repeats (ITRs).

[0012] In one aspect, the viral genome transduces cardiomyocytes upon delivery of the AAV particle. The delivery may be by any method known in the art, such as, but not limited to, intravenous administration or intracarotid artery delivery.

[0013] In one aspect, the capsid penetrates the blood brain barrier following delivery of the AAV particle. The delivery may be by any method known in the art, such as, but not limited to, intravenous administration or intracarotid artery delivery.

[0014] The AAV particles of the present invention may transduce CNS structures following administration. Non-limiting examples of CNS structures include brain, spinal cord, brainstem nuclei, cerebellum, cerebrum, motor cortex, caudate nucleus, thalamus, hypothalamus, cervical spinal cord, thoracic spinal cord, lumbar spinal cord, striatum, substantia nigra, hippocampus, amygdala and/or cerebral cortex.

[0015] In one aspect, the AAV particle comprises a viral genome which comprises a nucleic acid sequence that, when expressed, inhibits or suppresses the expression of a gene of interest (e.g., SOD1, HTT, APOE, and MAPT) in a cell. The nucleic acid sequence comprises a sense strand sequence and an antisense strand sequence which may be independently 30

nucleotides in length or less and, the sense and/or antisense strands may comprise a 3' overhang of at least 1 or at least 2 nucleotides. The sense sequence and antisense strand sequence may share a region of complementarity of at least four nucleotides in length (e.g., at least 17 nucleotides in length, between 19 and 21 nucleotides in length, or 19 nucleotides in length). The antisense strand may be excised from the AAV particle at a rate of at least 80%, 85%, 90%, 95%, or more than 95%, or more than 98%, or more than 99%. The antisense strand may be excised from the AAV particle at a rate greater than the excision of the sense strand (e.g., 2 times, 5 times, 10 times or more than 10 times greater).

[0016] Provided herein are compositions (e.g., pharmaceutical compositions) comprising AAV particles. The AAV particles may comprise a viral genome comprising a nucleic acid sequence encoding a protein of interest (e.g., an antibody, AADC, APOE2, Frataxin, ATP2A2, and/or S100A1). The AAV particles may comprise a viral genome comprising nucleic acid sequences that when expressed, inhibits or suppresses the expression of a gene of interest (e.g., SOD1, HTT, APOE, and/or MAPT) in a cell.

[0017] Provided herein are methods of using AAV particles.

[0018] In one aspect, provided are methods of inhibiting the expression of a target gene in a cell (e.g., mammalian cell, or mammalian cell of the CNS, or a cardiomyocyte).

[0019] In one aspect, provided are methods of increasing the expression of a target gene in a cell such as a mammalian cell (e.g., a mammalian cell of the CNS, or a cardiomyocyte)

[0020] In one aspect, provided are methods for treating and/or ameliorating a neurological disease in a subject by administering a therapeutically effective amount of a composition comprising the AAV particles described herein. The administration may be by intravenous or intracarotid artery delivery. The methods may be used to increase the expression of a protein of interest (e.g., an antibody, AADC, APOE2, and/or Frataxin). The methods may be used to decrease the amount of expression of a gene of interest (e.g., SOD1, HTT, APOE, and/or MAPT).

[0021] In one aspect, provided are methods for altering the level of a protein or gene of interest in a subject by administration of the AAV particles described herein. The administration may be by intravenous or intracarotid artery delivery. The methods may be used to increase the expression of a protein of interest (e.g., an antibody, AADC, APOE2, Frataxin, ATP2A2, and/or S100A1). The methods may be used to decrease the amount of expression of a gene of interest (e.g., SOD1, HTT, APOE, and/or MAPT).

[0022] Provided herein are methods for treating cardiovascular disease in a subject in need thereof by administering compositions of the AAV particles described herein. The delivery may be by any method known in the art, such as, but not limited to, intravenous administration or intracarotid artery delivery.

[0023] Provided herein are methods for treating heart failure in a subject in need thereof by administering compositions of the AAV particles described herein. The delivery may be by any method known in the art, such as, but not limited to, intravenous administration or intracarotid artery delivery.

[0024] The details of various embodiments of the invention are set forth in the description below. Other features, objects, and advantages of the invention will be apparent from the description, drawings, and the claims. In the description, the singular forms also include the plural unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. In the case of conflict, the present description will control.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] The foregoing and other objects, features and advantages will be apparent from the following description of particular embodiments of the invention, as illustrated in the accompanying drawings. The drawings are not necessarily to scale, emphasis instead being placed upon illustrating the principles of various embodiments of the invention.

[0026] FIG. 1 is a schematic of a viral genome of the invention.

DETAILED DESCRIPTION OF THE INVENTION

[0027] The details of one or more embodiments of the invention are set forth in the accompanying description below. Although any materials and methods similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred materials and methods are now described. Other features, objects and advantages of the invention will be apparent from the description. In the description, the singular forms also include the plural unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. In the case of conflict, the present description will control.

I. COMPOSITIONS OF THE INVENTION

Adeno-associated viruses (AAVs) and AAV particles

[0028] Viruses of the Parvoviridae family are small non-enveloped icosahedral capsid viruses characterized by a single stranded DNA genome. Parvoviridae family viruses consist of two subfamilies: Parvovirinae, which infect vertebrates, and Densovirinae, which infect invertebrates. Due to its relatively simple structure, easily manipulated using standard molecular biology techniques, this virus family is useful as a biological tool. The genome of the virus may be modified to contain a minimum of components for the assembly of a functional recombinant virus, or viral particle, which is loaded with or engineered to express or deliver a desired payload, which may be delivered to a target cell, tissue, organ, or organism.

[0029] The parvoviruses and other members of the Parvoviridae family are generally described in Kenneth I. Berns, "Parvoviridae: The Viruses and Their Replication," Chapter 69 in FIELDS VIROLOGY (3d Ed. 1996), the contents of which are incorporated by reference in their entirety.

[0030] The Parvoviridae family comprises the Dependovirus genus which includes adeno-associated viruses (AAV) capable of replication in vertebrate hosts including, but not limited to, human, primate, bovine, canine, equine, and ovine species.

[0031] The AAV viral genome is a linear, single-stranded DNA (ssDNA) molecule approximately 5,000 nucleotides (nt) in length. The AAV viral genome can comprise a payload region and at least one inverted terminal repeat (ITR) or ITR region. ITRs traditionally flank the coding nucleotide sequences for the non-structural proteins (encoded by Rep genes) and the structural proteins (encoded by capsid genes or Cap genes). While not wishing to be bound by theory, an AAV viral genome typically comprises two ITR sequences. The AAV vector genome comprises a characteristic T-shaped hairpin structure defined by the self-complementary terminal 145 nt of the 5' and 3' ends of the ssDNA which form an energetically stable double stranded region. The double stranded hairpin structures comprise multiple functions including, but not limited to, acting as an origin for DNA replication by functioning as primers for the endogenous DNA polymerase complex of the host viral replication cell.

[0032] In addition to the encoded heterologous payload, AAV particles may comprise the viral genome, in whole or in part, of any naturally occurring and/or recombinant AAV serotype nucleotide sequence or variant. AAV variants may have sequences of significant homology at the nucleic acid (genome or capsid) and amino acid levels (capsids), to produce

constructs which are generally physical and functional equivalents, replicate by similar mechanisms, and assemble by similar mechanisms. Chiorini et al., J. Vir. 71: 6823-33(1997); Srivastava et al., J. Vir. 45:555-64 (1983); Chiorini et al., J. Vir. 73:1309-1319 (1999); Rutledge et al., J. Vir. 72:309-319 (1998); and Wu et al., J. Vir. 74: 8635-47 (2000), the contents of each of which are incorporated herein by reference in their entirety.

[0033] In one embodiment, AAV particles of the present invention are recombinant AAV viral vectors which are replication defective, lacking sequences encoding functional Rep and Cap proteins within their viral genome. These defective AAV particles may lack most or all parental coding sequences and essentially carry only one or two AAV ITR sequences and the nucleic acid of interest for delivery to a cell, a tissue, an organ or an organism.

[0034] In one embodiment, the viral genome of the AAV particles of the present invention comprise at least one control element which provides for the replication, transcription and translation of a coding sequence encoded therein. Not all of the control elements need always be present as long as the coding sequence is capable of being replicated, transcribed and/or translated in an appropriate host cell. Non-limiting examples of expression control elements include sequences for transcription initiation and/or termination, promoter and/or enhancer sequences, efficient RNA processing signals such as splicing and polyadenylation signals, sequences that stabilize cytoplasmic mRNA, sequences that enhance translation efficacy (e.g., Kozak consensus sequence), sequences that enhance protein stability, and/or sequences that enhance protein processing and/or secretion.

[0035] According to the present invention, AAV particles for use in therapeutics and/or diagnostics comprise a virus that has been distilled or reduced to the minimum components necessary for transduction of a nucleic acid payload or cargo of interest. In this manner, AAV particles are engineered as vehicles for specific delivery while lacking the deleterious replication and/or integration features found in wild-type viruses.

[0036] AAV particles of the present invention may be produced recombinantly and may be based on adeno-associated virus (AAV) parent or reference sequences. As used herein, a "vector" is any molecule or moiety which transports, transduces or otherwise acts as a carrier of a heterologous molecule such as the nucleic acids described herein.

[0037] In addition to single stranded AAV viral genomes (e.g., ssAAVs), the present invention also provides for self-complementary AAV (scAAVs) viral genomes. scAAV vector genomes contain DNA strands which anneal together to form double stranded DNA. By skipping second strand synthesis, scAAVs allow for rapid expression in the cell.

[0038] In one embodiment, the AAV particle of the present invention is an scAAV.

[0039] In one embodiment, the AAV particle of the present invention is an ssAAV.

[0040] Methods for producing and/or modifying AAV particles are disclosed in the art such as pseudotyped AAV particles (PCT Patent Publication Nos. WO200028004; WO200123001; WO2004112727; WO 2005005610 and WO 2005072364, the contents of each of which are incorporated herein by reference in their entirety).

[0041] AAV particles may be modified to enhance the efficiency of delivery. Such modified AAV particles can be packaged efficiently and be used to successfully infect the target cells at high frequency and with minimal toxicity. In some embodiments the capsids of the AAV particles are engineered according to the methods described in US Patent Application Publication NO.US 20130195801, the contents of which are incorporated herein by reference in their entirety.

[0042] In one embodiment, the AAV particles comprising a payload region encoding the polypeptides of the invention may be introduced into mammalian cells.

[0043] AAV serotypes

[0044] AAV particles of the present invention may comprise or be derived from any natural or recombinant AAV serotype. According to the present invention, the AAV particles may utilize or be based on a serotype or include a peptide selected from any of the following VOY101, VOY201, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5 (G2B5), PHP.S, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1,

AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1,

AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-

R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, and/or AAVF9/HSC9 and variants thereof.

[0045] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20030138772, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV1 (SEQ ID NO: 6 and 64 of US20030138772), AAV2 (SEQ ID NO: 7 and 70 of US20030138772), AAV3 (SEQ ID NO: 8 and 71 of US20030138772), AAV4 (SEQ ID NO: 63 of US20030138772), AAV5 (SEQ ID NO: 114 of US20030138772), AAV6 (SEQ ID NO: 65 of US20030138772), AAV7 (SEQ ID NO: 1-3 of US20030138772), AAV8 (SEQ ID NO: 4 and 95 of US20030138772), AAV9 (SEQ ID NO: 5 and 100 of US20030138772), AAV10 (SEQ ID NO: 117 of US20030138772), AAV11 (SEQ ID NO: 118 of US20030138772), AAV12 (SEQ ID NO: 119 of US20030138772), AAVrh10 (amino acids 1 to 738 of SEQ ID NO: 81 of US20030138772), AAV16.3 (US20030138772 SEQ ID NO: 10), AAV29.3/bb.1 (US20030138772 SEQ ID NO: 11), AAV29.4 (US20030138772 SEQ ID NO: 12), AAV29.5/bb.2 (US20030138772 SEQ ID NO: 13), AAV1.3 (US20030138772 SEQ ID NO: 14), AAV13.3 (US20030138772 SEQ ID NO: 15), AAV24.1 (US20030138772 SEQ ID NO: 16), AAV27.3 (US20030138772 SEQ ID NO: 17), AAV7.2 (US20030138772 SEQ ID NO: 18), AAVC1 (US20030138772 SEQ ID NO: 19), AAVC3 (US20030138772 SEQ ID NO: 20), AAVC5 (US20030138772 SEQ ID NO: 21), AAVF1 (US20030138772 SEQ ID NO: 22), AAVF3 (US20030138772 SEQ ID NO: 23), AAVF5 (US20030138772 SEQ ID NO: 24), AAVH6 (US20030138772 SEQ ID NO: 25), AAVH2 (US20030138772 SEQ ID NO: 26), AAV42-8 (US20030138772 SEQ ID NO: 27), AAV42-15 (US20030138772 SEQ ID NO: 28), AAV42-5b (US20030138772 SEQ ID NO: 29), AAV42-1b (US20030138772 SEQ ID NO: 30), AAV42-13 (US20030138772 SEQ ID NO: 31), AAV42-3a (US20030138772 SEQ ID NO: 32), AAV42-4 (US20030138772 SEQ ID NO: 33), AAV42-5a (US20030138772 SEQ ID NO: 34), AAV42-10 (US20030138772 SEQ ID NO: 35), AAV42-3b (US20030138772 SEQ ID NO: 36), AAV42-11 (US20030138772 SEQ ID NO: 37),

AAV42-6b (US20030138772 SEQ ID NO: 38), AAV43-1 (US20030138772 SEQ ID NO: 39), AAV43-5 (US20030138772 SEQ ID NO: 40), AAV43-12 (US20030138772 SEQ ID NO: 41), AAV43-20 (US20030138772 SEQ ID NO: 42), AAV43-21 (US20030138772 SEQ ID NO: 43), AAV43-23 (US20030138772 SEQ ID NO: 44), AAV43-25 (US20030138772 SEQ ID NO: 45), AAV44.1 (US20030138772 SEQ ID NO: 46), AAV44.5 (US20030138772 SEQ ID NO: 47), AAV223.1 (US20030138772 SEQ ID NO: 48), AAV223.2 (US20030138772 SEQ ID NO: 49), AAV223.4 (US20030138772 SEQ ID NO: 50), AAV223.5 (US20030138772 SEQ ID NO: 51), AAV223.6 (US20030138772 SEQ ID NO: 52), AAV223.7 (US20030138772 SEQ ID NO: 53), AAVA3.4 (US20030138772 SEQ ID NO: 54), AAVA3.5 (US20030138772 SEQ ID NO: 55), AAVA3.7 (US20030138772 SEQ ID NO: 56), AAVA3.3 (US20030138772 SEQ ID NO: 57), AAV42.12 (US20030138772 SEQ ID NO: 58), AAV44.2 (US20030138772 SEQ ID NO: 59), AAV42-2 (US20030138772 SEQ ID NO: 9), or variants thereof.

[0046] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20150159173, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV2 (SEQ ID NO: 7 and 23 of US20150159173), rh20 (SEQ ID NO: 1 of US20150159173), rh32/33 (SEQ ID NO: 2 of US20150159173), rh39 (SEQ ID NO: 3, 20 and 36 of US20150159173), rh46 (SEQ ID NO: 4 and 22 of US20150159173), rh73 (SEQ ID NO: 5 of US20150159173), rh74 (SEQ ID NO: 6 of US20150159173), AAV6.1 (SEQ ID NO: 29 of US20150159173), rh.8 (SEQ ID NO: 41 of US20150159173), rh.48.1 (SEQ ID NO: 44 of US20150159173), hu.44 (SEQ ID NO: 45 of US20150159173), hu.29 (SEQ ID NO: 42 of US20150159173), hu.48 (SEQ ID NO: 38 of US20150159173), rh54 (SEQ ID NO: 49 of US20150159173), AAV2 (SEQ ID NO: 7 of US20150159173), cy.5 (SEQ ID NO: 8 and 24 of US20150159173), rh.10 (SEQ ID NO: 9 and 25 of US20150159173), rh.13 (SEQ ID NO: 10 and 26 of US20150159173), AAV1 (SEQ ID NO: 11 and 27 of US20150159173), AAV3 (SEQ ID NO: 12 and 28 of US20150159173), AAV6 (SEQ ID NO: 13 and 29 of US20150159173), AAV7 (SEQ ID NO: 14 and 30 of US20150159173), AAV8 (SEQ ID NO: 15 and 31 of US20150159173), hu.13 (SEQ ID NO: 16 and 32 of US20150159173), hu.26 (SEQ ID NO: 17 and 33 of US20150159173), hu.37 (SEQ ID NO: 18 and 34 of US20150159173), hu.53 (SEQ ID NO: 19 and 35 of US20150159173), rh.43 (SEQ ID NO: 21 and 37 of US20150159173), rh2 (SEQ ID NO: 39 of US20150159173), rh.37 (SEQ ID NO: 40 of US20150159173), rh.64 (SEQ ID NO: 43 of US20150159173), rh.48 (SEQ ID NO: 44 of US20150159173), ch.5

(SEQ ID NO 46 of US20150159173), rh.67 (SEQ ID NO: 47 of US20150159173), rh.58 (SEQ ID NO: 48 of US20150159173), or variants thereof including, but not limited to Cy5R1, Cy5R2, Cy5R3, Cy5R4, rh.13R, rh.37R2, rh.2R, rh.8R, rh.48.1, rh.48.2, rh.48.1.2, hu.44R1, hu.44R2, hu.44R3, hu.29R, ch.5R1, rh64R1, rh64R2, AAV6.2, AAV6.1, AAV6.12, hu.48R1, hu.48R2, and hu.48R3.

[0047] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent No. US 7198951, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 1-3 of US 7198951), AAV2 (SEQ ID NO: 4 of US 7198951), AAV1 (SEQ ID NO: 5 of US 7198951), AAV3 (SEQ ID NO: 6 of US 7198951), and AAV8 (SEQ ID NO: 7 of US7198951).

[0048] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV9 sequence as described by N Pulicherla et al. (Molecular Therapy 19(6):1070-1078 (2011), the contents of which are herein incorporated by reference in their entirety), such as but not limited to, AAV9.9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84.

[0049] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent No. US 6156303, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV3B (SEQ ID NO: 1 and 10 of US 6156303), AAV6 (SEQ ID NO: 2, 7 and 11 of US 6156303), AAV2 (SEQ ID NO: 3 and 8 of US 6156303), AAV3A (SEQ ID NO: 4 and 9, of US 6156303), or derivatives thereof.

[0050] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20140359799, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV8 (SEQ ID NO: 1 of US20140359799), AAVDJ (SEQ ID NO: 2 and 3 of US20140359799), or variants thereof.

[0051] In some embodiments, the serotype may be AAVDJ or a variant thereof, such as AAVDJ8 (or AAV-DJ8), as described by Grimm et al. (Journal of Virology 82(12): 5887-5911 (2008), herein incorporated by reference in its entirety). The amino acid sequence of AAVDJ8 may comprise two or more mutations in order to remove the heparin binding domain (HBD). As a non-limiting example, the AAV-DJ sequence described as SEQ ID NO: 1 in U.S. Patent No. 7,588,772, the contents of which are herein incorporated by reference in their entirety, may comprise two mutations: (1) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (2) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr). As another non-limiting example, may comprise three

mutations: (1) K406R where lysine (K; Lys) at amino acid 406 is changed to arginine (R; Arg), (2) R587Q where arginine (R; Arg) at amino acid 587 is changed to glutamine (Q; Gln) and (3) R590T where arginine (R; Arg) at amino acid 590 is changed to threonine (T; Thr).

[0052] In some embodiments, the AAV serotype may be, or have, a sequence of AAV4 as described in International Publication No. WO1998011244, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV4 (SEQ ID NO: 1-20 of WO1998011244).

[0053] In some embodiments, the AAV serotype may be, or have, a mutation in the AAV2 sequence to generate AAV2G9 as described in International Publication No. WO2014144229 and herein incorporated by reference in its entirety.

[0054] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2005033321, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV3-3 (SEQ ID NO: 217 of WO2005033321), AAV1 (SEQ ID NO: 219 and 202 of WO2005033321), AAV106.1/hu.37 (SEQ ID No: 10 of WO2005033321), AAV114.3/hu.40 (SEQ ID No: 11 of WO2005033321), AAV127.2/hu.41 (SEQ ID NO:6 and 8 of WO2005033321), AAV128.3/hu.44 (SEQ ID No: 81 of WO2005033321), AAV130.4/hu.48 (SEQ ID NO: 78 of WO2005033321), AAV145.1/hu.53 (SEQ ID No: 176 and 177 of WO2005033321), AAV145.6/hu.56 (SEQ ID NO: 168 and 192 of WO2005033321), AAV16.12/hu.11 (SEQ ID NO: 153 and 57 of WO2005033321), AAV16.8/hu.10 (SEQ ID NO: 156 and 56 of WO2005033321), AAV161.10/hu.60 (SEQ ID No: 170 of WO2005033321), AAV161.6/hu.61 (SEQ ID No: 174 of WO2005033321), AAV1-7/rh.48 (SEQ ID NO: 32 of WO2005033321), AAV1-8/rh.49 (SEQ ID NOs: 103 and 25 of WO2005033321), AAV2 (SEQ ID NO: 211 and 221 of WO2005033321), AAV2-15/rh.62 (SEQ ID No: 33 and 114 of WO2005033321), AAV2-3/rh.61 (SEQ ID NO: 21 of WO2005033321), AAV2-4/rh.50 (SEQ ID No: 23 and 108 of WO2005033321), AAV2-5/rh.51 (SEQ ID NO: 104 and 22 of WO2005033321), AAV3.1/hu.6 (SEQ ID NO: 5 and 84 of WO2005033321), AAV3.1/hu.9 (SEQ ID NO: 155 and 58 of WO2005033321), AAV3-11/rh.53 (SEQ ID NO: 186 and 176 of WO2005033321), AAV3-3 (SEQ ID NO: 200 of WO2005033321), AAV33.12/hu.17 (SEQ ID NO:4 of WO2005033321), AAV33.4/hu.15 (SEQ ID No: 50 of WO2005033321), AAV33.8/hu.16 (SEQ ID No: 51 of WO2005033321), AAV3-9/rh.52 (SEQ ID NO: 96 and 18 of WO2005033321), AAV4-19/rh.55 (SEQ ID NO: 117 of WO2005033321), AAV4-4 (SEQ ID NO: 201 and 218 of WO2005033321), AAV4-9/rh.54 (SEQ ID NO: 116 of

WO2005033321), AAV5 (SEQ ID NO: 199 and 216 of WO2005033321), AAV52.1/hu.20 (SEQ ID NO: 63 of WO2005033321), AAV52/hu.19 (SEQ ID NO: 133 of WO2005033321), AAV5-22/rh.58 (SEQ ID No: 27 of WO2005033321), AAV5-3/rh.57 (SEQ ID NO: 105 of WO2005033321), AAV5-3/rh.57 (SEQ ID No: 26 of WO2005033321), AAV58.2/hu.25 (SEQ ID No: 49 of WO2005033321), AAV6 (SEQ ID NO: 203 and 220 of WO2005033321), AAV7 (SEQ ID NO: 222 and 213 of WO2005033321), AAV7.3/hu.7 (SEQ ID No: 55 of WO2005033321), AAV8 (SEQ ID NO: 223 and 214 of WO2005033321), AAVH-1/hu.1 (SEQ ID No: 46 of WO2005033321), AAVH-5/hu.3 (SEQ ID No: 44 of WO2005033321), AAVhu.1 (SEQ ID NO: 144 of WO2005033321), AAVhu.10 (SEQ ID NO: 156 of WO2005033321), AAVhu.11 (SEQ ID NO: 153 of WO2005033321), AAVhu.12 (WO2005033321 SEQ ID NO: 59), AAVhu.13 (SEQ ID NO: 129 of WO2005033321), AAVhu.14/AAV9 (SEQ ID NO: 123 and 3 of WO2005033321), AAVhu.15 (SEQ ID NO: 147 of WO2005033321), AAVhu.16 (SEQ ID NO: 148 of WO2005033321), AAVhu.17 (SEQ ID NO: 83 of WO2005033321), AAVhu.18 (SEQ ID NO: 149 of WO2005033321), AAVhu.19 (SEQ ID NO: 133 of WO2005033321), AAVhu.2 (SEQ ID NO: 143 of WO2005033321), AAVhu.20 (SEQ ID NO: 134 of WO2005033321), AAVhu.21 (SEQ ID NO: 135 of WO2005033321), AAVhu.22 (SEQ ID NO: 138 of WO2005033321), AAVhu.23.2 (SEQ ID NO: 137 of WO2005033321), AAVhu.24 (SEQ ID NO: 136 of WO2005033321), AAVhu.25 (SEQ ID NO: 146 of WO2005033321), AAVhu.27 (SEQ ID NO: 140 of WO2005033321), AAVhu.29 (SEQ ID NO: 132 of WO2005033321), AAVhu.3 (SEQ ID NO: 145 of WO2005033321), AAVhu.31 (SEQ ID NO: 121 of WO2005033321), AAVhu.32 (SEQ ID NO: 122 of WO2005033321), AAVhu.34 (SEQ ID NO: 125 of WO2005033321), AAVhu.35 (SEQ ID NO: 164 of WO2005033321), AAVhu.37 (SEQ ID NO: 88 of WO2005033321), AAVhu.39 (SEQ ID NO: 102 of WO2005033321), AAVhu.4 (SEQ ID NO: 141 of WO2005033321), AAVhu.40 (SEQ ID NO: 87 of WO2005033321), AAVhu.41 (SEQ ID NO: 91 of WO2005033321), AAVhu.42 (SEQ ID NO: 85 of WO2005033321), AAVhu.43 (SEQ ID NO: 160 of WO2005033321), AAVhu.44 (SEQ ID NO: 144 of WO2005033321), AAVhu.45 (SEQ ID NO: 127 of WO2005033321), AAVhu.46 (SEQ ID NO: 159 of WO2005033321), AAVhu.47 (SEQ ID NO: 128 of WO2005033321), AAVhu.48 (SEQ ID NO: 157 of WO2005033321), AAVhu.49 (SEQ ID NO: 189 of WO2005033321), AAVhu.51 (SEQ ID NO: 190 of WO2005033321), AAVhu.52 (SEQ ID NO: 191 of WO2005033321), AAVhu.53 (SEQ ID NO: 186 of WO2005033321), AAVhu.54 (SEQ ID NO: 188 of WO2005033321), AAVhu.55 (SEQ ID NO: 187 of WO2005033321),

AAVhu.56 (SEQ ID NO: 192 of WO2005033321), AAVhu.57 (SEQ ID NO: 193 of WO2005033321), AAVhu.58 (SEQ ID NO: 194 of WO2005033321), AAVhu.6 (SEQ ID NO: 84 of WO2005033321), AAVhu.60 (SEQ ID NO: 184 of WO2005033321), AAVhu.61 (SEQ ID NO: 185 of WO2005033321), AAVhu.63 (SEQ ID NO: 195 of WO2005033321), AAVhu.64 (SEQ ID NO: 196 of WO2005033321), AAVhu.66 (SEQ ID NO: 197 of WO2005033321), AAVhu.67 (SEQ ID NO: 198 of WO2005033321), AAVhu.7 (SEQ ID NO: 150 of WO2005033321), AAVhu.8 (WO2005033321 SEQ ID NO: 12), AAVhu.9 (SEQ ID NO: 155 of WO2005033321), AAVLG-10/rh.40 (SEQ ID No: 14 of WO2005033321), AAVLG-4/rh.38 (SEQ ID NO: 86 of WO2005033321), AAVLG-4/rh.38 (SEQ ID No: 7 of WO2005033321), AAVN721-8/rh.43 (SEQ ID NO: 163 of WO2005033321), AAVN721-8/rh.43 (SEQ ID No: 43 of WO2005033321), AAVpi.1 (WO2005033321 SEQ ID NO: 28), AAVpi.2 (WO2005033321 SEQ ID NO: 30), AAVpi.3 (WO2005033321 SEQ ID NO: 29), AAVrh.38 (SEQ ID NO: 86 of WO2005033321), AAVrh.40 (SEQ ID NO: 92 of WO2005033321), AAVrh.43 (SEQ ID NO: 163 of WO2005033321), AAVrh.44 (WO2005033321 SEQ ID NO: 34), AAVrh.45 (WO2005033321 SEQ ID NO: 41), AAVrh.47 (WO2005033321 SEQ ID NO: 38), AAVrh.48 (SEQ ID NO: 115 of WO2005033321), AAVrh.49 (SEQ ID NO: 103 of WO2005033321), AAVrh.50 (SEQ ID NO: 108 of WO2005033321), AAVrh.51 (SEQ ID NO: 104 of WO2005033321), AAVrh.52 (SEQ ID NO: 96 of WO2005033321), AAVrh.53 (SEQ ID NO: 97 of WO2005033321), AAVrh.55 (WO2005033321 SEQ ID NO: 37), AAVrh.56 (SEQ ID NO: 152 of WO2005033321), AAVrh.57 (SEQ ID NO: 105 of WO2005033321), AAVrh.58 (SEQ ID NO: 106 of WO2005033321), AAVrh.59 (WO2005033321 SEQ ID NO: 42), AAVrh.60 (WO2005033321 SEQ ID NO: 31), AAVrh.61 (SEQ ID NO: 107 of WO2005033321), AAVrh.62 (SEQ ID NO: 114 of WO2005033321), AAVrh.64 (SEQ ID NO: 99 of WO2005033321), AAVrh.65 (WO2005033321 SEQ ID NO: 35), AAVrh.68 (WO2005033321 SEQ ID NO: 16), AAVrh.69 (WO2005033321 SEQ ID NO: 39), AAVrh.70 (WO2005033321 SEQ ID NO: 20), AAVrh.72 (WO2005033321 SEQ ID NO: 9), or variants thereof including, but not limited to, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVcy.6, AAVrh.12, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.25/42 15, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh14. Non limiting examples of variants include SEQ ID NO: 13, 15, 17, 19, 24, 36, 40, 45, 47, 48, 51-54, 60-62, 64-77, 79, 80, 82, 89, 90, 93-95, 98, 100, 101, , 109-113, 118-120, 124, 126, 131, 139, 142, 151,154, 158, 161, 162,

165-183, 202, 204-212, 215, 219, 224-236, of WO2005033321, the contents of which are herein incorporated by reference in their entirety.

[0055] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2015168666, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVrh8R (SEQ ID NO: 9 of WO2015168666), AAVrh8R A586R mutant (SEQ ID NO: 10 of WO2015168666), AAVrh8R R533A mutant (SEQ ID NO: 11 of WO2015168666), or variants thereof.

[0056] In some embodiments, the AAV serotype may be, or have, a sequence as described in United States Patent No. US9233131, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAVhE1.1 (SEQ ID NO:44 of US9233131), AAVhEr1.5 (SEQ ID NO:45 of US9233131), AAVhER1.14 (SEQ ID NO:46 of US9233131), AAVhEr1.8 (SEQ ID NO:47 of US9233131), AAVhEr1.16 (SEQ ID NO:48 of US9233131), AAVhEr1.18 (SEQ ID NO:49 of US9233131), AAVhEr1.35 (SEQ ID NO:50 of US9233131), AAVhEr1.7 (SEQ ID NO:51 of US9233131), AAVhEr1.36 (SEQ ID NO:52 of US9233131), AAVhEr2.29 (SEQ ID NO:53 of US9233131), AAVhEr2.4 (SEQ ID NO:54 of US9233131), AAVhEr2.16 (SEQ ID NO:55 of US9233131), AAVhEr2.30 (SEQ ID NO:56 of US9233131), AAVhEr2.31 (SEQ ID NO:58 of US9233131), AAVhEr2.36 (SEQ ID NO:57 of US9233131), AAVhER1.23 (SEQ ID NO:53 of US9233131), AAVhEr3.1 (SEQ ID NO:59 of US9233131), AAV2.5T (SEQ ID NO:42 of US9233131), or variants thereof.

[0057] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20150376607, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-PAEC (SEQ ID NO:1 of US20150376607), AAV-LK01 (SEQ ID NO:2 of US20150376607), AAV-LK02 (SEQ ID NO:3 of US20150376607), AAV-LK03 (SEQ ID NO:4 of US20150376607), AAV-LK04 (SEQ ID NO:5 of US20150376607), AAV-LK05 (SEQ ID NO:6 of US20150376607), AAV-LK06 (SEQ ID NO:7 of US20150376607), AAV-LK07 (SEQ ID NO:8 of US20150376607), AAV-LK08 (SEQ ID NO:9 of US20150376607), AAV-LK09 (SEQ ID NO:10 of US20150376607), AAV-LK10 (SEQ ID NO:11 of US20150376607), AAV-LK11 (SEQ ID NO:12 of US20150376607), AAV-LK12 (SEQ ID NO:13 of US20150376607), AAV-LK13 (SEQ ID NO:14 of US20150376607), AAV-LK14 (SEQ ID NO:15 of US20150376607), AAV-LK15 (SEQ ID NO:16 of US20150376607), AAV-LK16 (SEQ ID NO:17 of US20150376607), AAV-LK17 (SEQ ID NO:18 of US20150376607), AAV-LK18

(SEQ ID NO:19 of US20150376607), AAV-LK19 (SEQ ID NO:20 of US20150376607), AAV-PAEC2 (SEQ ID NO:21 of US20150376607), AAV-PAEC4 (SEQ ID NO:22 of US20150376607), AAV-PAEC6 (SEQ ID NO:23 of US20150376607), AAV-PAEC7 (SEQ ID NO:24 of US20150376607), AAV-PAEC8 (SEQ ID NO:25 of US20150376607), AAV-PAEC11 (SEQ ID NO:26 of US20150376607), AAV-PAEC12 (SEQ ID NO:27, of US20150376607), or variants thereof.

[0058] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent No. US9163261, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-2-pre-miRNA-101 (SEQ ID NO: 1 US9163261), or variants thereof.

[0059] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20150376240, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV-8h (SEQ ID NO: 6 of US20150376240), AAV-8b (SEQ ID NO: 5 of US20150376240), AAV-h (SEQ ID NO: 2 of US20150376240), AAV-b (SEQ ID NO: 1 of US20150376240), or variants thereof.

[0060] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20160017295, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV SM 10-2 (SEQ ID NO: 22 of US20160017295), AAV Shuffle 100-1 (SEQ ID NO: 23 of US20160017295), AAV Shuffle 100-3 (SEQ ID NO: 24 of US20160017295), AAV Shuffle 100-7 (SEQ ID NO: 25 of US20160017295), AAV Shuffle 10-2 (SEQ ID NO: 34 of US20160017295), AAV Shuffle 10-6 (SEQ ID NO: 35 of US20160017295), AAV Shuffle 10-8 (SEQ ID NO: 36 of US20160017295), AAV Shuffle 100-2 (SEQ ID NO: 37 of US20160017295), AAV SM 10-1 (SEQ ID NO: 38 of US20160017295), AAV SM 10-8 (SEQ ID NO: 39 of US20160017295), AAV SM 100-3 (SEQ ID NO: 40 of US20160017295), AAV SM 100-10 (SEQ ID NO: 41 of US20160017295), or variants thereof.

[0061] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20150238550, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BNP61 AAV (SEQ ID NO: 1 of US20150238550), BNP62 AAV (SEQ ID NO: 3 of US20150238550), BNP63 AAV (SEQ ID NO: 4 of US20150238550), or variants thereof.

[0062] In some embodiments, the AAV serotype may be or may have a sequence as described in United States Patent Publication No. US20150315612, the contents of which are

herein incorporated by reference in their entirety, such as, but not limited to, AAVrh.50 (SEQ ID NO: 108 of US20150315612), AAVrh.43 (SEQ ID NO: 163 of US20150315612), AAVrh.62 (SEQ ID NO: 114 of US20150315612), AAVrh.48 (SEQ ID NO: 115 of US20150315612), AAVhu.19 (SEQ ID NO: 133 of US20150315612), AAVhu.11 (SEQ ID NO: 153 of US20150315612), AAVhu.53 (SEQ ID NO: 186 of US20150315612), AAV4-8/rh.64 (SEQ ID No: 15 of US20150315612), AAVLG-9/hu.39 (SEQ ID No: 24 of US20150315612), AAV54.5/hu.23 (SEQ ID No: 60 of US20150315612), AAV54.2/hu.22 (SEQ ID No: 67 of US20150315612), AAV54.7/hu.24 (SEQ ID No: 66 of US20150315612), AAV54.1/hu.21 (SEQ ID No: 65 of US20150315612), AAV54.4R/hu.27 (SEQ ID No: 64 of US20150315612), AAV46.2/hu.28 (SEQ ID No: 68 of US20150315612), AAV46.6/hu.29 (SEQ ID No: 69 of US20150315612), AAV128.1/hu.43 (SEQ ID No: 80 of US20150315612), or variants thereof.

[0063] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2015121501, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, true type AAV (ttAAV) (SEQ ID NO: 2 of WO2015121501), "UPenn AAV10" (SEQ ID NO: 8 of WO2015121501), "Japanese AAV10" (SEQ ID NO: 9 of WO2015121501), or variants thereof.

[0064] According to the present invention, AAV capsid serotype selection or use may be from a variety of species. In one embodiment, the AAV may be an avian AAV (AAAV). The AAAV serotype may be, or have, a sequence as described in U.S. Patent No. US 9238800, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAAV (SEQ ID NO: 1, 2, 4, 6, 8, 10, 12, and 14 of US 9,238,800), or variants thereof.

[0065] In one embodiment, the AAV may be a bovine AAV (BAAV). The BAAV serotype may be, or have, a sequence as described in U.S. Patent No. US 9,193,769, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BAAV (SEQ ID NO: 1 and 6 of US 9,193,769), or variants thereof. The BAAV serotype may be or have a sequence as described in United States Patent No. US7,427,396, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, BAAV (SEQ ID NO: 5 and 6 of US7,427,396), or variants thereof.

[0066] In one embodiment, the AAV may be a caprine AAV. The caprine AAV serotype may be, or have, a sequence as described in United States Patent No. US7,427,396, the

contents of which are herein incorporated by reference in their entirety, such as, but not limited to, caprine AAV (SEQ ID NO: 3 of US7,427,396), or variants thereof.

[0067] In other embodiments the AAV may be engineered as a hybrid AAV from two or more parental serotypes. In one embodiment, the AAV may be AAV2G9 which comprises sequences from AAV2 and AAV9. The AAV2G9 AAV serotype may be, or have, a sequence as described in U.S. Patent Application Publication No. US20160017005, the contents of which are herein incorporated by reference in its entirety.

[0068] In one embodiment, the AAV may be a serotype generated by the AAV9 capsid library with mutations in amino acids 390-627 (VP1 numbering) as described by Pulicherla et al. (Molecular Therapy 19(6):1070-1078 (2011); the contents of which are herein incorporated by reference in their entirety. The serotype and corresponding nucleotide and amino acid substitutions may be, but is not limited to, AAV9.1 (G1594C; D532H), AAV6.2 (T1418A and T1436X; V473D and I479K), AAV9.3 (T1238A; F413Y), AAV9.4 (T1250C and A1617T; F417S), AAV9.5 (A1235G, A1314T, A1642G, C1760T; Q412R, T548A, A587V), AAV9.6 (T1231A; F411I), AAV9.9 (G1203A, G1785T; W595C), AAV9.10 (A1500G, T1676C; M559T), AAV9.11 (A1425T, A1702C, A1769T; T568P, Q590L), AAV9.13 (A1369C, A1720T; N457H, T574S), AAV9.14 (T1340A, T1362C, T1560C, G1713A; L447H), AAV9.16 (A1775T; Q592L), AAV9.24 (T1507C, T1521G; W503R), AAV9.26 (A1337G, A1769C; Y446C, Q590P), AAV9.33 (A1667C; D556A), AAV9.34 (A1534G, C1794T; N512D), AAV9.35 (A1289T, T1450A, C1494T, A1515T, C1794A, G1816A; Q430L, Y484N, N98K, V606I), AAV9.40 (A1694T, E565V), AAV9.41 (A1348T, T1362C; T450S), AAV9.44 (A1684C, A1701T, A1737G; N562H, K567N), AAV9.45 (A1492T, C1804T; N498Y, L602F), AAV9.46 (G1441C, T1525C, T1549G; G481R, W509R, L517V), 9.47 (G1241A, G1358A, A1669G, C1745T; S414N, G453D, K557E, T582I), AAV9.48 (C1445T, A1736T; P482L, Q579L), AAV9.50 (A1638T, C1683T, T1805A; Q546H, L602H), AAV9.53 (G1301A, A1405C, C1664T, G1811T; R134Q, S469R, A555V, G604V), AAV9.54 (C1531A, T1609A; L511I, L537M), AAV9.55 (T1605A; F535L), AAV9.58 (C1475T, C1579A; T492I, H527N), AAV.59 (T1336C; Y446H), AAV9.61 (A1493T; N498I), AAV9.64 (C1531A, A1617T; L511I), AAV9.65 (C1335T, T1530C, C1568A; A523D), AAV9.68 (C1510A; P504T), AAV9.80 (G1441A,;G481R), AAV9.83 (C1402A, A1500T; P468T, E500D), AAV9.87 (T1464C, T1468C; S490P), AAV9.90 (A1196T; Y399F), AAV9.91 (T1316G, A1583T, C1782G, T1806C; L439R, K528I), AAV9.93 (A1273G, A1421G, A1638C, C1712T, G1732A, A1744T, A1832T;

S425G, Q474R, Q546H, P571L, G578R, T582S, D611V), AAV9.94 (A1675T; M559L) and AAV9.95 (T1605A; F535L).

[0069] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2016049230, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAVF1/HSC1 (SEQ ID NO: 2 and 20 of WO2016049230), AAVF2/HSC2 (SEQ ID NO: 3 and 21 of WO2016049230), AAVF3/HSC3 (SEQ ID NO: 5 and 22 of WO2016049230), AAVF4/HSC4 (SEQ ID NO: 6 and 23 of WO2016049230), AAVF5/HSC5 (SEQ ID NO: 11 and 25 of WO2016049230), AAVF6/HSC6 (SEQ ID NO: 7 and 24 of WO2016049230), AAVF7/HSC7 (SEQ ID NO: 8 and 27 of WO2016049230), AAVF8/HSC8 (SEQ ID NO: 9 and 28 of WO2016049230), AAVF9/HSC9 (SEQ ID NO: 10 and 29 of WO2016049230), AAVF11/HSC11 (SEQ ID NO: 4 and 26 of WO2016049230), AAVF12/HSC12 (SEQ ID NO: 12 and 30 of WO2016049230), AAVF13/HSC13 (SEQ ID NO: 14 and 31 of WO2016049230), AAVF14/HSC14 (SEQ ID NO: 15 and 32 of WO2016049230), AAVF15/HSC15 (SEQ ID NO: 16 and 33 of WO2016049230), AAVF16/HSC16 (SEQ ID NO: 17 and 34 of WO2016049230), AAVF17/HSC17 (SEQ ID NO: 13 and 35 of WO2016049230), or variants or derivatives thereof.

[0070] In some embodiments, the AAV serotype may be, or have, a sequence as described in U.S. Patent No. US 8734809, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV CBr-E1 (SEQ ID NO: 13 and 87 of US8734809), AAV CBr-E2 (SEQ ID NO: 14 and 88 of US8734809), AAV CBr-E3 (SEQ ID NO: 15 and 89 of US8734809), AAV CBr-E4 (SEQ ID NO: 16 and 90 of US8734809), AAV CBr-E5 (SEQ ID NO: 17 and 91 of US8734809), AAV CBr-e5 (SEQ ID NO: 18 and 92 of US8734809), AAV CBr-E6 (SEQ ID NO: 19 and 93 of US8734809), AAV CBr-E7 (SEQ ID NO: 20 and 94 of US8734809), AAV CBr-E8 (SEQ ID NO: 21 and 95 of US8734809), AAV CLv-D1 (SEQ ID NO: 22 and 96 of US8734809), AAV CLv-D2 (SEQ ID NO: 23 and 97 of US8734809), AAV CLv-D3 (SEQ ID NO: 24 and 98 of US8734809), AAV CLv-D4 (SEQ ID NO: 25 and 99 of US8734809), AAV CLv-D5 (SEQ ID NO: 26 and 100 of US8734809), AAV CLv-D6 (SEQ ID NO: 27 and 101 of US8734809), AAV CLv-D7 (SEQ ID NO: 28 and 102 of US8734809), AAV CLv-D8 (SEQ ID NO: 29 and 103 of US8734809), AAV CLv-E1 (SEQ ID NO: 13 and 87 of US8734809), AAV CLv-R1 (SEQ ID NO: 30 and 104 of US8734809), AAV CLv-R2 (SEQ ID NO: 31 and 105 of US8734809), AAV CLv-R3 (SEQ ID NO: 32 and 106 of US8734809), AAV CLv-R4 (SEQ ID NO: 33 and 107 of US8734809),

AAV CLv-R5 (SEQ ID NO: 34 and 108 of US8734809), AAV CLv-R6 (SEQ ID NO: 35 and 109 of US8734809), AAV CLv-R7 (SEQ ID NO: 36 and 110 of US8734809), AAV CLv-R8 (SEQ ID NO: X and X of US8734809), AAV CLv-R9 (SEQ ID NO: X and X of US8734809), AAV CLg-F1 (SEQ ID NO: 39 and 113 of US8734809), AAV CLg-F2 (SEQ ID NO: 40 and 114 of US8734809), AAV CLg-F3 (SEQ ID NO: 41 and 115 of US8734809), AAV CLg-F4 (SEQ ID NO: 42 and 116 of US8734809), AAV CLg-F5 (SEQ ID NO: 43 and 117 of US8734809), AAV CLg-F6 (SEQ ID NO: 43 and 117 of US8734809), AAV CLg-F7 (SEQ ID NO: 44 and 118 of US8734809), AAV CLg-F8 (SEQ ID NO: 43 and 117 of US8734809), AAV CSp-1 (SEQ ID NO: 45 and 119 of US8734809), AAV CSp-10 (SEQ ID NO: 46 and 120 of US8734809), AAV CSp-11 (SEQ ID NO: 47 and 121 of US8734809), AAV CSp-2 (SEQ ID NO: 48 and 122 of US8734809), AAV CSp-3 (SEQ ID NO: 49 and 123 of US8734809), AAV CSp-4 (SEQ ID NO: 50 and 124 of US8734809), AAV CSp-6 (SEQ ID NO: 51 and 125 of US8734809), AAV CSp-7 (SEQ ID NO: 52 and 126 of US8734809), AAV CSp-8 (SEQ ID NO: 53 and 127 of US8734809), AAV CSp-9 (SEQ ID NO: 54 and 128 of US8734809), AAV CHt-2 (SEQ ID NO: 55 and 129 of US8734809), AAV CHt-3 (SEQ ID NO: 56 and 130 of US8734809), AAV CKd-1 (SEQ ID NO: 57 and 131 of US8734809), AAV CKd-10 (SEQ ID NO: 58 and 132 of US8734809), AAV CKd-2 (SEQ ID NO: 59 and 133 of US8734809), AAV CKd-3 (SEQ ID NO: 60 and 134 of US8734809), AAV CKd-4 (SEQ ID NO: 61 and 135 of US8734809), AAV CKd-6 (SEQ ID NO: 62 and 136 of US8734809), AAV CKd-7 (SEQ ID NO: 63 and 137 of US8734809), AAV CKd-8 (SEQ ID NO: 64 and 138 of US8734809), AAV CLv-1 (SEQ ID NO: 35 and 139 of US8734809), AAV CLv-12 (SEQ ID NO: 66 and 140 of US8734809), AAV CLv-13 (SEQ ID NO: 67 and 141 of US8734809), AAV CLv-2 (SEQ ID NO: 68 and 142 of US8734809), AAV CLv-3 (SEQ ID NO: 69 and 143 of US8734809), AAV CLv-4 (SEQ ID NO: 70 and 144 of US8734809), AAV CLv-6 (SEQ ID NO: 71 and 145 of US8734809), AAV CLv-8 (SEQ ID NO: 72 and 146 of US8734809), AAV CKd-B1 (SEQ ID NO: 73 and 147 of US8734809), AAV CKd-B2 (SEQ ID NO: 74 and 148 of US8734809), AAV CKd-B3 (SEQ ID NO: 75 and 149 of US8734809), AAV CKd-B4 (SEQ ID NO: 76 and 150 of US8734809), AAV CKd-B5 (SEQ ID NO: 77 and 151 of US8734809), AAV CKd-B6 (SEQ ID NO: 78 and 152 of US8734809), AAV CKd-B7 (SEQ ID NO: 79 and 153 of US8734809), AAV CKd-B8 (SEQ ID NO: 80 and 154 of US8734809), AAV CKd-H1 (SEQ ID NO: 81 and 155 of US8734809), AAV CKd-H2 (SEQ ID NO: 82 and 156 of US8734809), AAV CKd-H3 (SEQ ID NO: 83 and 157 of US8734809), AAV CKd-H4 (SEQ

ID NO: 84 and 158 of US8734809), AAV CKd-H5 (SEQ ID NO: 85 and 159 of US8734809), AAV CKd-H6 (SEQ ID NO: 77 and 151 of US8734809), AAV CHt-1 (SEQ ID NO: 86 and 160 of US8734809), AAV CLv1-1 (SEQ ID NO: 171 of US8734809), AAV CLv1-2 (SEQ ID NO: 172 of US8734809), AAV CLv1-3 (SEQ ID NO: 173 of US8734809), AAV CLv1-4 (SEQ ID NO: 174 of US8734809), AAV Clv1-7 (SEQ ID NO: 175 of US8734809), AAV Clv1-8 (SEQ ID NO: 176 of US8734809), AAV Clv1-9 (SEQ ID NO: 177 of US8734809), AAV Clv1-10 (SEQ ID NO: 178 of US8734809), AAV.VR-355 (SEQ ID NO: 181 of US8734809), AAV.hu.48R3 (SEQ ID NO: 183 of US8734809), or variants or derivatives thereof.

[0071] In some embodiments, the AAV serotype may be, or have, a sequence as described in International Publication No. WO2016065001, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to AAV CHt-P2 (SEQ ID NO: 1 and 51 of WO2016065001), AAV CHt-P5 (SEQ ID NO: 2 and 52 of WO2016065001), AAV CHt-P9 (SEQ ID NO: 3 and 53 of WO2016065001), AAV CBr-7.1 (SEQ ID NO: 4 and 54 of WO2016065001), AAV CBr-7.2 (SEQ ID NO: 5 and 55 of WO2016065001), AAV CBr-7.3 (SEQ ID NO: 6 and 56 of WO2016065001), AAV CBr-7.4 (SEQ ID NO: 7 and 57 of WO2016065001), AAV CBr-7.5 (SEQ ID NO: 8 and 58 of WO2016065001), AAV CBr-7.7 (SEQ ID NO: 9 and 59 of WO2016065001), AAV CBr-7.8 (SEQ ID NO: 10 and 60 of WO2016065001), AAV CBr-7.10 (SEQ ID NO: 11 and 61 of WO2016065001), AAV CKd-N3 (SEQ ID NO: 12 and 62 of WO2016065001), AAV CKd-N4 (SEQ ID NO: 13 and 63 of WO2016065001), AAV CKd-N9 (SEQ ID NO: 14 and 64 of WO2016065001), AAV CLv-L4 (SEQ ID NO: 15 and 65 of WO2016065001), AAV CLv-L5 (SEQ ID NO: 16 and 66 of WO2016065001), AAV CLv-L6 (SEQ ID NO: 17 and 67 of WO2016065001), AAV CLv-K1 (SEQ ID NO: 18 and 68 of WO2016065001), AAV CLv-K3 (SEQ ID NO: 19 and 69 of WO2016065001), AAV CLv-K6 (SEQ ID NO: 20 and 70 of WO2016065001), AAV CLv-M1 (SEQ ID NO: 21 and 71 of WO2016065001), AAV CLv-M11 (SEQ ID NO: 22 and 72 of WO2016065001), AAV CLv-M2 (SEQ ID NO: 23 and 73 of WO2016065001), AAV CLv-M5 (SEQ ID NO: 24 and 74 of WO2016065001), AAV CLv-M6 (SEQ ID NO: 25 and 75 of WO2016065001), AAV CLv-M7 (SEQ ID NO: 26 and 76 of WO2016065001), AAV CLv-M8 (SEQ ID NO: 27 and 77 of WO2016065001), AAV CLv-M9 (SEQ ID NO: 28 and 78 of WO2016065001), AAV CHt-P1 (SEQ ID NO: 29 and 79 of WO2016065001), AAV CHt-P6 (SEQ ID NO: 30 and 80 of WO2016065001), AAV CHt-P8 (SEQ ID NO: 31 and 81 of WO2016065001), AAV CHt-6.1 (SEQ ID NO: 32 and 82 of

WO2016065001), AAV CHt-6.10 (SEQ ID NO: 33 and 83 of WO2016065001), AAV CHt-6.5 (SEQ ID NO: 34 and 84 of WO2016065001), AAV CHt-6.6 (SEQ ID NO: 35 and 85 of WO2016065001), AAV CHt-6.7 (SEQ ID NO: 36 and 86 of WO2016065001), AAV CHt-6.8 (SEQ ID NO: 37 and 87 of WO2016065001), AAV CSp-8.10 (SEQ ID NO: 38 and 88 of WO2016065001), AAV CSp-8.2 (SEQ ID NO: 39 and 89 of WO2016065001), AAV CSp-8.4 (SEQ ID NO: 40 and 90 of WO2016065001), AAV CSp-8.5 (SEQ ID NO: 41 and 91 of WO2016065001), AAV CSp-8.6 (SEQ ID NO: 42 and 92 of WO2016065001), AAV CSp-8.7 (SEQ ID NO: 43 and 93 of WO2016065001), AAV CSp-8.8 (SEQ ID NO: 44 and 94 of WO2016065001), AAV CSp-8.9 (SEQ ID NO: 45 and 95 of WO2016065001), AAV CBr-B7.3 (SEQ ID NO: 46 and 96 of WO2016065001), AAV CBr-B7.4 (SEQ ID NO: 47 and 97 of WO2016065001), AAV3B (SEQ ID NO: 48 and 98 of WO2016065001), AAV4 (SEQ ID NO: 49 and 99 of WO2016065001), AAV5 (SEQ ID NO: 50 and 100 of WO2016065001), or variants or derivatives thereof.

[0072] In one embodiment, the AAV may be a serotype selected from any of those found in Table 1.

[0073] In one embodiment, the AAV may comprise a sequence, fragment or variant thereof, of the sequences in Table 1.

[0074] In one embodiment, the AAV may be encoded by a sequence, fragment or variant as described in Table 1.

Table 1. AAV Serotypes

Serotype	SEQ ID NO	Reference Information
VOY101	1 or 1809	-
VOY201	1810	-
PHP.N/PHP.B-DGT	2	WO2017100671 SEQ ID NO: 46
AAVPHP.B or G2B-26	3	WO2015038958 SEQ ID NO: 8 and 13
AAVPHP.B	4	WO2015038958 SEQ ID NO: 9
AAVG2B-13	5	WO2015038958 SEQ ID NO: 12
AAVTH1.1-32	6	WO2015038958 SEQ ID NO: 14
AAVTH1.1-35	7	WO2015038958 SEQ ID NO: 15
PHP.S/G2A12	8	WO2017100671 SEQ ID NO: 47
AAV9/hu.14 K449R	9	WO2017100671 SEQ ID NO: 45
AAV1	10	US20150159173 SEQ ID NO: 11, US20150315612 SEQ ID NO: 202
AAV1	11	US20160017295 SEQ ID NO: 1, US20030138772 SEQ ID NO: 64, US20150159173 SEQ ID NO: 27, US20150315612 SEQ ID NO: 219, US7198951 SEQ ID NO: 5
AAV1	12	US20030138772 SEQ ID NO: 6
AAV1.3	13	US20030138772 SEQ ID NO: 14
AAV10	14	US20030138772 SEQ ID NO: 117

AAV10	15	WO2015121501 SEQ ID NO: 9
AAV10	16	WO2015121501 SEQ ID NO: 8
AAV11	17	US20030138772 SEQ ID NO: 118
AAV12	18	US20030138772 SEQ ID NO: 119
AAV2	19	US20150159173 SEQ ID NO: 7, US20150315612 SEQ ID NO: 211
AAV2	20	US20030138772 SEQ ID NO: 70, US20150159173 SEQ ID NO: 23, US20150315612 SEQ ID NO: 221, US20160017295 SEQ ID NO: 2, US6156303 SEQ ID NO: 4, US7198951 SEQ ID NO: 4, WO2015121501 SEQ ID NO: 1
AAV2	21	US6156303 SEQ ID NO: 8
AAV2	22	US20030138772 SEQ ID NO: 7
AAV2	23	US6156303 SEQ ID NO: 3
AAV2.5T	24	US9233131 SEQ ID NO: 42
AAV223.10	25	US20030138772 SEQ ID NO: 75
AAV223.2	26	US20030138772 SEQ ID NO: 49
AAV223.2	27	US20030138772 SEQ ID NO: 76
AAV223.4	28	US20030138772 SEQ ID NO: 50
AAV223.4	29	US20030138772 SEQ ID NO: 73
AAV223.5	30	US20030138772 SEQ ID NO: 51
AAV223.5	31	US20030138772 SEQ ID NO: 74
AAV223.6	32	US20030138772 SEQ ID NO: 52
AAV223.6	33	US20030138772 SEQ ID NO: 78
AAV223.7	34	US20030138772 SEQ ID NO: 53
AAV223.7	35	US20030138772 SEQ ID NO: 77
AAV29.3	36	US20030138772 SEQ ID NO: 82
AAV29.4	37	US20030138772 SEQ ID NO: 12
AAV29.5	38	US20030138772 SEQ ID NO: 83
AAV29.5 (AAVbb.2)	39	US20030138772 SEQ ID NO: 13
AAV3	40	US20150159173 SEQ ID NO: 12
AAV3	41	US20030138772 SEQ ID NO: 71, US20150159173 SEQ ID NO: 28, US20160017295 SEQ ID NO: 3, US7198951 SEQ ID NO: 6
AAV3	42	US20030138772 SEQ ID NO: 8
AAV3.3b	43	US20030138772 SEQ ID NO: 72
AAV3-3	44	US20150315612 SEQ ID NO: 200
AAV3-3	45	US20150315612 SEQ ID NO: 217
AAV3a	46	US6156303 SEQ ID NO: 5
AAV3a	47	US6156303 SEQ ID NO: 9
AAV3b	48	US6156303 SEQ ID NO: 6
AAV3b	49	US6156303 SEQ ID NO: 10
AAV3b	50	US6156303 SEQ ID NO: 1
AAV4	51	US20140348794 SEQ ID NO: 17
AAV4	52	US20140348794 SEQ ID NO: 5
AAV4	53	US20140348794 SEQ ID NO: 3

AAV4	54	US20140348794 SEQ ID NO: 14
AAV4	55	US20140348794 SEQ ID NO: 15
AAV4	56	US20140348794 SEQ ID NO: 19
AAV4	57	US20140348794 SEQ ID NO: 12
AAV4	58	US20140348794 SEQ ID NO: 13
AAV4	59	US20140348794 SEQ ID NO: 7
AAV4	60	US20140348794 SEQ ID NO: 8
AAV4	61	US20140348794 SEQ ID NO: 9
AAV4	62	US20140348794 SEQ ID NO: 2
AAV4	63	US20140348794 SEQ ID NO: 10
AAV4	64	US20140348794 SEQ ID NO: 11
AAV4	65	US20140348794 SEQ ID NO: 18
AAV4	66	US20030138772 SEQ ID NO: 63, US20160017295 SEQ ID NO: 4, US20140348794 SEQ ID NO: 4
AAV4	67	US20140348794 SEQ ID NO: 16
AAV4	68	US20140348794 SEQ ID NO: 20
AAV4	69	US20140348794 SEQ ID NO: 6
AAV4	70	US20140348794 SEQ ID NO: 1
AAV42.2	71	US20030138772 SEQ ID NO: 9
AAV42.2	72	US20030138772 SEQ ID NO: 102
AAV42.3b	73	US20030138772 SEQ ID NO: 36
AAV42.3B	74	US20030138772 SEQ ID NO: 107
AAV42.4	75	US20030138772 SEQ ID NO: 33
AAV42.4	76	US20030138772 SEQ ID NO: 88
AAV42.8	77	US20030138772 SEQ ID NO: 27
AAV42.8	78	US20030138772 SEQ ID NO: 85
AAV43.1	79	US20030138772 SEQ ID NO: 39
AAV43.1	80	US20030138772 SEQ ID NO: 92
AAV43.12	81	US20030138772 SEQ ID NO: 41
AAV43.12	82	US20030138772 SEQ ID NO: 93
AAV43.20	83	US20030138772 SEQ ID NO: 42
AAV43.20	84	US20030138772 SEQ ID NO: 99
AAV43.21	85	US20030138772 SEQ ID NO: 43
AAV43.21	86	US20030138772 SEQ ID NO: 96
AAV43.23	87	US20030138772 SEQ ID NO: 44
AAV43.23	88	US20030138772 SEQ ID NO: 98
AAV43.25	89	US20030138772 SEQ ID NO: 45
AAV43.25	90	US20030138772 SEQ ID NO: 97
AAV43.5	91	US20030138772 SEQ ID NO: 40
AAV43.5	92	US20030138772 SEQ ID NO: 94
AAV4-4	93	US20150315612 SEQ ID NO: 201
AAV4-4	94	US20150315612 SEQ ID NO: 218
AAV44.1	95	US20030138772 SEQ ID NO: 46
AAV44.1	96	US20030138772 SEQ ID NO: 79

AAV44.5	97	US20030138772 SEQ ID NO: 47
AAV44.5	98	US20030138772 SEQ ID NO: 80
AAV4407	99	US20150315612 SEQ ID NO: 90
AAV5	100	US7427396 SEQ ID NO: 1
AAV5	101	US20030138772 SEQ ID NO: 114
AAV5	102	US20160017295 SEQ ID NO: 5, US7427396 SEQ ID NO: 2, US20150315612 SEQ ID NO: 216
AAV5	103	US20150315612 SEQ ID NO: 199
AAV6	104	US20150159173 SEQ ID NO: 13
AAV6	105	US20030138772 SEQ ID NO: 65, US20150159173 SEQ ID NO: 29, US20160017295 SEQ ID NO: 6, US6156303 SEQ ID NO: 7
AAV6	106	US6156303 SEQ ID NO: 11
AAV6	107	US6156303 SEQ ID NO: 2
AAV6	108	US20150315612 SEQ ID NO: 203
AAV6	109	US20150315612 SEQ ID NO: 220
AAV6.1	110	US20150159173
AAV6.12	111	US20150159173
AAV6.2	112	US20150159173
AAV7	113	US20150159173 SEQ ID NO: 14
AAV7	114	US20150315612 SEQ ID NO: 183
AAV7	115	US20030138772 SEQ ID NO: 2, US20150159173 SEQ ID NO: 30, US20150315612 SEQ ID NO: 181, US20160017295 SEQ ID NO: 7
AAV7	116	US20030138772 SEQ ID NO: 3
AAV7	117	US20030138772 SEQ ID NO: 1, US20150315612 SEQ ID NO: 180
AAV7	118	US20150315612 SEQ ID NO: 213
AAV7	119	US20150315612 SEQ ID NO: 222
AAV8	120	US20150159173 SEQ ID NO: 15
AAV8	121	US20150376240 SEQ ID NO: 7
AAV8	122	US20030138772 SEQ ID NO: 4, US20150315612 SEQ ID NO: 182
AAV8	123	US20030138772 SEQ ID NO: 95, US20140359799 SEQ ID NO: 1, US20150159173 SEQ ID NO: 31, US20160017295 SEQ ID NO: 8, US7198951 SEQ ID NO: 7, US20150315612 SEQ ID NO: 223
AAV8	124	US20150376240 SEQ ID NO: 8
AAV8	125	US20150315612 SEQ ID NO: 214
AAV-8b	126	US20150376240 SEQ ID NO: 5
AAV-8b	127	US20150376240 SEQ ID NO: 3
AAV-8h	128	US20150376240 SEQ ID NO: 6
AAV-8h	129	US20150376240 SEQ ID NO: 4
AAV9	130	US20030138772 SEQ ID NO: 5
AAV9	131	US7198951 SEQ ID NO: 1
AAV9	132	US20160017295 SEQ ID NO: 9
AAV9	133	US20030138772 SEQ ID NO: 100, US7198951 SEQ ID NO: 2

AAV9	134	US7198951 SEQ ID NO: 3
AAV9 (AAVhu.14)	135	US7906111 SEQ ID NO: 3; WO2015038958 SEQ ID NO: 11
AAV9 (AAVhu.14)	136	US7906111 SEQ ID NO: 123; WO2015038958 SEQ ID NO: 2
AAVA3.1	137	US20030138772 SEQ ID NO: 120
AAVA3.3	138	US20030138772 SEQ ID NO: 57
AAVA3.3	139	US20030138772 SEQ ID NO: 66
AAVA3.4	140	US20030138772 SEQ ID NO: 54
AAVA3.4	141	US20030138772 SEQ ID NO: 68
AAVA3.5	142	US20030138772 SEQ ID NO: 55
AAVA3.5	143	US20030138772 SEQ ID NO: 69
AAVA3.7	144	US20030138772 SEQ ID NO: 56
AAVA3.7	145	US20030138772 SEQ ID NO: 67
AAV29.3 (AAVbb.1)	146	US20030138772 SEQ ID NO: 11
AAVC2	147	US20030138772 SEQ ID NO: 61
AAVCh.5	148	US20150159173 SEQ ID NO: 46, US20150315612 SEQ ID NO: 234
AAVcy.2 (AAV13.3)	149	US20030138772 SEQ ID NO: 15
AAV24.1	150	US20030138772 SEQ ID NO: 101
AAVcy.3 (AAV24.1)	151	US20030138772 SEQ ID NO: 16
AAV27.3	152	US20030138772 SEQ ID NO: 104
AAVcy.4 (AAV27.3)	153	US20030138772 SEQ ID NO: 17
AAVcy.5	154	US20150315612 SEQ ID NO: 227
AAV7.2	155	US20030138772 SEQ ID NO: 103
AAVcy.5 (AAV7.2)	156	US20030138772 SEQ ID NO: 18
AAV16.3	157	US20030138772 SEQ ID NO: 105
AAVcy.6 (AAV16.3)	158	US20030138772 SEQ ID NO: 10
AAVcy.5	159	US20150159173 SEQ ID NO: 8
AAVcy.5	160	US20150159173 SEQ ID NO: 24
AAVCy.5R1	161	US20150159173
AAVCy.5R2	162	US20150159173
AAVCy.5R3	163	US20150159173
AAVCy.5R4	164	US20150159173
AAVDJ	165	US20140359799 SEQ ID NO: 3, US7588772 SEQ ID NO: 2
AAVDJ	166	US20140359799 SEQ ID NO: 2, US7588772 SEQ ID NO: 1
AAVDJ-8	167	US7588772; Grimm et al 2008
AAVDJ-8	168	US7588772; Grimm et al 2008
AAVF5	169	US20030138772 SEQ ID NO: 110
AAVH2	170	US20030138772 SEQ ID NO: 26
AAVH6	171	US20030138772 SEQ ID NO: 25
AAVhE1.1	172	US9233131 SEQ ID NO: 44
AAVhEr1.14	173	US9233131 SEQ ID NO: 46
AAVhEr1.16	174	US9233131 SEQ ID NO: 48

AAVhEr1.18	175	US9233131 SEQ ID NO: 49
AAVhEr1.23 (AAVhEr2.29)	176	US9233131 SEQ ID NO: 53
AAVhEr1.35	177	US9233131 SEQ ID NO: 50
AAVhEr1.36	178	US9233131 SEQ ID NO: 52
AAVhEr1.5	179	US9233131 SEQ ID NO: 45
AAVhEr1.7	180	US9233131 SEQ ID NO: 51
AAVhEr1.8	181	US9233131 SEQ ID NO: 47
AAVhEr2.16	182	US9233131 SEQ ID NO: 55
AAVhEr2.30	183	US9233131 SEQ ID NO: 56
AAVhEr2.31	184	US9233131 SEQ ID NO: 58
AAVhEr2.36	185	US9233131 SEQ ID NO: 57
AAVhEr2.4	186	US9233131 SEQ ID NO: 54
AAVhEr3.1	187	US9233131 SEQ ID NO: 59
AAVhu.1	188	US20150315612 SEQ ID NO: 46
AAVhu.1	189	US20150315612 SEQ ID NO: 144
AAVhu.10 (AAV16.8)	190	US20150315612 SEQ ID NO: 56
AAVhu.10 (AAV16.8)	191	US20150315612 SEQ ID NO: 156
AAVhu.11 (AAV16.12)	192	US20150315612 SEQ ID NO: 57
AAVhu.11 (AAV16.12)	193	US20150315612 SEQ ID NO: 153
AAVhu.12	194	US20150315612 SEQ ID NO: 59
AAVhu.12	195	US20150315612 SEQ ID NO: 154
AAVhu.13	196	US20150159173 SEQ ID NO: 16, US20150315612 SEQ ID NO: 71
AAVhu.13	197	US20150159173 SEQ ID NO: 32, US20150315612 SEQ ID NO: 129
AAVhu.136.1	198	US20150315612 SEQ ID NO: 165
AAVhu.140.1	199	US20150315612 SEQ ID NO: 166
AAVhu.140.2	200	US20150315612 SEQ ID NO: 167
AAVhu.145.6	201	US20150315612 SEQ ID No: 178
AAVhu.15	202	US20150315612 SEQ ID NO: 147
AAVhu.15 (AAV33.4)	203	US20150315612 SEQ ID NO: 50
AAVhu.156.1	204	US20150315612 SEQ ID No: 179
AAVhu.16	205	US20150315612 SEQ ID NO: 148
AAVhu.16 (AAV33.8)	206	US20150315612 SEQ ID NO: 51
AAVhu.17	207	US20150315612 SEQ ID NO: 83
AAVhu.17 (AAV33.12)	208	US20150315612 SEQ ID NO: 4
AAVhu.172.1	209	US20150315612 SEQ ID NO: 171
AAVhu.172.2	210	US20150315612 SEQ ID NO: 172
AAVhu.173.4	211	US20150315612 SEQ ID NO: 173
AAVhu.173.8	212	US20150315612 SEQ ID NO: 175
AAVhu.18	213	US20150315612 SEQ ID NO: 52
AAVhu.18	214	US20150315612 SEQ ID NO: 149
AAVhu.19	215	US20150315612 SEQ ID NO: 62
AAVhu.19	216	US20150315612 SEQ ID NO: 133
AAVhu.2	217	US20150315612 SEQ ID NO: 48

AAVhu.2	218	US20150315612 SEQ ID NO: 143
AAVhu.20	219	US20150315612 SEQ ID NO: 63
AAVhu.20	220	US20150315612 SEQ ID NO: 134
AAVhu.21	221	US20150315612 SEQ ID NO: 65
AAVhu.21	222	US20150315612 SEQ ID NO: 135
AAVhu.22	223	US20150315612 SEQ ID NO: 67
AAVhu.22	224	US20150315612 SEQ ID NO: 138
AAVhu.23	225	US20150315612 SEQ ID NO: 60
AAVhu.23.2	226	US20150315612 SEQ ID NO: 137
AAVhu.24	227	US20150315612 SEQ ID NO: 66
AAVhu.24	228	US20150315612 SEQ ID NO: 136
AAVhu.25	229	US20150315612 SEQ ID NO: 49
AAVhu.25	230	US20150315612 SEQ ID NO: 146
AAVhu.26	231	US20150159173 SEQ ID NO: 17, US20150315612 SEQ ID NO: 61
AAVhu.26	232	US20150159173 SEQ ID NO: 33, US20150315612 SEQ ID NO: 139
AAVhu.27	233	US20150315612 SEQ ID NO: 64
AAVhu.27	234	US20150315612 SEQ ID NO: 140
AAVhu.28	235	US20150315612 SEQ ID NO: 68
AAVhu.28	236	US20150315612 SEQ ID NO: 130
AAVhu.29	237	US20150315612 SEQ ID NO: 69
AAVhu.29	238	US20150159173 SEQ ID NO: 42, US20150315612 SEQ ID NO: 132
AAVhu.29	239	US20150315612 SEQ ID NO: 225
AAVhu.29R	240	US20150159173
AAVhu.3	241	US20150315612 SEQ ID NO: 44
AAVhu.3	242	US20150315612 SEQ ID NO: 145
AAVhu.30	243	US20150315612 SEQ ID NO: 70
AAVhu.30	244	US20150315612 SEQ ID NO: 131
AAVhu.31	245	US20150315612 SEQ ID NO: 1
AAVhu.31	246	US20150315612 SEQ ID NO: 121
AAVhu.32	247	US20150315612 SEQ ID NO: 2
AAVhu.32	248	US20150315612 SEQ ID NO: 122
AAVhu.33	249	US20150315612 SEQ ID NO: 75
AAVhu.33	250	US20150315612 SEQ ID NO: 124
AAVhu.34	251	US20150315612 SEQ ID NO: 72
AAVhu.34	252	US20150315612 SEQ ID NO: 125
AAVhu.35	253	US20150315612 SEQ ID NO: 73
AAVhu.35	254	US20150315612 SEQ ID NO: 164
AAVhu.36	255	US20150315612 SEQ ID NO: 74
AAVhu.36	256	US20150315612 SEQ ID NO: 126
AAVhu.37	257	US20150159173 SEQ ID NO: 34, US20150315612 SEQ ID NO: 88
AAVhu.37 (AAV106.1)	258	US20150315612 SEQ ID NO: 10, US20150159173 SEQ ID NO: 18

AAVhu.38	259	US20150315612 SEQ ID NO: 161
AAVhu.39	260	US20150315612 SEQ ID NO: 102
AAVhu.39 (AAVLG-9)	261	US20150315612 SEQ ID NO: 24
AAVhu.4	262	US20150315612 SEQ ID NO: 47
AAVhu.4	263	US20150315612 SEQ ID NO: 141
AAVhu.40	264	US20150315612 SEQ ID NO: 87
AAVhu.40 (AAV114.3)	265	US20150315612 SEQ ID No: 11
AAVhu.41	266	US20150315612 SEQ ID NO: 91
AAVhu.41 (AAV127.2)	267	US20150315612 SEQ ID NO: 6
AAVhu.42	268	US20150315612 SEQ ID NO: 85
AAVhu.42 (AAV127.5)	269	US20150315612 SEQ ID NO: 8
AAVhu.43	270	US20150315612 SEQ ID NO: 160
AAVhu.43	271	US20150315612 SEQ ID NO: 236
AAVhu.43 (AAV128.1)	272	US20150315612 SEQ ID NO: 80
AAVhu.44	273	US20150159173 SEQ ID NO: 45, US20150315612 SEQ ID NO: 158
AAVhu.44 (AAV128.3)	274	US20150315612 SEQ ID NO: 81
AAVhu.44R1	275	US20150159173
AAVhu.44R2	276	US20150159173
AAVhu.44R3	277	US20150159173
AAVhu.45	278	US20150315612 SEQ ID NO: 76
AAVhu.45	279	US20150315612 SEQ ID NO: 127
AAVhu.46	280	US20150315612 SEQ ID NO: 82
AAVhu.46	281	US20150315612 SEQ ID NO: 159
AAVhu.46	282	US20150315612 SEQ ID NO: 224
AAVhu.47	283	US20150315612 SEQ ID NO: 77
AAVhu.47	284	US20150315612 SEQ ID NO: 128
AAVhu.48	285	US20150159173 SEQ ID NO: 38
AAVhu.48	286	US20150315612 SEQ ID NO: 157
AAVhu.48 (AAV130.4)	287	US20150315612 SEQ ID NO: 78
AAVhu.48R1	288	US20150159173
AAVhu.48R2	289	US20150159173
AAVhu.48R3	290	US20150159173
AAVhu.49	291	US20150315612 SEQ ID NO: 209
AAVhu.49	292	US20150315612 SEQ ID NO: 189
AAVhu.5	293	US20150315612 SEQ ID NO: 45
AAVhu.5	294	US20150315612 SEQ ID NO: 142
AAVhu.51	295	US20150315612 SEQ ID NO: 208
AAVhu.51	296	US20150315612 SEQ ID NO: 190
AAVhu.52	297	US20150315612 SEQ ID NO: 210
AAVhu.52	298	US20150315612 SEQ ID NO: 191
AAVhu.53	299	US20150159173 SEQ ID NO: 19
AAVhu.53	300	US20150159173 SEQ ID NO: 35
AAVhu.53 (AAV145.1)	301	US20150315612 SEQ ID NO: 176

AAVhu.54	302	US20150315612 SEQ ID NO: 188
AAVhu.54 (AAV145.5)	303	US20150315612 SEQ ID No: 177
AAVhu.55	304	US20150315612 SEQ ID NO: 187
AAVhu.56	305	US20150315612 SEQ ID NO: 205
AAVhu.56 (AAV145.6)	306	US20150315612 SEQ ID NO: 168
AAVhu.56 (AAV145.6)	307	US20150315612 SEQ ID NO: 192
AAVhu.57	308	US20150315612 SEQ ID NO: 206
AAVhu.57	309	US20150315612 SEQ ID NO: 169
AAVhu.57	310	US20150315612 SEQ ID NO: 193
AAVhu.58	311	US20150315612 SEQ ID NO: 207
AAVhu.58	312	US20150315612 SEQ ID NO: 194
AAVhu.6 (AAV3.1)	313	US20150315612 SEQ ID NO: 5
AAVhu.6 (AAV3.1)	314	US20150315612 SEQ ID NO: 84
AAVhu.60	315	US20150315612 SEQ ID NO: 184
AAVhu.60 (AAV161.10)	316	US20150315612 SEQ ID NO: 170
AAVhu.61	317	US20150315612 SEQ ID NO: 185
AAVhu.61 (AAV161.6)	318	US20150315612 SEQ ID NO: 174
AAVhu.63	319	US20150315612 SEQ ID NO: 204
AAVhu.63	320	US20150315612 SEQ ID NO: 195
AAVhu.64	321	US20150315612 SEQ ID NO: 212
AAVhu.64	322	US20150315612 SEQ ID NO: 196
AAVhu.66	323	US20150315612 SEQ ID NO: 197
AAVhu.67	324	US20150315612 SEQ ID NO: 215
AAVhu.67	325	US20150315612 SEQ ID NO: 198
AAVhu.7	326	US20150315612 SEQ ID NO: 226
AAVhu.7	327	US20150315612 SEQ ID NO: 150
AAVhu.7 (AAV7.3)	328	US20150315612 SEQ ID NO: 55
AAVhu.71	329	US20150315612 SEQ ID NO: 79
AAVhu.8	330	US20150315612 SEQ ID NO: 53
AAVhu.8	331	US20150315612 SEQ ID NO: 12
AAVhu.8	332	US20150315612 SEQ ID NO: 151
AAVhu.9 (AAV3.1)	333	US20150315612 SEQ ID NO: 58
AAVhu.9 (AAV3.1)	334	US20150315612 SEQ ID NO: 155
AAV-LK01	335	US20150376607 SEQ ID NO: 2
AAV-LK01	336	US20150376607 SEQ ID NO: 29
AAV-LK02	337	US20150376607 SEQ ID NO: 3
AAV-LK02	338	US20150376607 SEQ ID NO: 30
AAV-LK03	339	US20150376607 SEQ ID NO: 4
AAV-LK03	340	WO2015121501 SEQ ID NO: 12, US20150376607 SEQ ID NO: 31
AAV-LK04	341	US20150376607 SEQ ID NO: 5
AAV-LK04	342	US20150376607 SEQ ID NO: 32
AAV-LK05	343	US20150376607 SEQ ID NO: 6
AAV-LK05	344	US20150376607 SEQ ID NO: 33

AAV-LK06	345	US20150376607 SEQ ID NO: 7
AAV-LK06	346	US20150376607 SEQ ID NO: 34
AAV-LK07	347	US20150376607 SEQ ID NO: 8
AAV-LK07	348	US20150376607 SEQ ID NO: 35
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AAV-LK11	355	US20150376607 SEQ ID NO: 12
AAV-LK11	356	US20150376607 SEQ ID NO: 39
AAV-LK12	357	US20150376607 SEQ ID NO: 13
AAV-LK12	358	US20150376607 SEQ ID NO: 40
AAV-LK13	359	US20150376607 SEQ ID NO: 14
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AAV-LK15	363	US20150376607 SEQ ID NO: 16
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AAV-LK16	365	US20150376607 SEQ ID NO: 17
AAV-LK16	366	US20150376607 SEQ ID NO: 44
AAV-LK17	367	US20150376607 SEQ ID NO: 18
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AAV-PAEC	374	US20150376607 SEQ ID NO: 48
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AAV-PAEC11	376	US20150376607 SEQ ID NO: 54
AAV-PAEC12	377	US20150376607 SEQ ID NO: 27
AAV-PAEC12	378	US20150376607 SEQ ID NO: 51
AAV-PAEC13	379	US20150376607 SEQ ID NO: 28
AAV-PAEC13	380	US20150376607 SEQ ID NO: 49
AAV-PAEC2	381	US20150376607 SEQ ID NO: 21
AAV-PAEC2	382	US20150376607 SEQ ID NO: 56
AAV-PAEC4	383	US20150376607 SEQ ID NO: 22
AAV-PAEC4	384	US20150376607 SEQ ID NO: 55
AAV-PAEC6	385	US20150376607 SEQ ID NO: 23
AAV-PAEC6	386	US20150376607 SEQ ID NO: 52
AAV-PAEC7	387	US20150376607 SEQ ID NO: 24
AAV-PAEC7	388	US20150376607 SEQ ID NO: 53

AAV-PAEC8	389	US20150376607 SEQ ID NO: 25
AAV-PAEC8	390	US20150376607 SEQ ID NO: 50
AAVpi.1	391	US20150315612 SEQ ID NO: 28
AAVpi.1	392	US20150315612 SEQ ID NO: 93
AAVpi.2	393	US20150315612 SEQ ID NO: 30
AAVpi.2	394	US20150315612 SEQ ID NO: 95
AAVpi.3	395	US20150315612 SEQ ID NO: 29
AAVpi.3	396	US20150315612 SEQ ID NO: 94
AAVrh.10	397	US20150159173 SEQ ID NO: 9
AAVrh.10	398	US20150159173 SEQ ID NO: 25
AAV44.2	399	US20030138772 SEQ ID NO: 59
AAVrh.10 (AAV44.2)	400	US20030138772 SEQ ID NO: 81
AAV42.1B	401	US20030138772 SEQ ID NO: 90
AAVrh.12 (AAV42.1b)	402	US20030138772 SEQ ID NO: 30
AAVrh.13	403	US20150159173 SEQ ID NO: 10
AAVrh.13	404	US20150159173 SEQ ID NO: 26
AAVrh.13	405	US20150315612 SEQ ID NO: 228
AAVrh.13R	406	US20150159173
AAV42.3A	407	US20030138772 SEQ ID NO: 87
AAVrh.14 (AAV42.3a)	408	US20030138772 SEQ ID NO: 32
AAV42.5A	409	US20030138772 SEQ ID NO: 89
AAVrh.17 (AAV42.5a)	410	US20030138772 SEQ ID NO: 34
AAV42.5B	411	US20030138772 SEQ ID NO: 91
AAVrh.18 (AAV42.5b)	412	US20030138772 SEQ ID NO: 29
AAV42.6B	413	US20030138772 SEQ ID NO: 112
AAVrh.19 (AAV42.6b)	414	US20030138772 SEQ ID NO: 38
AAVrh.2	415	US20150159173 SEQ ID NO: 39
AAVrh.2	416	US20150315612 SEQ ID NO: 231
AAVrh.20	417	US20150159173 SEQ ID NO: 1
AAV42.10	418	US20030138772 SEQ ID NO: 106
AAVrh.21 (AAV42.10)	419	US20030138772 SEQ ID NO: 35
AAV42.11	420	US20030138772 SEQ ID NO: 108
AAVrh.22 (AAV42.11)	421	US20030138772 SEQ ID NO: 37
AAV42.12	422	US20030138772 SEQ ID NO: 113
AAVrh.23 (AAV42.12)	423	US20030138772 SEQ ID NO: 58
AAV42.13	424	US20030138772 SEQ ID NO: 86
AAVrh.24 (AAV42.13)	425	US20030138772 SEQ ID NO: 31
AAV42.15	426	US20030138772 SEQ ID NO: 84
AAVrh.25 (AAV42.15)	427	US20030138772 SEQ ID NO: 28
AAVrh.2R	428	US20150159173
AAVrh.31 (AAV223.1)	429	US20030138772 SEQ ID NO: 48
AAVC1	430	US20030138772 SEQ ID NO: 60
AAVrh.32 (AAVC1)	431	US20030138772 SEQ ID NO: 19
AAVrh.32/33	432	US20150159173 SEQ ID NO: 2

AAVrh.33 (AAVC3)	433	US20030138772 SEQ ID NO: 20
AAVC5	434	US20030138772 SEQ ID NO: 62
AAVrh.34 (AAVC5)	435	US20030138772 SEQ ID NO: 21
AAVF1	436	US20030138772 SEQ ID NO: 109
AAVrh.35 (AAVF1)	437	US20030138772 SEQ ID NO: 22
AAVF3	438	US20030138772 SEQ ID NO: 111
AAVrh.36 (AAVF3)	439	US20030138772 SEQ ID NO: 23
AAVrh.37	440	US20030138772 SEQ ID NO: 24
AAVrh.37	441	US20150159173 SEQ ID NO: 40
AAVrh.37	442	US20150315612 SEQ ID NO: 229
AAVrh.37R2	443	US20150159173
AAVrh.38 (AAVLG-4)	444	US20150315612 SEQ ID NO: 7
AAVrh.38 (AAVLG-4)	445	US20150315612 SEQ ID NO: 86
AAVrh.39	446	US20150159173 SEQ ID NO: 20, US20150315612 SEQ ID NO: 13
AAVrh.39	447	US20150159173 SEQ ID NO: 3, US20150159173 SEQ ID NO: 36, US20150315612 SEQ ID NO: 89
AAVrh.40	448	US20150315612 SEQ ID NO: 92
AAVrh.40 (AAVLG-10)	449	US20150315612 SEQ ID No: 14
AAVrh.43 (AAVN721-8)	450	US20150315612 SEQ ID NO: 43, US20150159173 SEQ ID NO: 21
AAVrh.43 (AAVN721-8)	451	US20150315612 SEQ ID NO: 163, US20150159173 SEQ ID NO: 37
AAVrh.44	452	US20150315612 SEQ ID NO: 34
AAVrh.44	453	US20150315612 SEQ ID NO: 111
AAVrh.45	454	US20150315612 SEQ ID NO: 41
AAVrh.45	455	US20150315612 SEQ ID NO: 109
AAVrh.46	456	US20150159173 SEQ ID NO: 22, US20150315612 SEQ ID NO: 19
AAVrh.46	457	US20150159173 SEQ ID NO: 4, US20150315612 SEQ ID NO: 101
AAVrh.47	458	US20150315612 SEQ ID NO: 38
AAVrh.47	459	US20150315612 SEQ ID NO: 118
AAVrh.48	460	US20150159173 SEQ ID NO: 44, US20150315612 SEQ ID NO: 115
AAVrh.48.1	461	US20150159173
AAVrh.48.1.2	462	US20150159173
AAVrh.48.2	463	US20150159173
AAVrh.48 (AAV1-7)	464	US20150315612 SEQ ID NO: 32
AAVrh.49 (AAV1-8)	465	US20150315612 SEQ ID NO: 25
AAVrh.49 (AAV1-8)	466	US20150315612 SEQ ID NO: 103
AAVrh.50 (AAV2-4)	467	US20150315612 SEQ ID NO: 23
AAVrh.50 (AAV2-4)	468	US20150315612 SEQ ID NO: 108
AAVrh.51 (AAV2-5)	469	US20150315612 SEQ ID No: 22
AAVrh.51 (AAV2-5)	470	US20150315612 SEQ ID NO: 104
AAVrh.52 (AAV3-9)	471	US20150315612 SEQ ID NO: 18
AAVrh.52 (AAV3-9)	472	US20150315612 SEQ ID NO: 96

AAVrh.53	473	US20150315612 SEQ ID NO: 97
AAVrh.53 (AAV3-11)	474	US20150315612 SEQ ID NO: 17
AAVrh.53 (AAV3-11)	475	US20150315612 SEQ ID NO: 186
AAVrh.54	476	US20150315612 SEQ ID NO: 40
AAVrh.54	477	US20150159173 SEQ ID NO: 49, US20150315612 SEQ ID NO: 116
AAVrh.55	478	US20150315612 SEQ ID NO: 37
AAVrh.55 (AAV4-19)	479	US20150315612 SEQ ID NO: 117
AAVrh.56	480	US20150315612 SEQ ID NO: 54
AAVrh.56	481	US20150315612 SEQ ID NO: 152
AAVrh.57	482	US20150315612 SEQ ID NO: 26
AAVrh.57	483	US20150315612 SEQ ID NO: 105
AAVrh.58	484	US20150315612 SEQ ID NO: 27
AAVrh.58	485	US20150159173 SEQ ID NO: 48, US20150315612 SEQ ID NO: 106
AAVrh.58	486	US20150315612 SEQ ID NO: 232
AAVrh.59	487	US20150315612 SEQ ID NO: 42
AAVrh.59	488	US20150315612 SEQ ID NO: 110
AAVrh.60	489	US20150315612 SEQ ID NO: 31
AAVrh.60	490	US20150315612 SEQ ID NO: 120
AAVrh.61	491	US20150315612 SEQ ID NO: 107
AAVrh.61 (AAV2-3)	492	US20150315612 SEQ ID NO: 21
AAVrh.62 (AAV2-15)	493	US20150315612 SEQ ID No: 33
AAVrh.62 (AAV2-15)	494	US20150315612 SEQ ID NO: 114
AAVrh.64	495	US20150315612 SEQ ID No: 15
AAVrh.64	496	US20150159173 SEQ ID NO: 43, US20150315612 SEQ ID NO: 99
AAVrh.64	497	US20150315612 SEQ ID NO: 233
AAVRh.64R1	498	US20150159173
AAVRh.64R2	499	US20150159173
AAVrh.65	500	US20150315612 SEQ ID NO: 35
AAVrh.65	501	US20150315612 SEQ ID NO: 112
AAVrh.67	502	US20150315612 SEQ ID NO: 36
AAVrh.67	503	US20150315612 SEQ ID NO: 230
AAVrh.67	504	US20150159173 SEQ ID NO: 47, US20150315612 SEQ ID NO: 113
AAVrh.68	505	US20150315612 SEQ ID NO: 16
AAVrh.68	506	US20150315612 SEQ ID NO: 100
AAVrh.69	507	US20150315612 SEQ ID NO: 39
AAVrh.69	508	US20150315612 SEQ ID NO: 119
AAVrh.70	509	US20150315612 SEQ ID NO: 20
AAVrh.70	510	US20150315612 SEQ ID NO: 98
AAVrh.71	511	US20150315612 SEQ ID NO: 162
AAVrh.72	512	US20150315612 SEQ ID NO: 9
AAVrh.73	513	US20150159173 SEQ ID NO: 5
AAVrh.74	514	US20150159173 SEQ ID NO: 6

AAVrh.8	515	US20150159173 SEQ ID NO: 41
AAVrh.8	516	US20150315612 SEQ ID NO: 235
AAVrh.8R	517	US20150159173, WO2015168666 SEQ ID NO: 9
AAVrh.8R A586R mutant	518	WO2015168666 SEQ ID NO: 10
AAVrh.8R R533A mutant	519	WO2015168666 SEQ ID NO: 11
BAAV (bovine AAV)	520	US9193769 SEQ ID NO: 8
BAAV (bovine AAV)	521	US9193769 SEQ ID NO: 10
BAAV (bovine AAV)	522	US9193769 SEQ ID NO: 4
BAAV (bovine AAV)	523	US9193769 SEQ ID NO: 2
BAAV (bovine AAV)	524	US9193769 SEQ ID NO: 6
BAAV (bovine AAV)	525	US9193769 SEQ ID NO: 1
BAAV (bovine AAV)	526	US9193769 SEQ ID NO: 5
BAAV (bovine AAV)	527	US9193769 SEQ ID NO: 3
BAAV (bovine AAV)	528	US9193769 SEQ ID NO: 11
BAAV (bovine AAV)	529	US7427396 SEQ ID NO: 5
BAAV (bovine AAV)	530	US7427396 SEQ ID NO: 6
BAAV (bovine AAV)	531	US9193769 SEQ ID NO: 7
BAAV (bovine AAV)	532	US9193769 SEQ ID NO: 9
BNP61 AAV	533	US20150238550 SEQ ID NO: 1
BNP61 AAV	534	US20150238550 SEQ ID NO: 2
BNP62 AAV	535	US20150238550 SEQ ID NO: 3
BNP63 AAV	536	US20150238550 SEQ ID NO: 4
caprine AAV	537	US7427396 SEQ ID NO: 3
caprine AAV	538	US7427396 SEQ ID NO: 4
true type AAV (ttAAV)	539	WO2015121501 SEQ ID NO: 2
AAAV (Avian AAV)	540	US9238800 SEQ ID NO: 12
AAAV (Avian AAV)	541	US9238800 SEQ ID NO: 2
AAAV (Avian AAV)	542	US9238800 SEQ ID NO: 6
AAAV (Avian AAV)	543	US9238800 SEQ ID NO: 4
AAAV (Avian AAV)	544	US9238800 SEQ ID NO: 8
AAAV (Avian AAV)	545	US9238800 SEQ ID NO: 14
AAAV (Avian AAV)	546	US9238800 SEQ ID NO: 10
AAAV (Avian AAV)	547	US9238800 SEQ ID NO: 15
AAAV (Avian AAV)	548	US9238800 SEQ ID NO: 5
AAAV (Avian AAV)	549	US9238800 SEQ ID NO: 9
AAAV (Avian AAV)	550	US9238800 SEQ ID NO: 3
AAAV (Avian AAV)	551	US9238800 SEQ ID NO: 7
AAAV (Avian AAV)	552	US9238800 SEQ ID NO: 11
AAAV (Avian AAV)	553	US9238800 SEQ ID NO: 13
AAAV (Avian AAV)	554	US9238800 SEQ ID NO: 1
AAV Shuffle 100-1	555	US20160017295 SEQ ID NO: 23
AAV Shuffle 100-1	556	US20160017295 SEQ ID NO: 11
AAV Shuffle 100-2	557	US20160017295 SEQ ID NO: 37
AAV Shuffle 100-2	558	US20160017295 SEQ ID NO: 29
AAV Shuffle 100-3	559	US20160017295 SEQ ID NO: 24

AAV Shuffle 100-3	560	US20160017295 SEQ ID NO: 12
AAV Shuffle 100-7	561	US20160017295 SEQ ID NO: 25
AAV Shuffle 100-7	562	US20160017295 SEQ ID NO: 13
AAV Shuffle 10-2	563	US20160017295 SEQ ID NO: 34
AAV Shuffle 10-2	564	US20160017295 SEQ ID NO: 26
AAV Shuffle 10-6	565	US20160017295 SEQ ID NO: 35
AAV Shuffle 10-6	566	US20160017295 SEQ ID NO: 27
AAV Shuffle 10-8	567	US20160017295 SEQ ID NO: 36
AAV Shuffle 10-8	568	US20160017295 SEQ ID NO: 28
AAV SM 100-10	569	US20160017295 SEQ ID NO: 41
AAV SM 100-10	570	US20160017295 SEQ ID NO: 33
AAV SM 100-3	571	US20160017295 SEQ ID NO: 40
AAV SM 100-3	572	US20160017295 SEQ ID NO: 32
AAV SM 10-1	573	US20160017295 SEQ ID NO: 38
AAV SM 10-1	574	US20160017295 SEQ ID NO: 30
AAV SM 10-2	575	US20160017295 SEQ ID NO: 10
AAV SM 10-2	576	US20160017295 SEQ ID NO: 22
AAV SM 10-8	577	US20160017295 SEQ ID NO: 39
AAV SM 10-8	578	US20160017295 SEQ ID NO: 31
AAVF1/HSC1	579	WO2016049230 SEQ ID NO: 20
AAVF2/HSC2	580	WO2016049230 SEQ ID NO: 21
AAVF3/HSC3	581	WO2016049230 SEQ ID NO: 22
AAVF4/HSC4	582	WO2016049230 SEQ ID NO: 23
AAVF5/HSC5	583	WO2016049230 SEQ ID NO: 25
AAVF6/HSC6	584	WO2016049230 SEQ ID NO: 24
AAVF7/HSC7	585	WO2016049230 SEQ ID NO: 27
AAVF8/HSC8	586	WO2016049230 SEQ ID NO: 28
AAVF9/HSC9	587	WO2016049230 SEQ ID NO: 29
AAVF11/HSC11	588	WO2016049230 SEQ ID NO: 26
AAVF12/HSC12	589	WO2016049230 SEQ ID NO: 30
AAVF13/HSC13	590	WO2016049230 SEQ ID NO: 31
AAVF14/HSC14	591	WO2016049230 SEQ ID NO: 32
AAVF15/HSC15	592	WO2016049230 SEQ ID NO: 33
AAVF16/HSC16	593	WO2016049230 SEQ ID NO: 34
AAVF17/HSC17	594	WO2016049230 SEQ ID NO: 35
AAVF1/HSC1	595	WO2016049230 SEQ ID NO: 2
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AAVF3/HSC3	597	WO2016049230 SEQ ID NO: 5
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AAVF6/HSC6	600	WO2016049230 SEQ ID NO: 7
AAVF7/HSC7	601	WO2016049230 SEQ ID NO: 8
AAVF8/HSC8	602	WO2016049230 SEQ ID NO: 9
AAVF9/HSC9	603	WO2016049230 SEQ ID NO: 10

AAVF11/HSC11	604	WO2016049230 SEQ ID NO: 4
AAVF12/HSC12	605	WO2016049230 SEQ ID NO: 12
AAVF13/HSC13	606	WO2016049230 SEQ ID NO: 14
AAVF14/HSC14	607	WO2016049230 SEQ ID NO: 15
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AAVF16/HSC16	609	WO2016049230 SEQ ID NO: 17
AAVF17/HSC17	610	WO2016049230 SEQ ID NO: 13
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AAV CBr-E3	613	US8734809 SEQ ID NO: 15
AAV CBr-E4	614	US8734809 SEQ ID NO: 16
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AAV CBr-E6	617	US8734809 SEQ ID NO: 19
AAV CBr-E7	618	US8734809 SEQ ID NO: 20
AAV CBr-E8	619	US8734809 SEQ ID NO: 21
AAV CLv-D1	620	US8734809 SEQ ID NO: 22
AAV CLv-D2	621	US8734809 SEQ ID NO: 23
AAV CLv-D3	622	US8734809 SEQ ID NO: 24
AAV CLv-D4	623	US8734809 SEQ ID NO: 25
AAV CLv-D5	624	US8734809 SEQ ID NO: 26
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AAV CLv-D7	626	US8734809 SEQ ID NO: 28
AAV CLv-D8	627	US8734809 SEQ ID NO: 29
AAV CLv-E1	628	US8734809 SEQ ID NO: 13
AAV CLv-R1	629	US8734809 SEQ ID NO: 30
AAV CLv-R2	630	US8734809 SEQ ID NO: 31
AAV CLv-R3	631	US8734809 SEQ ID NO: 32
AAV CLv-R4	632	US8734809 SEQ ID NO: 33
AAV CLv-R5	633	US8734809 SEQ ID NO: 34
AAV CLv-R6	634	US8734809 SEQ ID NO: 35
AAV CLv-R7	635	US8734809 SEQ ID NO: 36
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AAV CLv-R9	637	US8734809 SEQ ID NO: 38
AAV CLg-F1	638	US8734809 SEQ ID NO: 39
AAV CLg-F2	639	US8734809 SEQ ID NO: 40
AAV CLg-F3	640	US8734809 SEQ ID NO: 41
AAV CLg-F4	641	US8734809 SEQ ID NO: 42
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AAV CLg-F6	643	US8734809 SEQ ID NO: 43
AAV CLg-F7	644	US8734809 SEQ ID NO: 44
AAV CLg-F8	645	US8734809 SEQ ID NO: 43
AAV CSp-1	646	US8734809 SEQ ID NO: 45
AAV CSp-10	647	US8734809 SEQ ID NO: 46

AAV CSp-11	648	US8734809 SEQ ID NO: 47
AAV CSp-2	649	US8734809 SEQ ID NO: 48
AAV CSp-3	650	US8734809 SEQ ID NO: 49
AAV CSp-4	651	US8734809 SEQ ID NO: 50
AAV CSp-6	652	US8734809 SEQ ID NO: 51
AAV CSp-7	653	US8734809 SEQ ID NO: 52
AAV CSp-8	654	US8734809 SEQ ID NO: 53
AAV CSp-9	655	US8734809 SEQ ID NO: 54
AAV CHt-2	656	US8734809 SEQ ID NO: 55
AAV CHt-3	657	US8734809 SEQ ID NO: 56
AAV CKd-1	658	US8734809 SEQ ID NO: 57
AAV CKd-10	659	US8734809 SEQ ID NO: 58
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AAV CKd-4	662	US8734809 SEQ ID NO: 61
AAV CKd-6	663	US8734809 SEQ ID NO: 62
AAV CKd-7	664	US8734809 SEQ ID NO: 63
AAV CKd-8	665	US8734809 SEQ ID NO: 64
AAV CLv-1	666	US8734809 SEQ ID NO: 65
AAV CLv-12	667	US8734809 SEQ ID NO: 66
AAV CLv-13	668	US8734809 SEQ ID NO: 67
AAV CLv-2	669	US8734809 SEQ ID NO: 68
AAV CLv-3	670	US8734809 SEQ ID NO: 69
AAV CLv-4	671	US8734809 SEQ ID NO: 70
AAV CLv-6	672	US8734809 SEQ ID NO: 71
AAV CLv-8	673	US8734809 SEQ ID NO: 72
AAV CKd-B1	674	US8734809 SEQ ID NO: 73
AAV CKd-B2	675	US8734809 SEQ ID NO: 74
AAV CKd-B3	676	US8734809 SEQ ID NO: 75
AAV CKd-B4	677	US8734809 SEQ ID NO: 76
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AAV CKd-B8	681	US8734809 SEQ ID NO: 80
AAV CKd-H1	682	US8734809 SEQ ID NO: 81
AAV CKd-H2	683	US8734809 SEQ ID NO: 82
AAV CKd-H3	684	US8734809 SEQ ID NO: 83
AAV CKd-H4	685	US8734809 SEQ ID NO: 84
AAV CKd-H5	686	US8734809 SEQ ID NO: 85
AAV CKd-H6	687	US8734809 SEQ ID NO: 77
AAV CHt-1	688	US8734809 SEQ ID NO: 86
AAV CLv1-1	689	US8734809 SEQ ID NO: 171
AAV CLv1-2	690	US8734809 SEQ ID NO: 172
AAV CLv1-3	691	US8734809 SEQ ID NO: 173

AAV CLv1-4	692	US8734809 SEQ ID NO: 174
AAV Clv1-7	693	US8734809 SEQ ID NO: 175
AAV Clv1-8	694	US8734809 SEQ ID NO: 176
AAV Clv1-9	695	US8734809 SEQ ID NO: 177
AAV Clv1-10	696	US8734809 SEQ ID NO: 178
AAV.VR-355	697	US8734809 SEQ ID NO: 181
AAV.hu.48R3	698	US8734809 SEQ ID NO: 183
AAV CBr-E1	699	US8734809 SEQ ID NO: 87
AAV CBr-E2	700	US8734809 SEQ ID NO: 88
AAV CBr-E3	701	US8734809 SEQ ID NO: 89
AAV CBr-E4	702	US8734809 SEQ ID NO: 90
AAV CBr-E5	703	US8734809 SEQ ID NO: 91
AAV CBr-e5	704	US8734809 SEQ ID NO: 92
AAV CBr-E6	705	US8734809 SEQ ID NO: 93
AAV CBr-E7	706	US8734809 SEQ ID NO: 94
AAV CBr-E8	707	US8734809 SEQ ID NO: 95
AAV CLv-D1	708	US8734809 SEQ ID NO: 96
AAV CLv-D2	709	US8734809 SEQ ID NO: 97
AAV CLv-D3	710	US8734809 SEQ ID NO: 98
AAV CLv-D4	711	US8734809 SEQ ID NO: 99
AAV CLv-D5	712	US8734809 SEQ ID NO: 100
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AAV CLv-D7	714	US8734809 SEQ ID NO: 102
AAV CLv-D8	715	US8734809 SEQ ID NO: 103
AAV CLv-E1	716	US8734809 SEQ ID NO: 87
AAV CLv-R1	717	US8734809 SEQ ID NO: 104
AAV CLv-R2	718	US8734809 SEQ ID NO: 105
AAV CLv-R3	719	US8734809 SEQ ID NO: 106
AAV CLv-R4	720	US8734809 SEQ ID NO: 107
AAV CLv-R5	721	US8734809 SEQ ID NO: 108
AAV CLv-R6	722	US8734809 SEQ ID NO: 109
AAV CLv-R7	723	US8734809 SEQ ID NO: 110
AAV CLv-R8	724	US8734809 SEQ ID NO: 111
AAV CLv-R9	725	US8734809 SEQ ID NO: 112
AAV CLg-F1	726	US8734809 SEQ ID NO: 113
AAV CLg-F2	727	US8734809 SEQ ID NO: 114
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AAV CLg-F4	729	US8734809 SEQ ID NO: 116
AAV CLg-F5	730	US8734809 SEQ ID NO: 117
AAV CLg-F6	731	US8734809 SEQ ID NO: 117
AAV CLg-F7	732	US8734809 SEQ ID NO: 118
AAV CLg-F8	733	US8734809 SEQ ID NO: 117
AAV CSp-1	734	US8734809 SEQ ID NO: 119
AAV CSp-10	735	US8734809 SEQ ID NO: 120

AAV CSp-11	736	US8734809 SEQ ID NO: 121
AAV CSp-2	737	US8734809 SEQ ID NO: 122
AAV CSp-3	738	US8734809 SEQ ID NO: 123
AAV CSp-4	739	US8734809 SEQ ID NO: 124
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AAV CSp-7	741	US8734809 SEQ ID NO: 126
AAV CSp-8	742	US8734809 SEQ ID NO: 127
AAV CSp-9	743	US8734809 SEQ ID NO: 128
AAV CHt-2	744	US8734809 SEQ ID NO: 129
AAV CHt-3	745	US8734809 SEQ ID NO: 130
AAV CKd-1	746	US8734809 SEQ ID NO: 131
AAV CKd-10	747	US8734809 SEQ ID NO: 132
AAV CKd-2	748	US8734809 SEQ ID NO: 133
AAV CKd-3	749	US8734809 SEQ ID NO: 134
AAV CKd-4	750	US8734809 SEQ ID NO: 135
AAV CKd-6	751	US8734809 SEQ ID NO: 136
AAV CKd-7	752	US8734809 SEQ ID NO: 137
AAV CKd-8	753	US8734809 SEQ ID NO: 138
AAV CLv-1	754	US8734809 SEQ ID NO: 139
AAV CLv-12	755	US8734809 SEQ ID NO: 140
AAV CLv-13	756	US8734809 SEQ ID NO: 141
AAV CLv-2	757	US8734809 SEQ ID NO: 142
AAV CLv-3	758	US8734809 SEQ ID NO: 143
AAV CLv-4	759	US8734809 SEQ ID NO: 144
AAV CLv-6	760	US8734809 SEQ ID NO: 145
AAV CLv-8	761	US8734809 SEQ ID NO: 146
AAV CKd-B1	762	US8734809 SEQ ID NO: 147
AAV CKd-B2	763	US8734809 SEQ ID NO: 148
AAV CKd-B3	764	US8734809 SEQ ID NO: 149
AAV CKd-B4	765	US8734809 SEQ ID NO: 150
AAV CKd-B5	766	US8734809 SEQ ID NO: 151
AAV CKd-B6	767	US8734809 SEQ ID NO: 152
AAV CKd-B7	768	US8734809 SEQ ID NO: 153
AAV CKd-B8	769	US8734809 SEQ ID NO: 154
AAV CKd-H1	770	US8734809 SEQ ID NO: 155
AAV CKd-H2	771	US8734809 SEQ ID NO: 156
AAV CKd-H3	772	US8734809 SEQ ID NO: 157
AAV CKd-H4	773	US8734809 SEQ ID NO: 158
AAV CKd-H5	774	US8734809 SEQ ID NO: 159
AAV CKd-H6	775	US8734809 SEQ ID NO: 151
AAV CHt-1	776	US8734809 SEQ ID NO: 160
AAV CHt-P2	777	WO2016065001 SEQ ID NO: 1
AAV CHt-P5	778	WO2016065001 SEQ ID NO: 2
AAV CHt-P9	779	WO2016065001 SEQ ID NO: 3

AAV CBr-7.1	780	WO2016065001 SEQ ID NO: 4
AAV CBr-7.2	781	WO2016065001 SEQ ID NO: 5
AAV CBr-7.3	782	WO2016065001 SEQ ID NO: 6
AAV CBr-7.4	783	WO2016065001 SEQ ID NO: 7
AAV CBr-7.5	784	WO2016065001 SEQ ID NO: 8
AAV CBr-7.7	785	WO2016065001 SEQ ID NO: 9
AAV CBr-7.8	786	WO2016065001 SEQ ID NO: 10
AAV CBr-7.10	787	WO2016065001 SEQ ID NO: 11
AAV CKd-N3	788	WO2016065001 SEQ ID NO: 12
AAV CKd-N4	789	WO2016065001 SEQ ID NO: 13
AAV CKd-N9	790	WO2016065001 SEQ ID NO: 14
AAV CLv-L4	791	WO2016065001 SEQ ID NO: 15
AAV CLv-L5	792	WO2016065001 SEQ ID NO: 16
AAV CLv-L6	793	WO2016065001 SEQ ID NO: 17
AAV CLv-K1	794	WO2016065001 SEQ ID NO: 18
AAV CLv-K3	795	WO2016065001 SEQ ID NO: 19
AAV CLv-K6	796	WO2016065001 SEQ ID NO: 20
AAV CLv-M1	797	WO2016065001 SEQ ID NO: 21
AAV CLv-M11	798	WO2016065001 SEQ ID NO: 22
AAV CLv-M2	799	WO2016065001 SEQ ID NO: 23
AAV CLv-M5	800	WO2016065001 SEQ ID NO: 24
AAV CLv-M6	801	WO2016065001 SEQ ID NO: 25
AAV CLv-M7	802	WO2016065001 SEQ ID NO: 26
AAV CLv-M8	803	WO2016065001 SEQ ID NO: 27
AAV CLv-M9	804	WO2016065001 SEQ ID NO: 28
AAV CHt-P1	805	WO2016065001 SEQ ID NO: 29
AAV CHt-P6	806	WO2016065001 SEQ ID NO: 30
AAV CHt-P8	807	WO2016065001 SEQ ID NO: 31
AAV CHt-6.1	808	WO2016065001 SEQ ID NO: 32
AAV CHt-6.10	809	WO2016065001 SEQ ID NO: 33
AAV CHt-6.5	810	WO2016065001 SEQ ID NO: 34
AAV CHt-6.6	811	WO2016065001 SEQ ID NO: 35
AAV CHt-6.7	812	WO2016065001 SEQ ID NO: 36
AAV CHt-6.8	813	WO2016065001 SEQ ID NO: 37
AAV CSp-8.10	814	WO2016065001 SEQ ID NO: 38
AAV CSp-8.2	815	WO2016065001 SEQ ID NO: 39
AAV CSp-8.4	816	WO2016065001 SEQ ID NO: 40
AAV CSp-8.5	817	WO2016065001 SEQ ID NO: 41
AAV CSp-8.6	818	WO2016065001 SEQ ID NO: 42
AAV CSp-8.7	819	WO2016065001 SEQ ID NO: 43
AAV CSp-8.8	820	WO2016065001 SEQ ID NO: 44
AAV CSp-8.9	821	WO2016065001 SEQ ID NO: 45
AAV CBr-B7.3	822	WO2016065001 SEQ ID NO: 46
AAV CBr-B7.4	823	WO2016065001 SEQ ID NO: 47

AAV3B	824	WO2016065001 SEQ ID NO: 48
AAV4	825	WO2016065001 SEQ ID NO: 49
AAV5	826	WO2016065001 SEQ ID NO: 50
AAV CHt-P2	827	WO2016065001 SEQ ID NO: 51
AAV CHt-P5	828	WO2016065001 SEQ ID NO: 52
AAV CHt-P9	829	WO2016065001 SEQ ID NO: 53
AAV CBr-7.1	830	WO2016065001 SEQ ID NO: 54
AAV CBr-7.2	831	WO2016065001 SEQ ID NO: 55
AAV CBr-7.3	832	WO2016065001 SEQ ID NO: 56
AAV CBr-7.4	833	WO2016065001 SEQ ID NO: 57
AAV CBr-7.5	834	WO2016065001 SEQ ID NO: 58
AAV CBr-7.7	835	WO2016065001 SEQ ID NO: 59
AAV CBr-7.8	836	WO2016065001 SEQ ID NO: 60
AAV CBr-7.10	837	WO2016065001 SEQ ID NO: 61
AAV CKd-N3	838	WO2016065001 SEQ ID NO: 62
AAV CKd-N4	839	WO2016065001 SEQ ID NO: 63
AAV CKd-N9	840	WO2016065001 SEQ ID NO: 64
AAV CLv-L4	841	WO2016065001 SEQ ID NO: 65
AAV CLv-L5	842	WO2016065001 SEQ ID NO: 66
AAV CLv-L6	843	WO2016065001 SEQ ID NO: 67
AAV CLv-K1	844	WO2016065001 SEQ ID NO: 68
AAV CLv-K3	845	WO2016065001 SEQ ID NO: 69
AAV CLv-K6	846	WO2016065001 SEQ ID NO: 70
AAV CLv-M1	847	WO2016065001 SEQ ID NO: 71
AAV CLv-M11	848	WO2016065001 SEQ ID NO: 72
AAV CLv-M2	849	WO2016065001 SEQ ID NO: 73
AAV CLv-M5	850	WO2016065001 SEQ ID NO: 74
AAV CLv-M6	851	WO2016065001 SEQ ID NO: 75
AAV CLv-M7	852	WO2016065001 SEQ ID NO: 76
AAV CLv-M8	853	WO2016065001 SEQ ID NO: 77
AAV CLv-M9	854	WO2016065001 SEQ ID NO: 78
AAV CHt-P1	855	WO2016065001 SEQ ID NO: 79
AAV CHt-P6	856	WO2016065001 SEQ ID NO: 80
AAV CHt-P8	857	WO2016065001 SEQ ID NO: 81
AAV CHt-6.1	858	WO2016065001 SEQ ID NO: 82
AAV CHt-6.10	859	WO2016065001 SEQ ID NO: 83
AAV CHt-6.5	860	WO2016065001 SEQ ID NO: 84
AAV CHt-6.6	861	WO2016065001 SEQ ID NO: 85
AAV CHt-6.7	862	WO2016065001 SEQ ID NO: 86
AAV CHt-6.8	863	WO2016065001 SEQ ID NO: 87
AAV CSp-8.10	864	WO2016065001 SEQ ID NO: 88
AAV CSp-8.2	865	WO2016065001 SEQ ID NO: 89
AAV CSp-8.4	866	WO2016065001 SEQ ID NO: 90
AAV CSp-8.5	867	WO2016065001 SEQ ID NO: 91

AAV CSp-8.6	868	WO2016065001 SEQ ID NO: 92
AAV CSp-8.7	869	WO2016065001 SEQ ID NO: 93
AAV CSp-8.8	870	WO2016065001 SEQ ID NO: 94
AAV CSp-8.9	871	WO2016065001 SEQ ID NO: 95
AAV CBr-B7.3	872	WO2016065001 SEQ ID NO: 96
AAV CBr-B7.4	873	WO2016065001 SEQ ID NO: 97
AAV3B	874	WO2016065001 SEQ ID NO: 98
AAV4	875	WO2016065001 SEQ ID NO: 99
AAV5	876	WO2016065001 SEQ ID NO: 100
GPV	877	US9624274B2 SEQ ID NO: 192
B19	878	US9624274B2 SEQ ID NO: 193
MVM	879	US9624274B2 SEQ ID NO: 194
FPV	880	US9624274B2 SEQ ID NO: 195
CPV	881	US9624274B2 SEQ ID NO: 196
AAV6	882	US9546112B2 SEQ ID NO: 5
AAV6	883	US9457103B2 SEQ ID NO: 1
AAV2	884	US9457103B2 SEQ ID NO: 2
ShH10	885	US9457103B2 SEQ ID NO: 3
ShH13	886	US9457103B2 SEQ ID NO: 4
ShH10	887	US9457103B2 SEQ ID NO: 5
ShH10	888	US9457103B2 SEQ ID NO: 6
ShH10	889	US9457103B2 SEQ ID NO: 7
ShH10	890	US9457103B2 SEQ ID NO: 8
ShH10	891	US9457103B2 SEQ ID NO: 9
rh74	892	US9434928B2 SEQ ID NO: 1, US2015023924A1 SEQ ID NO: 2
rh74	893	US9434928B2 SEQ ID NO: 2, US2015023924A1 SEQ ID NO: 1
AAV8	894	US9434928B2 SEQ ID NO: 4
rh74	895	US9434928B2 SEQ ID NO: 5
rh74 (RHM4-1)	896	US2015023924A1 SEQ ID NO: 5, US20160375110A1 SEQ ID NO: 4
rh74 (RHM15-1)	897	US2015023924A1 SEQ ID NO: 6, US20160375110A1 SEQ ID NO: 5
rh74 (RHM15-2)	898	US2015023924A1 SEQ ID NO: 7, US20160375110A1 SEQ ID NO: 6
rh74 (RHM15-3/RHM15-5)	899	US2015023924A1 SEQ ID NO: 8, US20160375110A1 SEQ ID NO: 7
rh74 (RHM15-4)	900	US2015023924A1 SEQ ID NO: 9, US20160375110A1 SEQ ID NO: 8
rh74 (RHM15-6)	901	US2015023924A1 SEQ ID NO: 10, US20160375110A1 SEQ ID NO: 9
rh74 (RHM4-1)	902	US2015023924A1 SEQ ID NO: 11
rh74 (RHM15-1)	903	US2015023924A1 SEQ ID NO: 12
rh74 (RHM15-2)	904	US2015023924A1 SEQ ID NO: 13
rh74 (RHM15-3/RHM15-5)	905	US2015023924A1 SEQ ID NO: 14
rh74 (RHM15-4)	906	US2015023924A1 SEQ ID NO: 15
rh74 (RHM15-6)	907	US2015023924A1 SEQ ID NO: 16

AAV2 (comprising lung specific polypeptide)	908	US20160175389A1 SEQ ID NO: 9
AAV2 (comprising lung specific polypeptide)	909	US20160175389A1 SEQ ID NO: 10
Anc80	910	US20170051257A1 SEQ ID NO: 1
Anc80	911	US20170051257A1 SEQ ID NO: 2
Anc81	912	US20170051257A1 SEQ ID NO: 3
Anc80	913	US20170051257A1 SEQ ID NO: 4
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Anc113	922	US20170051257A1 SEQ ID NO: 13
Anc113	923	US20170051257A1 SEQ ID NO: 14
Anc126	924	US20170051257A1 SEQ ID NO: 15
Anc126	925	US20170051257A1 SEQ ID NO: 16
Anc127	926	US20170051257A1 SEQ ID NO: 17
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Anc80L62	931	US20170051257A1 SEQ ID NO: 22
Anc80L65	932	US20170051257A1 SEQ ID NO: 23
Anc80L33	933	US20170051257A1 SEQ ID NO: 24
Anc80L36	934	US20170051257A1 SEQ ID NO: 25
Anc80L44	935	US20170051257A1 SEQ ID NO: 26
Anc80L1	936	US20170051257A1 SEQ ID NO: 35
Anc80L1	937	US20170051257A1 SEQ ID NO: 36
AAV-X1	938	US8283151B2 SEQ ID NO: 11
AAV-X1b	939	US8283151B2 SEQ ID NO: 12
AAV-X5	940	US8283151B2 SEQ ID NO: 13
AAV-X19	941	US8283151B2 SEQ ID NO: 14
AAV-X21	942	US8283151B2 SEQ ID NO: 15
AAV-X22	943	US8283151B2 SEQ ID NO: 16
AAV-X23	944	US8283151B2 SEQ ID NO: 17
AAV-X24	945	US8283151B2 SEQ ID NO: 18
AAV-X25	946	US8283151B2 SEQ ID NO: 19
AAV-X26	947	US8283151B2 SEQ ID NO: 20
AAV-X1	948	US8283151B2 SEQ ID NO: 21
AAV-X1b	949	US8283151B2 SEQ ID NO: 22
AAV-X5	950	US8283151B2 SEQ ID NO: 23

AAV-X19	951	US8283151B2 SEQ ID NO: 24
AAV-X21	952	US8283151B2 SEQ ID NO: 25
AAV-X22	953	US8283151B2 SEQ ID NO: 26
AAV-X23	954	US8283151B2 SEQ ID NO: 27
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AAV-X25	956	US8283151B2 SEQ ID NO: 29
AAV-X26	957	US8283151B2 SEQ ID NO: 30
AAVrh8	958	WO2016054554A1 SEQ ID NO: 8
AAVrh8VP2FC5	959	WO2016054554A1 SEQ ID NO: 9
AAVrh8VP2FC44	960	WO2016054554A1 SEQ ID NO: 10
AAVrh8VP2ApoB100	961	WO2016054554A1 SEQ ID NO: 11
AAVrh8VP2RVG	962	WO2016054554A1 SEQ ID NO: 12
AAVrh8VP2Angiopep-2 VP2	963	WO2016054554A1 SEQ ID NO: 13
AAV9.47VP1.3	964	WO2016054554A1 SEQ ID NO: 14
AAV9.47VP2ICAMg3	965	WO2016054554A1 SEQ ID NO: 15
AAV9.47VP2RVG	966	WO2016054554A1 SEQ ID NO: 16
AAV9.47VP2Angiopep-2	967	WO2016054554A1 SEQ ID NO: 17
AAV9.47VP2A-string	968	WO2016054554A1 SEQ ID NO: 18
AAVrh8VP2FC5 VP2	969	WO2016054554A1 SEQ ID NO: 19
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AAVrh8VP2ApoB100 VP2	971	WO2016054554A1 SEQ ID NO: 21
AAVrh8VP2RVG VP2	972	WO2016054554A1 SEQ ID NO: 22
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AAV9.47VP2ICAMg3 VP2	974	WO2016054554A1 SEQ ID NO: 24
AAV9.47VP2RVG VP2	975	WO2016054554A1 SEQ ID NO: 25
AAV9.47VP2Angiopep-2 VP2	976	WO2016054554A1 SEQ ID NO: 26
AAV9.47VP2A-string VP2	977	WO2016054554A1 SEQ ID NO: 27
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rAAV-B2	979	WO2016054557A1 SEQ ID NO: 2
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rAAV-B1	982	WO2016054557A1 SEQ ID NO: 5
rAAV-B2	983	WO2016054557A1 SEQ ID NO: 6
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rAAV-L4	989	WO2016054557A1 SEQ ID NO: 12
rAAV-L1	990	WO2016054557A1 SEQ ID NO: 13
rAAV-L2	991	WO2016054557A1 SEQ ID NO: 14
rAAV-L3	992	WO2016054557A1 SEQ ID NO: 15

rAAV-L4	993	WO2016054557A1 SEQ ID NO: 16
AAV9	994	WO2016073739A1 SEQ ID NO: 3
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rAAV	1079	WO2016081811A1 SEQ ID NO: 85
rAAV	1080	WO2016081811A1 SEQ ID NO: 86

rAAV	1081	WO2016081811A1 SEQ ID NO: 87
rAAV	1082	WO2016081811A1 SEQ ID NO: 88
rAAV	1083	WO2016081811A1 SEQ ID NO: 89
rAAV	1084	WO2016081811A1 SEQ ID NO: 90
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rAAV	1109	WO2016081811A1 SEQ ID NO: 115
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rAAV	1119	WO2016081811A1 SEQ ID NO: 125
rAAV	1120	WO2016081811A1 SEQ ID NO: 126
rAAV	1121	WO2016081811A1 SEQ ID NO: 127
rAAV	1122	WO2016081811A1 SEQ ID NO: 128
AAV8 E532K	1123	WO2016081811A1 SEQ ID NO: 133
AAV8 E532K	1124	WO2016081811A1 SEQ ID NO: 134

rAAV4	1125	WO2016115382A1 SEQ ID NO: 2
rAAV4	1126	WO2016115382A1 SEQ ID NO: 3
rAAV4	1127	WO2016115382A1 SEQ ID NO: 4
rAAV4	1128	WO2016115382A1 SEQ ID NO: 5
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AAV11	1145	WO2016115382A1 SEQ ID NO: 22
AAV12	1146	WO2016115382A1 SEQ ID NO: 23
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rh34	1149	WO2016115382A1 SEQ ID NO: 27
rAAV4	1150	WO2016115382A1 SEQ ID NO: 28
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rAAV4	1152	WO2016115382A1 SEQ ID NO: 30
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rAAV4	1154	WO2016115382A1 SEQ ID NO: 32
rAAV4	1155	WO2016115382A1 SEQ ID NO: 33
AAV2/8	1156	WO2016131981A1 SEQ ID NO: 47
AAV2/8	1157	WO2016131981A1 SEQ ID NO: 48
ancestral AAV	1158	WO2016154344A1 SEQ ID NO: 7
ancestral AAV variant C4	1159	WO2016154344A1 SEQ ID NO: 13
ancestral AAV variant C7	1160	WO2016154344A1 SEQ ID NO: 14
ancestral AAV variant G4	1161	WO2016154344A1 SEQ ID NO: 15
consensus amino acid sequence of ancestral AAV variants, C4, C7 and G4	1162	WO2016154344A1 SEQ ID NO: 16
consensus amino acid sequence of ancestral AAV variants, C4 and C7	1163	WO2016154344A1 SEQ ID NO: 17
AAV8 (with an AAV2 phospholipase domain)	1164	WO2016150403A1 SEQ ID NO: 13
AAV VR-942n	1165	US20160289275A1 SEQ ID NO: 10

AAV5-A (M569V)	1166	US20160289275A1 SEQ ID NO: 13
AAV5-A (M569V)	1167	US20160289275A1 SEQ ID NO: 14
AAV5-A (Y585V)	1168	US20160289275A1 SEQ ID NO: 16
AAV5-A (Y585V)	1169	US20160289275A1 SEQ ID NO: 17
AAV5-A (L587T)	1170	US20160289275A1 SEQ ID NO: 19
AAV5-A (L587T)	1171	US20160289275A1 SEQ ID NO: 20
AAV5-A (Y585V/L587T)	1172	US20160289275A1 SEQ ID NO: 22
AAV5-A (Y585V/L587T)	1173	US20160289275A1 SEQ ID NO: 23
AAV5-B (D652A)	1174	US20160289275A1 SEQ ID NO: 25
AAV5-B (D652A)	1175	US20160289275A1 SEQ ID NO: 26
AAV5-B (T362M)	1176	US20160289275A1 SEQ ID NO: 28
AAV5-B (T362M)	1177	US20160289275A1 SEQ ID NO: 29
AAV5-B (Q359D)	1178	US20160289275A1 SEQ ID NO: 31
AAV5-B (Q359D)	1179	US20160289275A1 SEQ ID NO: 32
AAV5-B (E350Q)	1180	US20160289275A1 SEQ ID NO: 34
AAV5-B (E350Q)	1181	US20160289275A1 SEQ ID NO: 35
AAV5-B (P533S)	1182	US20160289275A1 SEQ ID NO: 37
AAV5-B (P533S)	1183	US20160289275A1 SEQ ID NO: 38
AAV5-B (P533G)	1184	US20160289275A1 SEQ ID NO: 40
AAV5-B (P533G)	1185	US20160289275A1 SEQ ID NO: 41
AAV5-mutation in loop VII	1186	US20160289275A1 SEQ ID NO: 43
AAV5-mutation in loop VII	1187	US20160289275A1 SEQ ID NO: 44
AAV8	1188	US20160289275A1 SEQ ID NO: 47
Mut A (LK03/AAV8)	1189	WO2016181123A1 SEQ ID NO: 1
Mut B (LK03/AAV5)	1190	WO2016181123A1 SEQ ID NO: 2
Mut C (AAV8/AAV3B)	1191	WO2016181123A1 SEQ ID NO: 3
Mut D (AAV5/AAV3B)	1192	WO2016181123A1 SEQ ID NO: 4
Mut E (AAV8/AAV3B)	1193	WO2016181123A1 SEQ ID NO: 5
Mut F (AAV3B/AAV8)	1194	WO2016181123A1 SEQ ID NO: 6
AAV44.9	1195	WO2016183297A1 SEQ ID NO: 4
AAV44.9	1196	WO2016183297A1 SEQ ID NO: 5
AAVrh8	1197	WO2016183297A1 SEQ ID NO: 6
AAV44.9 (S470N)	1198	WO2016183297A1 SEQ ID NO: 9
rh74 VP1	1199	US20160375110A1 SEQ ID NO: 1
AAV-LK03 (L125I)	1200	WO2017015102A1 SEQ ID NO: 5
AAV3B (S663V+T492V)	1201	WO2017015102A1 SEQ ID NO: 6
Anc80	1202	WO2017019994A2 SEQ ID NO: 1
Anc80	1203	WO2017019994A2 SEQ ID NO: 2
Anc81	1204	WO2017019994A2 SEQ ID NO: 3
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Anc82	1206	WO2017019994A2 SEQ ID NO: 5
Anc82	1207	WO2017019994A2 SEQ ID NO: 6
Anc83	1208	WO2017019994A2 SEQ ID NO: 7
Anc83	1209	WO2017019994A2 SEQ ID NO: 8

Anc84	1210	WO2017019994A2 SEQ ID NO: 9
Anc84	1211	WO2017019994A2 SEQ ID NO: 10
Anc94	1212	WO2017019994A2 SEQ ID NO: 11
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Anc80L62	1223	WO2017019994A2 SEQ ID NO: 22
Anc80L65	1224	WO2017019994A2 SEQ ID NO: 23
Anc80L33	1225	WO2017019994A2 SEQ ID NO: 24
Anc80L36	1226	WO2017019994A2 SEQ ID NO: 25
Anc80L44	1227	WO2017019994A2 SEQ ID NO: 26
Anc80L1	1228	WO2017019994A2 SEQ ID NO: 35
Anc80L1	1229	WO2017019994A2 SEQ ID NO: 36
AAVrh10	1230	WO2017019994A2 SEQ ID NO: 41
Anc110	1231	WO2017019994A2 SEQ ID NO: 42
Anc110	1232	WO2017019994A2 SEQ ID NO: 43
AAVrh32.33	1233	WO2017019994A2 SEQ ID NO: 45
AAVrh74	1234	WO2017049031A1 SEQ ID NO: 1
AAV2	1235	WO2017053629A2 SEQ ID NO: 49
AAV2	1236	WO2017053629A2 SEQ ID NO: 50
AAV2	1237	WO2017053629A2 SEQ ID NO: 82
Parvo-like virus	1238	WO2017070476A2 SEQ ID NO: 1
Parvo-like virus	1239	WO2017070476A2 SEQ ID NO: 2
Parvo-like virus	1240	WO2017070476A2 SEQ ID NO: 3
Parvo-like virus	1241	WO2017070476A2 SEQ ID NO: 4
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Parvo-like virus	1243	WO2017070476A2 SEQ ID NO: 6
AAVrh.10	1244	WO2017070516A1 SEQ ID NO: 7
AAVrh.10	1245	WO2017070516A1 SEQ ID NO: 14
AAV2tYF	1246	WO2017070491A1 SEQ ID NO: 1
AAV-SPK	1247	WO2017075619A1 SEQ ID NO:28
AAV2.5	1248	US20170128528A1 SEQ ID NO: 13
AAV1.1	1249	US20170128528A1 SEQ ID NO: 15
AAV6.1	1250	US20170128528A1 SEQ ID NO: 17
AAV6.3.1	1251	US20170128528A1 SEQ ID NO: 18
AAV2i8	1252	US20170128528A1 SEQ ID NO: 28
AAV2i8	1253	US20170128528A1 SEQ ID NO: 29

ttAAV	1254	US20170128528A1 SEQ ID NO: 30
ttAAV-S312N	1255	US20170128528A1 SEQ ID NO: 32
ttAAV-S312N	1256	US20170128528A1 SEQ ID NO: 33
AAV6 (Y705, Y731, and T492)	1257	WO2016134337A1 SEQ ID NO: 24
AAV2	1258	WO2016134375A1 SEQ ID NO: 9
AAV2	1259	WO2016134375A1 SEQ ID NO: 10

[0075] In one embodiment, the AAV serotype may be, or may have a sequence as described in International Patent Publication WO2015038958, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 2 and 11 of WO2015038958 or SEQ ID NO: 135 and 136 respectively herein), PHP.B (SEQ ID NO: 8 and 9 of WO2015038958, herein SEQ ID NO: 3 and 4), G2B-13 (SEQ ID NO: 12 of WO2015038958, herein SEQ ID NO: 5), G2B-26 (SEQ ID NO: 13 of WO2015038958, herein SEQ ID NO: 3), TH1.1-32 (SEQ ID NO: 14 of WO2015038958, herein SEQ ID NO: 6), TH1.1-35 (SEQ ID NO: 15 of WO2015038958, herein SEQ ID NO: 7) or variants thereof. Further, any of the targeting peptides or amino acid inserts described in WO2015038958, may be inserted into any parent AAV serotype, such as, but not limited to, AAV9 (SEQ ID NO: 135 for the DNA sequence and SEQ ID NO: 136 for the amino acid sequence). In one embodiment, the amino acid insert is inserted between amino acids 586-592 of the parent AAV (e.g., AAV9). In another embodiment, the amino acid insert is inserted between amino acids 588-589 of the parent AAV sequence. The amino acid insert may be, but is not limited to, any of the following amino acid sequences, TLAVPFK (SEQ ID NO: 1 of WO2015038958; herein SEQ ID NO: 1260), KFPVALT (SEQ ID NO: 3 of WO2015038958; herein SEQ ID NO: 1261), LAVPFK (SEQ ID NO: 31 of WO2015038958; herein SEQ ID NO: 1262), AVPFK (SEQ ID NO: 32 of WO2015038958; herein SEQ ID NO: 1263), VPFK (SEQ ID NO: 33 of WO2015038958; herein SEQ ID NO: 1264), TLAVPF (SEQ ID NO: 34 of WO2015038958; herein SEQ ID NO: 1265), TLAVP (SEQ ID NO: 35 of WO2015038958; herein SEQ ID NO: 1266), TLAV (SEQ ID NO: 36 of WO2015038958; herein SEQ ID NO: 1267), SVSKPFL (SEQ ID NO: 28 of WO2015038958; herein SEQ ID NO: 1268), FTLTTPK (SEQ ID NO: 29 of WO2015038958; herein SEQ ID NO: 1269), MNATKNV (SEQ ID NO: 30 of WO2015038958; herein SEQ ID NO: 1270), QSSQTPR (SEQ ID NO: 54 of WO2015038958; herein SEQ ID NO: 1271), ILGTGTS (SEQ ID NO: 55 of WO2015038958; herein SEQ ID NO: 1272), TRTNPEA (SEQ ID NO: 56 of WO2015038958; herein SEQ ID NO: 1273), NGGTSSS (SEQ ID NO: 58 of

WO2015038958; herein SEQ ID NO: 1274), or YTLSQGW (SEQ ID NO: 60 of WO2015038958; herein SEQ ID NO: 1275). Non-limiting examples of nucleotide sequences that may encode the amino acid inserts include the following, AAGTTTCCTGTGGCGTTGACT (for SEQ ID NO: 3 of WO2015038958; herein SEQ ID NO: 1276), ACTTTGGCGGTGCCTTTTAAG (SEQ ID NO: 24 and 49 of WO2015038958; herein SEQ ID NO: 1277), AGTGTGAGTAAGCCTTTTTTG (SEQ ID NO: 25 of WO2015038958; herein SEQ ID NO: 1278), TTTACGTTGACGACGCCTAAG (SEQ ID NO: 26 of WO2015038958; herein SEQ ID NO: 1279), ATGAATGCTACGAAGAATGTG (SEQ ID NO: 27 of WO2015038958; herein SEQ ID NO: 1280), CAGTCGTCGCAGACGCCTAGG (SEQ ID NO: 48 of WO2015038958; herein SEQ ID NO: 1281), ATTCTGGGGACTGGTACTTCG (SEQ ID NO: 50 and 52 of WO2015038958; herein SEQ ID NO: 1282), ACGCGGACTAATCCTGAGGCT (SEQ ID NO: 51 of WO2015038958; herein SEQ ID NO: 1283), AATGGGGGGACTAGTAGTTCT (SEQ ID NO: 53 of WO2015038958; herein SEQ ID NO: 1284), or TATACTTTGTCGCAGGGTTGG (SEQ ID NO: 59 of WO2015038958; herein SEQ ID NO: 1285).

[0076] In one embodiment, the AAV serotype may be, or may have a sequence as described in International Patent Publication WO2017100671, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV9 (SEQ ID NO: 45 of WO2017100671, herein SEQ ID NO: 9), PHP.N (SEQ ID NO: 46 of WO2017100671, herein SEQ ID NO: 2), PHP.S (SEQ ID NO: 47 of WO2017100671, herein SEQ ID NO: 8), or variants thereof. Further, any of the targeting peptides or amino acid inserts described in WO2017100671 may be inserted into any parent AAV serotype, such as, but not limited to, AAV9 (SEQ ID NO: 9 or SEQ ID NO: 131). In one embodiment, the amino acid insert is inserted between amino acids 586-592 of the parent AAV (e.g., AAV9). In another embodiment, the amino acid insert is inserted between amino acids 588-589 of the parent AAV sequence. The amino acid insert may be, but is not limited to, any of the following amino acid sequences, AQTLAVPFKAQ (SEQ ID NO: 1 of WO2017100671; herein SEQ ID NO: 1286), AQSVSKPFLAQ (SEQ ID NO: 2 of WO2017100671; herein SEQ ID NO: 1287), AQFTLTTPKAQ (SEQ ID NO: 3 in the sequence listing of WO2017100671; herein SEQ ID NO: 1288), DGTLAVPFKAQ (SEQ ID NO: 4 in the sequence listing of WO2017100671; herein SEQ ID NO: 1289), ESTLAVPFKAQ (SEQ ID NO: 5 of WO2017100671; herein SEQ ID NO: 1290), GGTLAVPFKAQ (SEQ ID NO: 6 of

WO2017100671; herein SEQ ID NO: 1291), AQTLATPFKAQ (SEQ ID NO: 7 and 33 of WO2017100671; herein SEQ ID NO: 1292), ATTLATPFKAQ (SEQ ID NO: 8 of WO2017100671; herein SEQ ID NO: 1293), DGTLATPFKAQ (SEQ ID NO: 9 of WO2017100671; herein SEQ ID NO: 1294), GGTLATPFKAQ (SEQ ID NO: 10 of WO2017100671; herein SEQ ID NO: 1295), SGSLAVPFKAQ (SEQ ID NO: 11 of WO2017100671; herein SEQ ID NO: 1296), AQTLAQPFKAQ (SEQ ID NO: 12 of WO2017100671; herein SEQ ID NO: 1297), AQTLQQPFKAQ (SEQ ID NO: 13 of WO2017100671; herein SEQ ID NO: 1298), AQTLSNPFKAQ (SEQ ID NO: 14 of WO2017100671; herein SEQ ID NO: 1299), AQTLAVPFSNP (SEQ ID NO: 15 of WO2017100671; herein SEQ ID NO: 1300), QGTLAVPFKAQ (SEQ ID NO: 16 of WO2017100671; herein SEQ ID NO: 1301), NQTLAVPFKAQ (SEQ ID NO: 17 of WO2017100671; herein SEQ ID NO: 1302), EGSLAVPFKAQ (SEQ ID NO: 18 of WO2017100671; herein SEQ ID NO: 1303), SGNLAVPFKAQ (SEQ ID NO: 19 of WO2017100671; herein SEQ ID NO: 1304), EGTLAVPFKAQ (SEQ ID NO: 20 of WO2017100671; herein SEQ ID NO: 1305), DSTLAVPFKAQ (SEQ ID NO: 21 in Table 1 of WO2017100671; herein SEQ ID NO: 1306), AVTLAVPFKAQ (SEQ ID NO: 22 of WO2017100671; herein SEQ ID NO: 1307), AQTLSTPFKAQ (SEQ ID NO: 23 of WO2017100671; herein SEQ ID NO: 1308), AQTLPQPFKAQ (SEQ ID NO: 24 and 32 of WO2017100671; herein SEQ ID NO: 1309), AQTLSQPFKAQ (SEQ ID NO: 25 of WO2017100671; herein SEQ ID NO: 1310), AQTLQLPFKAQ (SEQ ID NO: 26 of WO2017100671; herein SEQ ID NO: 1311), AQTLTMPFKAQ (SEQ ID NO: 27, and 34 of WO2017100671 and SEQ ID NO: 35 in the sequence listing of WO2017100671; herein SEQ ID NO: 1312), AQTLTTPFKAQ (SEQ ID NO: 28 of WO2017100671; herein SEQ ID NO: 1313), AQYTLSQGWAQ (SEQ ID NO: 29 of WO2017100671; herein SEQ ID NO: 1314), AQMNATKNVAQ (SEQ ID NO: 30 of WO2017100671; herein SEQ ID NO: 1315), AQVSGGHHSAQ (SEQ ID NO: 31 of WO2017100671; herein SEQ ID NO: 1316), AQTLTAPFKAQ (SEQ ID NO: 35 in Table 1 of WO2017100671; herein SEQ ID NO: 1317), AQTLSKPFKAQ (SEQ ID NO: 36 of WO2017100671; herein SEQ ID NO: 1318), QAVRTSL (SEQ ID NO: 37 of WO2017100671; herein SEQ ID NO: 1319), YTLSQGW (SEQ ID NO: 38 of WO2017100671; herein SEQ ID NO: 1275), LAKERLS (SEQ ID NO: 39 of WO2017100671; herein SEQ ID NO: 1320), TLAVPFK (SEQ ID NO: 40 in the sequence listing of WO2017100671; herein SEQ ID NO: 1260), SVSKPFL (SEQ ID NO: 41 of WO2017100671; herein SEQ ID NO: 1268), FTLTTPK (SEQ ID NO: 42 of

WO2017100671; herein SEQ ID NO: 1269), MNSTKNV (SEQ ID NO: 43 of WO2017100671; herein SEQ ID NO: 1321), VSGGHHS (SEQ ID NO: 44 of WO2017100671; herein SEQ ID NO: 1322), SAQTLAVPFKAQAQ (SEQ ID NO: 48 of WO2017100671; herein SEQ ID NO: 1323), SXXXLAVPFKAQAQ (SEQ ID NO: 49 of WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 1324), SAQXXXVPFKAQAQ (SEQ ID NO: 50 of WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 1325), SAQTLXXXFKAQAQ (SEQ ID NO: 51 of WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 1326), SAQTLAVXXXAQAQ (SEQ ID NO: 52 of WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 1327), SAQTLAVPFXXXAQ (SEQ ID NO: 53 of WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 1328), TNHQSAQ (SEQ ID NO: 65 of WO2017100671; herein SEQ ID NO: 1329), AQAQTGW (SEQ ID NO: 66 of WO2017100671; herein SEQ ID NO: 1330), DGTLATPFK (SEQ ID NO: 67 of WO2017100671; herein SEQ ID NO: 1331), DGTLATPFKXX (SEQ ID NO: 68 of WO2017100671 wherein X may be any amino acid; herein SEQ ID NO: 1332), LAVPFKAQ (SEQ ID NO: 80 of WO2017100671; herein SEQ ID NO: 1333), VPFKAQ (SEQ ID NO: 81 of WO2017100671; herein SEQ ID NO: 1334), FKAQ (SEQ ID NO: 82 of WO2017100671; herein SEQ ID NO: 1335), AQTLAV (SEQ ID NO: 83 of WO2017100671; herein SEQ ID NO: 1336), AQTLAVPF (SEQ ID NO: 84 of WO2017100671; herein SEQ ID NO: 1337), QAVR (SEQ ID NO: 85 of WO2017100671; herein SEQ ID NO: 1338), AVRT (SEQ ID NO: 86 of WO2017100671; herein SEQ ID NO: 1339), VRTS (SEQ ID NO: 87 of WO2017100671; herein SEQ ID NO: 1340), RTSL (SEQ ID NO: 88 of WO2017100671; herein SEQ ID NO: 1341), QAVRT (SEQ ID NO: 89 of WO2017100671; herein SEQ ID NO: 1342), AVRTS (SEQ ID NO: 90 of WO2017100671; herein SEQ ID NO: 1343), VRTSL (SEQ ID NO: 91 of WO2017100671; herein SEQ ID NO: 1344), QAVRTS (SEQ ID NO: 92 of WO2017100671; herein SEQ ID NO: 1345), or AVRTSL (SEQ ID NO: 93 of WO2017100671; herein SEQ ID NO: 1346).

[0077] Non-limiting examples of nucleotide sequences that may encode the amino acid inserts include the following, GATGGGACTTTGGCGGTGCCTTTTAAGGCACAG (SEQ ID NO: 54 of WO2017100671; herein SEQ ID NO: 1347), GATGGGACGTTGGCGGTGCCTTTTAAGGCACAG (SEQ ID NO: 55 of WO2017100671; herein SEQ ID NO: 1348), CAGGCGGTTAGGACGTCTTTG (SEQ ID NO: 56 of WO2017100671; herein SEQ ID NO: 1349),

CAGGTCTTCACGGACTCAGACTATCAG (SEQ ID NO: 57 and 78 of WO2017100671; herein SEQ ID NO: 1350), CAAGTAAAACCTCTACAAATGTGGTAAAATCG (SEQ ID NO: 58 of WO2017100671; herein SEQ ID NO: 1351), ACTCATCGACCAATACTTGTACTATCTCTCTAGAAC (SEQ ID NO: 59 of WO2017100671; herein SEQ ID NO: 1352), GGAAGTATTCCTTGGTTTTGAACCCA (SEQ ID NO: 60 of WO2017100671; herein SEQ ID NO: 1353), GGTCGCGGTTCTTGTTTGTGGAT (SEQ ID NO: 61 of WO2017100671; herein SEQ ID NO: 1354), CGACCTTGAAGCGCATGAACTCCT (SEQ ID NO: 62 of WO2017100671; herein SEQ ID NO: 1355), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCMNNMNNMNNMNNMNNNMNNMNNTTGGGCACTCTGGTGGTTTGTC (SEQ ID NO: 63 of WO2017100671 wherein N may be A, C, T, or G; herein SEQ ID NO: 1356), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCMNNMNNMNNAAAAGGCACCGCCAAAGTTTG (SEQ ID NO: 69 of WO2017100671 wherein N may be A, C, T, or G; herein SEQ ID NO: 1357), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCMNNMNNMNNCACCGCCAAAGTTTGGGCACT (SEQ ID NO: 70 of WO2017100671 wherein N may be A, C, T, or G; herein SEQ ID NO: 1358), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCCTTAAAMNNMNNMNNCAAAGTTTGGGCACTCTGGTGG (SEQ ID NO: 71 of WO2017100671 wherein N may be A, C, T, or G; herein SEQ ID NO: 1359), GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCCTTAAAAGGCACMNNMNNMNNTTGGGCACTCTGGTGGTTTGTG (SEQ ID NO: 72 of WO2017100671 wherein N may be A, C, T, or G; herein SEQ ID NO: 1360), ACTTTGGCGGTGCCTTTTAAG (SEQ ID NO: 74 of WO2017100671; herein SEQ ID NO: 1277), AGTGTGAGTAAGCCTTTTTTG (SEQ ID NO: 75 of WO2017100671; herein SEQ ID NO: 1278), TTTACGTTGACGACGCCTAAG (SEQ ID NO: 76 of WO2017100671; herein SEQ ID NO: 1279), TATACTTTGTCGCAGGGTTGG (SEQ ID NO: 77 of WO2017100671; herein SEQ ID NO: 1285), or CTTGCGAAGGAGCGGCTTTCG (SEQ ID NO: 79 of WO2017100671; herein SEQ ID NO: 1361).

[0078] In one embodiment, the AAV serotype may be, or may have a sequence as described in U.S. Patent No. US 9624274, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV1 (SEQ ID NO: 181 of

US9624274), AAV6 (SEQ ID NO: 182 of US9624274), AAV2 (SEQ ID NO: 183 of US9624274), AAV3b (SEQ ID NO: 184 of US9624274), AAV7 (SEQ ID NO: 185 of US9624274), AAV8 (SEQ ID NO: 186 of US9624274), AAV10 (SEQ ID NO: 187 of US9624274), AAV4 (SEQ ID NO: 188 of US9624274), AAV11 (SEQ ID NO: 189 of US9624274), bAAV (SEQ ID NO: 190 of US9624274), AAV5 (SEQ ID NO: 191 of US9624274), GPV (SEQ ID NO: 192 of US9624274; herein SEQ ID NO: 992), B19 (SEQ ID NO: 193 of US9624274; herein SEQ ID NO: 993), MVM (SEQ ID NO: 194 of US9624274; herein SEQ ID NO: 994), FPV (SEQ ID NO: 195 of US9624274; herein SEQ ID NO: 995), CPV (SEQ ID NO: 196 of US9624274; herein SEQ ID NO: 996) or variants thereof. Further, any of the structural protein inserts described in US 9624274, may be inserted into, but not limited to, I-453 and I-587 of any parent AAV serotype, such as, but not limited to, AAV2 (SEQ ID NO: 183 of US9624274). The amino acid insert may be, but is not limited to, any of the following amino acid sequences, VNLTWSRASG (SEQ ID NO: 50 of US9624274; herein SEQ ID NO: 1362), EFCINHRGYWVCGD (SEQ ID NO:55 of US9624274; herein SEQ ID NO: 1363), EDGQVMDVDLS (SEQ ID NO: 85 of US9624274; herein SEQ ID NO: 1364), EKQRNGTLT (SEQ ID NO: 86 of US9624274; herein SEQ ID NO: 1365), TYQCRVTHPHLPRALMR (SEQ ID NO: 87 of US9624274; herein SEQ ID NO: 1366), RHSTTQPRKTKGSG (SEQ ID NO: 88 of US9624274; herein SEQ ID NO: 1367), DSNPRGVSAYLSR (SEQ ID NO: 89 of US9624274; herein SEQ ID NO: 1368), TITCLWDLAPSK (SEQ ID NO: 90 of US9624274; herein SEQ ID NO: 1369), KTKGSGFFVF (SEQ ID NO: 91 of US9624274; herein SEQ ID NO: 1370), THPHLPRALMRS (SEQ ID NO: 92 of US9624274; herein SEQ ID NO: 1371), GETYQCRVTHPHLPRALMRSTTK (SEQ ID NO: 93 of US9624274; herein SEQ ID NO: 1372), LPRALMRS (SEQ ID NO: 94 of US9624274; herein SEQ ID NO: 1373), INHRGYWV (SEQ ID NO: 95 of US9624274; herein SEQ ID NO: 1374), CDAGSVRTNAPD (SEQ ID NO: 60 of US9624274; herein SEQ ID NO: 1375), AKAVSNLTESRSESLQS (SEQ ID NO: 96 of US9624274; herein SEQ ID NO: 1376), SLTGDEFKKVLET (SEQ ID NO: 97 of US9624274; herein SEQ ID NO: 1377), REAVAYRFEED (SEQ ID NO: 98 of US9624274; herein SEQ ID NO: 1378), INPEIITLDG (SEQ ID NO: 99 of US9624274; herein SEQ ID NO: 1379), DISVTGAPVITATYL (SEQ ID NO: 100 of US9624274; herein SEQ ID NO: 1380), DISVTGAPVITA (SEQ ID NO: 101 of US9624274; herein SEQ ID NO: 1381), PKTVSNLTESSSESVQS (SEQ ID NO: 102 of US9624274; herein SEQ ID NO: 1382), SLMGDEFKAVLET (SEQ ID NO: 103 of

US9624274; herein SEQ ID NO: 1383), QHSVAYTFEED (SEQ ID NO: 104 of US9624274; herein SEQ ID NO: 1384), INPEIITRDG (SEQ ID NO: 105 of US9624274; herein SEQ ID NO: 1385), DISLTGDPVITASYL (SEQ ID NO: 106 of US9624274; herein SEQ ID NO: 1386), DISLTGDPVITA (SEQ ID NO: 107 of US9624274; herein SEQ ID NO: 1387), DQSIDFEIDSA (SEQ ID NO: 108 of US9624274; herein SEQ ID NO: 1388), KNVSEDLPLPTFSPTLLGDS (SEQ ID NO: 109 of US9624274; herein SEQ ID NO: 1389), KNVSEDLPLPT (SEQ ID NO: 110 of US9624274; herein SEQ ID NO: 1390), CDSGRVRTDAPD (SEQ ID NO: 111 of US9624274; herein SEQ ID NO: 1391), FPEHLLVDFLQSLS (SEQ ID NO: 112 of US9624274; herein SEQ ID NO: 1392), DAEFRHDSG (SEQ ID NO: 65 of US9624274; herein SEQ ID NO: 1393), HYAAAQWDFGNTMCQL (SEQ ID NO: 113 of US9624274; herein SEQ ID NO: 1394), YAAQWDFGNTMCQ (SEQ ID NO: 114 of US9624274; herein SEQ ID NO: 1395), RSQKEGLHYT (SEQ ID NO: 115 of US9624274; herein SEQ ID NO: 1396), SSRTPSDKPVAHWANPQAE (SEQ ID NO: 116 of US9624274; herein SEQ ID NO: 1397), SRTPSDKPVAHWANP (SEQ ID NO: 117 of US9624274; herein SEQ ID NO: 1398), SSRTPSDKP (SEQ ID NO: 118 of US9624274; herein SEQ ID NO: 1399), NADGNVDYHMNSVP (SEQ ID NO: 119 of US9624274; herein SEQ ID NO: 1400), DGNVDYHMNSV (SEQ ID NO: 120 of US9624274; herein SEQ ID NO: 1401), RSFKEFLQSSLRALRQ (SEQ ID NO: 121 of US9624274; herein SEQ ID NO: 1402); FKEFLQSSLRA (SEQ ID NO: 122 of US9624274; herein SEQ ID NO: 1403), or QMWAPQWGPD (SEQ ID NO: 123 of US9624274; herein SEQ ID NO: 1404).

[0079] In one embodiment, the AAV serotype may be, or may have a sequence as described in U.S. Patent No. US 9475845, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, AAV capsid proteins comprising modification of one or more amino acids at amino acid positions 585 to 590 of the native AAV2 capsid protein. Further the modification may result in, but not limited to, the amino acid sequence RGNRQA (SEQ ID NO: 3 of US9475845; herein SEQ ID NO: 1405), SSSTDP (SEQ ID NO: 4 of US9475845; herein SEQ ID NO: 1406), SSNTAP (SEQ ID NO: 5 of US9475845; herein SEQ ID NO: 1407), SNSNLP (SEQ ID NO: 6 of US9475845; herein SEQ ID NO: 1408), SSTTAP (SEQ ID NO: 7 of US9475845; herein SEQ ID NO: 1409), AANTAA (SEQ ID NO: 8 of US9475845; herein SEQ ID NO: 1410), QQNTAP (SEQ ID NO: 9 of US9475845; herein SEQ ID NO: 1411), SAQAQA (SEQ ID NO: 10 of US9475845; herein SEQ ID NO: 1412), QANTGP (SEQ ID NO: 11 of US9475845; herein

SEQ ID NO: 1413), NATTAP (SEQ ID NO: 12 of US9475845; herein SEQ ID NO: 1414), SSTAGP (SEQ ID NO: 13 and 20 of US9475845; herein SEQ ID NO: 1415), QQNTAA (SEQ ID NO: 14 of US9475845; herein SEQ ID NO: 1416), PSTAGP (SEQ ID NO: 15 of US9475845; herein SEQ ID NO: 1417), NQNTAP (SEQ ID NO: 16 of US9475845; herein SEQ ID NO: 1418), QAANAP (SEQ ID NO: 17 of US9475845; herein SEQ ID NO: 1419), SIVGLP (SEQ ID NO: 18 of US9475845; herein SEQ ID NO: 1420), AASTAA (SEQ ID NO: 19, and 27 of US9475845; herein SEQ ID NO: 1421), SQNTTA (SEQ ID NO: 21 of US9475845; herein SEQ ID NO: 1422), QQDTAP (SEQ ID NO: 22 of US9475845; herein SEQ ID NO: 1423), QTNTGP (SEQ ID NO: 23 of US9475845; herein SEQ ID NO: 1424), QTNGAP (SEQ ID NO: 24 of US9475845; herein SEQ ID NO: 1425), QQNAAP (SEQ ID NO: 25 of US9475845; herein SEQ ID NO: 1426), or AANTQA (SEQ ID NO: 26 of US9475845; herein SEQ ID NO: 1427). In one embodiment, the amino acid modification is a substitution at amino acid positions 262 through 265 in the native AAV2 capsid protein or the corresponding position in the capsid protein of another AAV with a targeting sequence. The targeting sequence may be, but is not limited to, any of the amino acid sequences, NGRAHA (SEQ ID NO: 38 of US9475845; herein SEQ ID NO: 1428), QPEHSST (SEQ ID NO: 39 and 50 of US9475845; herein SEQ ID NO: 1429), VNTANST (SEQ ID NO: 40 of US9475845; herein SEQ ID NO: 1430), HGPMQKS (SEQ ID NO: 41 of US9475845; herein SEQ ID NO: 1431), PHKPPLA (SEQ ID NO: 42 of US9475845; herein SEQ ID NO: 1432), IKNNEMW (SEQ ID NO: 43 of US9475845; herein SEQ ID NO: 1433), RNLDTPM (SEQ ID NO: 44 of US9475845; herein SEQ ID NO: 1434), VDSHRQS (SEQ ID NO: 45 of US9475845; herein SEQ ID NO: 1435), YDSKTKT (SEQ ID NO: 46 of US9475845; herein SEQ ID NO: 1436), SQLPHQK (SEQ ID NO: 47 of US9475845; herein SEQ ID NO: 1437), STMQQNT (SEQ ID NO: 48 of US9475845; herein SEQ ID NO: 1438), TERYMTQ (SEQ ID NO: 49 of US9475845; herein SEQ ID NO: 1439), DASLSTS (SEQ ID NO: 51 of US9475845; herein SEQ ID NO: 1440), DLPNKKT (SEQ ID NO: 52 of US9475845; herein SEQ ID NO: 1441), DLTAARL (SEQ ID NO: 53 of US9475845; herein SEQ ID NO: 1442), EPHQFNY (SEQ ID NO: 54 of US9475845; herein SEQ ID NO: 1443), EPQSNHT (SEQ ID NO: 55 of US9475845; herein SEQ ID NO: 1444), MSSWPSQ (SEQ ID NO: 56 of US9475845; herein SEQ ID NO: 1445), NPKHNAT (SEQ ID NO: 57 of US9475845; herein SEQ ID NO: 1446), PDGMRTT (SEQ ID NO: 58 of US9475845; herein SEQ ID NO: 1447), PNNNKTT (SEQ ID NO: 59 of US9475845; herein SEQ ID NO: 1448), QSTTHDS (SEQ ID NO: 60 of US9475845; herein SEQ ID NO: 1449), TGSKQKQ (SEQ ID NO: 61 of US9475845; herein

SEQ ID NO: 1450), SLKHQAL (SEQ ID NO: 62 of US9475845; herein SEQ ID NO: 1451), SPIDGEQ (SEQ ID NO: 63 of US9475845; herein SEQ ID NO: 1452), WIFPWIQL (SEQ ID NO: 64 and 112 of US9475845; herein SEQ ID NO: 1453), CDCRGDCFC (SEQ ID NO: 65 of US9475845; herein SEQ ID NO: 1454), CNGRC (SEQ ID NO: 66 of US9475845; herein SEQ ID NO: 1455), CPRECES (SEQ ID NO: 67 of US9475845; herein SEQ ID NO: 1456), CTTHWGFTLC (SEQ ID NO: 68 and 123 of US9475845; herein SEQ ID NO: 1457), CGRRAGGSC (SEQ ID NO: 69 of US9475845; herein SEQ ID NO: 1458), CKGGRAKDC (SEQ ID NO: 70 of US9475845; herein SEQ ID NO: 1459), CVPELGHEC (SEQ ID NO: 71 and 115 of US9475845; herein SEQ ID NO: 1460), CRRETAWAK (SEQ ID NO: 72 of US9475845; herein SEQ ID NO: 1461), VSWFSHRYSPFAVS (SEQ ID NO: 73 of US9475845; herein SEQ ID NO: 1462), GYRDGYAGPILYN (SEQ ID NO: 74 of US9475845; herein SEQ ID NO: 1463), XXXYXXX (SEQ ID NO: 75 of US9475845; herein SEQ ID NO: 1464), YXNW (SEQ ID NO: 76 of US9475845; herein SEQ ID NO: 1465), RPLPPLP (SEQ ID NO: 77 of US9475845; herein SEQ ID NO: 1466), APPLPPR (SEQ ID NO: 78 of US9475845; herein SEQ ID NO: 1467), DVFYPYPYASGS (SEQ ID NO: 79 of US9475845; herein SEQ ID NO: 1468), MYWYPY (SEQ ID NO: 80 of US9475845; herein SEQ ID NO: 1469), DITWDQLWDLMK (SEQ ID NO: 81 of US9475845; herein SEQ ID NO: 1470), CWDDXWLC (SEQ ID NO: 82 of US9475845; herein SEQ ID NO: 1471), EWCEYLGGYLRCYA (SEQ ID NO: 83 of US9475845; herein SEQ ID NO: 1472), YXCXXGPXTWXCXP (SEQ ID NO: 84 of US9475845; herein SEQ ID NO: 1473), IEGPTLRQWLAARA (SEQ ID NO: 85 of US9475845; herein SEQ ID NO: 1474), LWXXX (SEQ ID NO: 86 of US9475845; herein SEQ ID NO: 1475), XFXXYLW (SEQ ID NO: 87 of US9475845; herein SEQ ID NO: 1476), SSIISHFRWGLCD (SEQ ID NO: 88 of US9475845; herein SEQ ID NO: 1477), MSRPACPPNDKYE (SEQ ID NO: 89 of US9475845; herein SEQ ID NO: 1478), CLRSGRGC (SEQ ID NO: 90 of US9475845; herein SEQ ID NO: 1479), CHWMFSPWC (SEQ ID NO: 91 of US9475845; herein SEQ ID NO: 1480), WXXF (SEQ ID NO: 92 of US9475845; herein SEQ ID NO: 1481), CSSRLDAC (SEQ ID NO: 93 of US9475845; herein SEQ ID NO: 1482), CLPVASC (SEQ ID NO: 94 of US9475845; herein SEQ ID NO: 1483), CGFECVRQCPERC (SEQ ID NO: 95 of US9475845; herein SEQ ID NO: 1484), CVALCREACGEGC (SEQ ID NO: 96 of US9475845; herein SEQ ID NO: 1485), SWCEPGWCR (SEQ ID NO: 97 of US9475845; herein SEQ ID NO: 1486), YSGKWGW (SEQ ID NO: 98 of US9475845; herein SEQ ID NO: 1487), GLSGGRS (SEQ ID NO: 99 of US9475845; herein SEQ ID NO: 1488),

LMLPRAD (SEQ ID NO: 100 of US9475845; herein SEQ ID NO: 1489), CSCFRDVCC (SEQ ID NO: 101 of US9475845; herein SEQ ID NO: 1490), CRDVVSVIC (SEQ ID NO: 102 of US9475845; herein SEQ ID NO: 1491), MARSGL (SEQ ID NO: 103 of US9475845; herein SEQ ID NO: 1492), MARAKE (SEQ ID NO: 104 of US9475845; herein SEQ ID NO: 1493), MSRTMS (SEQ ID NO: 105 of US9475845; herein SEQ ID NO: 1494), KCCYSL (SEQ ID NO: 106 of US9475845; herein SEQ ID NO: 1495), MYWGDSHWLQYWYE (SEQ ID NO: 107 of US9475845; herein SEQ ID NO: 1496), MQLPLAT (SEQ ID NO: 108 of US9475845; herein SEQ ID NO: 1497), EWLS (SEQ ID NO: 109 of US9475845; herein SEQ ID NO: 1498), SNEW (SEQ ID NO: 110 of US9475845; herein SEQ ID NO: 1499), TNYL (SEQ ID NO: 111 of US9475845; herein SEQ ID NO: 1500), WDLAWMFRLPVG (SEQ ID NO: 113 of US9475845; herein SEQ ID NO: 1501), CTVALPGGYVRVC (SEQ ID NO: 114 of US9475845; herein SEQ ID NO: 1502), CVAYCIEHHCWTC (SEQ ID NO: 116 of US9475845; herein SEQ ID NO: 1503), CVFAHNYDYLVC (SEQ ID NO: 117 of US9475845; herein SEQ ID NO: 1504), CVFTSNYAFC (SEQ ID NO: 118 of US9475845; herein SEQ ID NO: 1505), VHSPNKK (SEQ ID NO: 119 of US9475845; herein SEQ ID NO: 1506), CRGDGWC (SEQ ID NO: 120 of US9475845; herein SEQ ID NO: 1507), XRGCDX (SEQ ID NO: 121 of US9475845; herein SEQ ID NO: 1508), PXXX (SEQ ID NO: 122 of US9475845; herein SEQ ID NO: 1509), SGKGPRQITAL (SEQ ID NO: 124 of US9475845; herein SEQ ID NO: 1510), AAAAAAAAAXXXXX (SEQ ID NO: 125 of US9475845; herein SEQ ID NO: 1511), VYMSPF (SEQ ID NO: 126 of US9475845; herein SEQ ID NO: 1512), ATWLPPR (SEQ ID NO: 127 of US9475845; herein SEQ ID NO: 1513), HTMYYHHYQHHL (SEQ ID NO: 128 of US9475845; herein SEQ ID NO: 1514), SEVGCRAGPLQWLCEKYFG (SEQ ID NO: 129 of US9475845; herein SEQ ID NO: 1515), CGLLPVGRPDRNVWRWLC (SEQ ID NO: 130 of US9475845; herein SEQ ID NO: 1516), CKGQCDRFKGLPWEC (SEQ ID NO: 131 of US9475845; herein SEQ ID NO: 1517), SGRSA (SEQ ID NO: 132 of US9475845; herein SEQ ID NO: 1518), WGFP (SEQ ID NO: 133 of US9475845; herein SEQ ID NO: 1519), AEPMPHSLNFSQYLWYT (SEQ ID NO: 134 of US9475845; herein SEQ ID NO: 1520), WAYXSP (SEQ ID NO: 135 of US9475845; herein SEQ ID NO: 1521), IELLQAR (SEQ ID NO: 136 of US9475845; herein SEQ ID NO: 1522), AYTKCSRQWRTCMTTH (SEQ ID NO: 137 of US9475845; herein SEQ ID NO: 1523), PQNSKIPGPTFLDPH (SEQ ID NO: 138 of US9475845; herein SEQ ID NO: 1524), SMEPALPDWWWKMFK (SEQ ID NO: 139 of US9475845; herein SEQ ID NO: 1525), ANTPCGPYTHDCPVKR (SEQ ID NO: 140 of US9475845; herein SEQ ID NO:

1526), TACHQHVRMVRP (SEQ ID NO: 141 of US9475845; herein SEQ ID NO: 1527), VPWMEPAYQRFL (SEQ ID NO: 142 of US9475845; herein SEQ ID NO: 1528), DPRATPGS (SEQ ID NO: 143 of US9475845; herein SEQ ID NO: 1529), FRPNRAQDYNTN (SEQ ID NO: 144 of US9475845; herein SEQ ID NO: 1530), CTKNSYLMC (SEQ ID NO: 145 of US9475845; herein SEQ ID NO: 1531), CXXTXXXGXGC (SEQ ID NO: 146 of US9475845; herein SEQ ID NO: 1532), CPIEDRPMC (SEQ ID NO: 147 of US9475845; herein SEQ ID NO: 1533), HEWSYLAPYPWF (SEQ ID NO: 148 of US9475845; herein SEQ ID NO: 1534), MCPKHPLGC (SEQ ID NO: 149 of US9475845; herein SEQ ID NO: 1535), RMWPSSTVNLSAGRR (SEQ ID NO: 150 of US9475845; herein SEQ ID NO: 1536), SAKTAVSQRVWLPSHRGGEP (SEQ ID NO: 151 of US9475845; herein SEQ ID NO: 1537), KSREHVNNSACPSKRITAAL (SEQ ID NO: 152 of US9475845; herein SEQ ID NO: 1538), EGFR (SEQ ID NO: 153 of US9475845; herein SEQ ID NO: 1539), AGLGVR (SEQ ID NO: 154 of US9475845; herein SEQ ID NO: 1540), GTRQGHTMRLGVSDG (SEQ ID NO: 155 of US9475845; herein SEQ ID NO: 1541), IAGLATPGWSHWLAL (SEQ ID NO: 156 of US9475845; herein SEQ ID NO: 1542), SMSIARL (SEQ ID NO: 157 of US9475845; herein SEQ ID NO: 1543), HTFEPGV (SEQ ID NO: 158 of US9475845; herein SEQ ID NO: 1544), NTSLKRISNKRIRRK (SEQ ID NO: 159 of US9475845; herein SEQ ID NO: 1545), LRIKRKRRKRKKTRK (SEQ ID NO: 160 of US9475845; herein SEQ ID NO: 1546), GGG, GFS, LWS, EGG, LLV, LSP, LBS, AGG, GRR, GGH and GTV.

[0080] In one embodiment, the AAV serotype may be, or may have a sequence as described in United States Publication No. US 20160369298, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to, site-specific mutated capsid protein of AAV2 (SEQ ID NO: 97 of US 20160369298; herein SEQ ID NO: 1547) or variants thereof, wherein the specific site is at least one site selected from sites R447, G453, S578, N587, N587+1, S662 of VP1 or fragment thereof.

[0081] Further, any of the mutated sequences described in U.S. Patent Application Publication No. US20160369298, may be or may have, but not limited to, any of the following sequences SDSGASN (SEQ ID NO: 1 and SEQ ID NO: 231 of US20160369298; herein SEQ ID NO: 1548), SPSGASN (SEQ ID NO: 2 of US20160369298; herein SEQ ID NO: 1549), SHSGASN (SEQ ID NO: 3 of US20160369298; herein SEQ ID NO: 1550), SRSGASN (SEQ ID NO: 4 of US20160369298; herein SEQ ID NO: 1551), SKSGASN (SEQ ID NO: 5 of US20160369298; herein SEQ ID NO: 1552), SNSGASN (SEQ ID NO: 6

of US20160369298; herein SEQ ID NO: 1553), SGSGASN (SEQ ID NO: 7 of US20160369298; herein SEQ ID NO: 1554), SASGASN (SEQ ID NO: 8, 175, and 221 of US20160369298; herein SEQ ID NO: 1555), SESGTSN (SEQ ID NO: 9 of US20160369298; herein SEQ ID NO: 1556), STTGGSN (SEQ ID NO: 10 of US20160369298; herein SEQ ID NO: 1557), SSAGSTN (SEQ ID NO: 11 of US20160369298; herein SEQ ID NO: 1558), NNDSQA (SEQ ID NO: 12 of US20160369298; herein SEQ ID NO: 1559), NNRNQA (SEQ ID NO: 13 of US20160369298; herein SEQ ID NO: 1560), NNNKQA (SEQ ID NO: 14 of US20160369298; herein SEQ ID NO: 1561), NAKRQA (SEQ ID NO: 15 of US20160369298; herein SEQ ID NO: 1562), NDEHQA (SEQ ID NO: 16 of US20160369298; herein SEQ ID NO: 1563), NTSQKA (SEQ ID NO: 17 of US20160369298; herein SEQ ID NO: 1564), YYLSRTNTPSGTDTQSRLVFSQAGA (SEQ ID NO: 18 of US20160369298; herein SEQ ID NO: 1565), YYLSRTNTDSGTETQSGLDFSQAGA (SEQ ID NO: 19 of US20160369298; herein SEQ ID NO: 1566), YYLSRTNTESGTPTQSALEFSQAGA (SEQ ID NO: 20 of US20160369298; herein SEQ ID NO: 1567), YYLSRTNTHSGTHTQSPLHFSQAGA (SEQ ID NO: 21 of US20160369298; herein SEQ ID NO: 1568), YYLSRTNTSSGTITISHLIFSQAGA (SEQ ID NO: 22 of US20160369298; herein SEQ ID NO: 1569), YYLSRTNTRSGIMTKSSLMFSQAGA (SEQ ID NO: 23 of US20160369298; herein SEQ ID NO: 1570), YYLSRTNTKSGRKTLSNLSFSQAGA (SEQ ID NO: 24 of US20160369298; herein SEQ ID NO: 1571), YYLSRTNDGSGPVTPSKLRFSQRGA (SEQ ID NO: 25 of US20160369298; herein SEQ ID NO: 1572), YYLSRTNAASGHATHSDLKFSQPGA (SEQ ID NO: 26 of US20160369298; herein SEQ ID NO: 1573), YYLSRTNGQAGSLTMSELGFSQVGA (SEQ ID NO: 27 of US20160369298; herein SEQ ID NO: 1574), YYLSRTNSTGGNQTTSQLLFSQLSA (SEQ ID NO: 28 of US20160369298; herein SEQ ID NO: 1575), YFLSRTNNNTGLNTNSTLNFSQGRA (SEQ ID NO: 29 of US20160369298; herein SEQ ID NO: 1576), SKTGADNNNSEYSWTG (SEQ ID NO: 30 of US20160369298; herein SEQ ID NO: 1577), SKTDADNNNSEYSWTG (SEQ ID NO: 31 of US20160369298; herein SEQ ID NO: 1578), SKTEADNNNSEYSWTG (SEQ ID NO: 32 of US20160369298; herein SEQ ID NO: 1579), SKTPADNNNSEYSWTG (SEQ ID NO: 33 of US20160369298; herein SEQ ID NO: 1580), SKTHADNNNSEYSWTG (SEQ ID NO: 34 of US20160369298; herein SEQ ID NO: 1581), SKTQADNNNSEYSWTG (SEQ ID NO: 35 of US20160369298; herein SEQ ID NO: 1582), SKTIADNNNSEYSWTG (SEQ ID NO: 36 of US20160369298; herein SEQ

ID NO: 1583), SKTMADNNNSEYSWTG (SEQ ID NO: 37 of US20160369298; herein SEQ ID NO: 1584), SKTRADNNNSEYSWTG (SEQ ID NO: 38 of US20160369298; herein SEQ ID NO: 1585), SKTNADNNNSEYSWTG (SEQ ID NO: 39 of US20160369298; herein SEQ ID NO: 1586), SKTVGRNNNSEYSWTG (SEQ ID NO: 40 of US20160369298; herein SEQ ID NO: 1587), SKTADRNNNSEYSWTG (SEQ ID NO: 41 of US20160369298; herein SEQ ID NO: 1588), SKKLSQNNNSKYSWQG (SEQ ID NO: 42 of US20160369298; herein SEQ ID NO: 1589), SKPTTGNNNSDYSWPG (SEQ ID NO: 43 of US20160369298; herein SEQ ID NO: 1590), STQKNENNNSNYSWPG (SEQ ID NO: 44 of US20160369298; herein SEQ ID NO: 1591), HKDDEGKF (SEQ ID NO: 45 of US20160369298; herein SEQ ID NO: 1592), HKDDNRKF (SEQ ID NO: 46 of US20160369298; herein SEQ ID NO: 1593), HKDDTNKF (SEQ ID NO: 47 of US20160369298; herein SEQ ID NO: 1594), HEDSDKNF (SEQ ID NO: 48 of US20160369298; herein SEQ ID NO: 1595), HRDGADSF (SEQ ID NO: 49 of US20160369298; herein SEQ ID NO: 1596), HGDNKSRF (SEQ ID NO: 50 of US20160369298; herein SEQ ID NO: 1597), KQGSEKTNVDFEEV (SEQ ID NO: 51 of US20160369298; herein SEQ ID NO: 1598), KQGSEKTNVDSEEV (SEQ ID NO: 52 of US20160369298; herein SEQ ID NO: 1599), KQGSEKTNVDVEEV (SEQ ID NO: 53 of US20160369298; herein SEQ ID NO: 1600), KQGSDKTNVDDAGV (SEQ ID NO: 54 of US20160369298; herein SEQ ID NO: 1601), KQGSSKTNVDPREV (SEQ ID NO: 55 of US20160369298; herein SEQ ID NO: 1602), KQGSRKTNVDHKQV (SEQ ID NO: 56 of US20160369298; herein SEQ ID NO: 1603), KQGSKGGNVDTNRV (SEQ ID NO: 57 of US20160369298; herein SEQ ID NO: 1604), KQGSGEANVDNGDV (SEQ ID NO: 58 of US20160369298; herein SEQ ID NO: 1605), KQDAAADNIDYDHV (SEQ ID NO: 59 of US20160369298; herein SEQ ID NO: 1606), KQSGTRSNAAASSV (SEQ ID NO: 60 of US20160369298; herein SEQ ID NO: 1607), KENTNTNDTELTNV (SEQ ID NO: 61 of US20160369298; herein SEQ ID NO: 1608), QRGNNVAATADVNT (SEQ ID NO: 62 of US20160369298; herein SEQ ID NO: 1609), QRGNNEAATADVNT (SEQ ID NO: 63 of US20160369298; herein SEQ ID NO: 1610), QRGNNPAATADVNT (SEQ ID NO: 64 of US20160369298; herein SEQ ID NO: 1611), QRGNNHAATADVNT (SEQ ID NO: 65 of US20160369298; herein SEQ ID NO: 1612), QEENNIAATPGVNT (SEQ ID NO: 66 of US20160369298; herein SEQ ID NO: 1613), QPPNNMAATHEVNT (SEQ ID NO: 67 of US20160369298; herein SEQ ID NO: 1614), QHHNNSAATTIVNT (SEQ ID NO: 68 of US20160369298; herein SEQ ID NO: 1615), QTTNNRAAFNMVET (SEQ ID NO: 69 of US20160369298; herein SEQ ID NO: 1616), QKKNNNAASKKVAT (SEQ ID NO: 70 of

US20160369298; herein SEQ ID NO: 1617), QGGNNKAADDAVKT (SEQ ID NO: 71 of US20160369298; herein SEQ ID NO: 1618), QAAKGGAADDAVKT (SEQ ID NO: 72 of US20160369298; herein SEQ ID NO: 1619), QDDRAAAANESVDT (SEQ ID NO: 73 of US20160369298; herein SEQ ID NO: 1620), QQQHDDAAYQRVHT (SEQ ID NO: 74 of US20160369298; herein SEQ ID NO: 1621), QSSSSLAAVSTVQT (SEQ ID NO: 75 of US20160369298; herein SEQ ID NO: 1622), QNNQTTAAIRNVTT (SEQ ID NO: 76 of US20160369298; herein SEQ ID NO: 1623), NYNKKSDNVDFT (SEQ ID NO: 77 of US20160369298; herein SEQ ID NO: 1624), NYNKKSENVDFT (SEQ ID NO: 78 of US20160369298; herein SEQ ID NO: 1625), NYNKKSLNVDFT (SEQ ID NO: 79 of US20160369298; herein SEQ ID NO: 1626), NYNKKSPNVDFT (SEQ ID NO: 80 of US20160369298; herein SEQ ID NO: 1627), NYSKKSHCVDFT (SEQ ID NO: 81 of US20160369298; herein SEQ ID NO: 1628), NYRKTIYVDFT (SEQ ID NO: 82 of US20160369298; herein SEQ ID NO: 1629), NYKEKKDVHFT (SEQ ID NO: 83 of US20160369298; herein SEQ ID NO: 1630), NYGHRAIVQFT (SEQ ID NO: 84 of US20160369298; herein SEQ ID NO: 1631), NYANHQFVVCT (SEQ ID NO: 85 of US20160369298; herein SEQ ID NO: 1632), NYDDDPTGVLLT (SEQ ID NO: 86 of US20160369298; herein SEQ ID NO: 1633), NYDDPTGVLLT (SEQ ID NO: 87 of US20160369298; herein SEQ ID NO: 1634), NFEQQNSVEWT (SEQ ID NO: 88 of US20160369298; herein SEQ ID NO: 1635), SQSGASN (SEQ ID NO: 89 and SEQ ID NO: 241 of US20160369298; herein SEQ ID NO: 1636), NNGSQA (SEQ ID NO: 90 of US20160369298; herein SEQ ID NO: 1637), YYLSRTNTPSGTTTWSRLQFSQAGA (SEQ ID NO: 91 of US20160369298; herein SEQ ID NO: 1638), SKTSADNNNSEYSWTG (SEQ ID NO: 92 of US20160369298; herein SEQ ID NO: 1639), HKDDEEKF (SEQ ID NO: 93, 209, 214, 219, 224, 234, 239, and 244 of US20160369298; herein SEQ ID NO: 1640), KQGSEKTNVDIEEV (SEQ ID NO: 94 of US20160369298; herein SEQ ID NO: 1641), QRGNNQAATADVNT (SEQ ID NO: 95 of US20160369298; herein SEQ ID NO: 1642), NYNKKSVNVDFT (SEQ ID NO: 96 of US20160369298; herein SEQ ID NO: 1643), SQSGASNYNTPSGTTTQSRLQFSTSADNNNSEYSWTGATKYH (SEQ ID NO: 106 of US20160369298; herein SEQ ID NO: 1644), SASGASNFNSEGGSLTQSSLGFSTDGENNNSDFSWTGATKYH (SEQ ID NO: 107 of US20160369298; herein SEQ ID NO: 1645), SQSGASNYNTPSGTTTQSRLQFSTDGENNNSDFSWTGATKYH (SEQ ID NO: 108 of US20160369298; herein SEQ ID NO: 1646),

SASGASNYNTPSGTTTQSRLQFSTSADNNNSEFSWPGATTYH (SEQ ID NO: 109 of US20160369298; herein SEQ ID NO: 1647), SQSGASNFNSEGGSLTQSSLGFSTDGENNNSDFSWTGATKYH (SEQ ID NO: 110 of US20160369298; herein SEQ ID NO: 1648), SASGASNYNTPSGSLTQSSLGFSTDGENNNSDFSWTGATKYH (SEQ ID NO: 111 of US20160369298; herein SEQ ID NO: 1649), SQSGASNYNTPSGTTTQSRLQFSTSADNNNSDFSWTGATKYH (SEQ ID NO: 112 of US20160369298; herein SEQ ID NO: 1650), SGAGASNFNSEGGSLTQSSLGFSTDGENNNSDFSWTGATKYH (SEQ ID NO: 113 of US20160369298; herein SEQ ID NO: 1651), SGAGASN (SEQ ID NO: 176 of US20160369298; herein SEQ ID NO: 1652), NSEGGSLTQSSLGFS (SEQ ID NO: 177, 185, 193 and 202 of US20160369298; herein SEQ ID NO: 1653), TDGENNNSDFS (SEQ ID NO: 178 of US20160369298; herein SEQ ID NO: 1654), SEFSWPGATT (SEQ ID NO: 179 of US20160369298; herein SEQ ID NO: 1655), TSADNNNSDFSWT (SEQ ID NO: 180 of US20160369298; herein SEQ ID NO: 1656), SQSGASNY (SEQ ID NO: 181, 187, and 198 of US20160369298; herein SEQ ID NO: 1657), NTPSGTTTQSRLQFS (SEQ ID NO: 182, 188, 191, and 199 of US20160369298; herein SEQ ID NO: 1658), TSADNNNSEYSWTGATKYH (SEQ ID NO: 183 of US20160369298; herein SEQ ID NO: 1659), SASGASNF (SEQ ID NO: 184 of US20160369298; herein SEQ ID NO: 1660), TDGENNNSDFSWTGATKYH (SEQ ID NO: 186, 189, 194, 197, and 203 of US20160369298; herein SEQ ID NO: 1661), SASGASNY (SEQ ID NO: 190 and SEQ ID NO: 195 of US20160369298; herein SEQ ID NO: 1662), TSADNNNSEFSWPGATTYH (SEQ ID NO: 192 of US20160369298; herein SEQ ID NO: 1663), NTPSGSLTQSSLGFS (SEQ ID NO: 196 of US20160369298; herein SEQ ID NO: 1664), TSADNNNSDFSWTGATKYH (SEQ ID NO: 200 of US20160369298; herein SEQ ID NO: 1665), SGAGASNF (SEQ ID NO: 201 of US20160369298; herein SEQ ID NO: 1666), CTCCAGVVSVVSMRSRVCVNSGCAGCTDHCVVSRNSGTCVMSACACAA (SEQ ID NO: 204 of US20160369298; herein SEQ ID NO: 1667), CTCCAGAGAGGCAACAGACAAGCAGCTACCGCAGATGTCAACACACAA (SEQ ID NO: 205 of US20160369298; herein SEQ ID NO: 1668), SAAGASN (SEQ ID NO: 206 of US20160369298; herein SEQ ID NO: 1669), YFLSRTNTESGSTTQSTLRFSQAG (SEQ ID NO: 207 of US20160369298; herein SEQ ID NO: 1670), SKTSADNNNSDFS (SEQ ID NO: 208, 228, and 253 of US20160369298; herein SEQ ID NO: 1671), KQGSEKTDVDIDKV

(SEQ ID NO: 210 of US20160369298; herein SEQ ID NO: 1672), STAGASN (SEQ ID NO: 211 of US20160369298; herein SEQ ID NO: 1673), YFLSRTNTTSGIETQSTLRFSQAG (SEQ ID NO: 212 and SEQ ID NO: 247 of US20160369298; herein SEQ ID NO: 1674), SKTDGENNNSDFS (SEQ ID NO: 213 and SEQ ID NO: 248 of US20160369298; herein SEQ ID NO: 1675), KQGAAADDVEIDGV (SEQ ID NO: 215 and SEQ ID NO: 250 of US20160369298; herein SEQ ID NO: 1676), SEAGASN (SEQ ID NO: 216 of US20160369298; herein SEQ ID NO: 1677), YYLSRTNTPSGTTTQSRLQFSQAG (SEQ ID NO: 217, 232 and 242 of US20160369298; herein SEQ ID NO: 1678), SKTSADNNNSEYS (SEQ ID NO: 218, 233, 238, and 243 of US20160369298; herein SEQ ID NO: 1679), KQGSEKTNVDIEKV (SEQ ID NO: 220, 225 and 245 of US20160369298; herein SEQ ID NO: 1680), YFLSRTNDASGSDTKSTLLFSQAG (SEQ ID NO: 222 of US20160369298; herein SEQ ID NO: 1681), STTPSENNNSEYS (SEQ ID NO: 223 of US20160369298; herein SEQ ID NO: 1682), SAAGATN (SEQ ID NO: 226 and SEQ ID NO: 251 of US20160369298; herein SEQ ID NO: 1683), YFLSRTNGEAGSATLSELRFSQAG (SEQ ID NO: 227 of US20160369298; herein SEQ ID NO: 1684), HGDDADRF (SEQ ID NO: 229 and SEQ ID NO: 254 of US20160369298; herein SEQ ID NO: 1685), KQGAEKSDVEVDRV (SEQ ID NO: 230 and SEQ ID NO: 255 of US20160369298; herein SEQ ID NO: 1686), KQDSGGDNIDIDQV (SEQ ID NO: 235 of US20160369298; herein SEQ ID NO: 1687), SDAGASN (SEQ ID NO: 236 of US20160369298; herein SEQ ID NO: 1688), YFLSRTNTEGGHDTQSTLRFSQAG (SEQ ID NO: 237 of US20160369298; herein SEQ ID NO: 1689), KEDGGGSDVAIDEV (SEQ ID NO: 240 of US20160369298; herein SEQ ID NO: 1690), SNAGASN (SEQ ID NO: 246 of US20160369298; herein SEQ ID NO: 1691), and YFLSRTNGEAGSATLSELRFSQPG (SEQ ID NO: 252 of US20160369298; herein SEQ ID NO: 1692). Non-limiting examples of nucleotide sequences that may encode the amino acid mutated sites include the following, AGCVVMDCAGGARSCASCAAC (SEQ ID NO: 97 of US20160369298; herein SEQ ID NO: 1693), AACRACRRSMRSMAGGCA (SEQ ID NO: 98 of US20160369298; herein SEQ ID NO: 1694), CACRRGGACRRCRMSRRSARSTTT (SEQ ID NO: 99 of US20160369298; herein SEQ ID NO: 1695), TATTTCTTGAGCAGAACAAACRVCVVSRSCGGAMNCVHSACGMHSTCAVVSCTTV DSTTTTCTCAGSBCRGSGCG (SEQ ID NO: 100 of US20160369298; herein SEQ ID NO: 1696), TCAAMAMMAVNSRVCSRSAACAACAACAGTRASTTCTCGTGGMMAGGA (SEQ ID NO: 101 of US20160369298; herein SEQ ID NO: 1697),

AAGSAARRCRSCRVSRVARVCRATRYCGMSNHCRVMVRSGTC (SEQ ID NO: 102 of US20160369298; herein SEQ ID NO: 1698), CAGVVSVVSMRSRVCVNSGCAGCTDHCVVSRNSGTCVMSACA (SEQ ID NO: 103 of US20160369298; herein SEQ ID NO: 1699), AACTWCRVSVASMVSVHSDDTGTGSWSTKSACT (SEQ ID NO: 104 of US20160369298; herein SEQ ID NO: 1700), TTGTTGAACATCACCACGTGACGCACGTTC (SEQ ID NO: 256 of US20160369298; herein SEQ ID NO: 1701), TCCCCGTGGTTCTACTACATAATGTGGCCG (SEQ ID NO: 257 of US20160369298; herein SEQ ID NO: 1702), TTCCACACTCCGTTTTGGATAATGTTGAAC (SEQ ID NO: 258 of US20160369298; herein SEQ ID NO: 1703), AGGGACATCCCCAGCTCCATGCTGTGGTCG (SEQ ID NO: 259 of US20160369298; herein SEQ ID NO: 1704), AGGGACAACCCCTCCGACTCGCCCTAATCC (SEQ ID NO: 260 of US20160369298; herein SEQ ID NO: 1705), TCCTAGTAGAAGACACCCTCTCACTGCCCG (SEQ ID NO: 261 of US20160369298; herein SEQ ID NO: 1706), AGTACCATGTACACCCACTCTCCCAGTGCC (SEQ ID NO: 262 of US20160369298; herein SEQ ID NO: 1707), ATATGGACGTTCATGCTGATCACCATACCG (SEQ ID NO: 263 of US20160369298; herein SEQ ID NO: 1708), AGCAGGAGCTCCTTGGCCTCAGCGTGCGAG (SEQ ID NO: 264 of US20160369298; herein SEQ ID NO: 1709), ACAAGCAGCTTCACTATGACAACCACTGAC (SEQ ID NO: 265 of US20160369298; herein SEQ ID NO: 1710), CAGCCTAGGAACTGGCTTCCTGGACCCTGTTACCGCCAGCAGAGAGTCTCAAMA MMAVNSRVCSRSAACAACAACAGTRASTTCTCCTGGMMAGGAGCTACCAAGTAC CACCTCAATGGCAGAGACTCTCTGGTGAATCCCGGACCAGCTATGGCAAGCCAC RRGGACRRCRMSRRSARSTTTTTTCCTCAGAGCGGGGTTCTCATCTTTGGGAAGSA ARRCRSCRVSRVARVCRATRYCGMSNHCRVMVRSGTCATGATTACAGACGAAGA GGAGATCTGGAC (SEQ ID NO: 266 of US20160369298; herein SEQ ID NO: 1711), TGGGACAATGGCGGTCGTCTCTCAGAGTTKTKKT (SEQ ID NO: 267 of US20160369298; herein SEQ ID NO: 1712), AGAGGACCKKTCCTCGATGGTTCATGGTGGAGTTA (SEQ ID NO: 268 of US20160369298; herein SEQ ID NO: 1713), CCACTTAGGGCCTGGTCGATACCGTTCGGTG (SEQ ID NO: 269 of US20160369298;

herein SEQ ID NO: 1714), and TCTCGCCCCAAGAGTAGAAACCCTTCSTTYYG (SEQ ID NO: 270 of US20160369298; herein SEQ ID NO: 1715).

[0082] In some embodiments, the AAV serotype may comprise an ocular cell targeting peptide as described in International Patent Publication WO2016134375, the contents of which are herein incorporated by reference in their entirety, such as, but not limited to SEQ ID NO: 9, and SEQ ID NO:10 of WO2016134375. Further, any of the ocular cell targeting peptides or amino acids described in WO2016134375, may be inserted into any parent AAV serotype, such as, but not limited to, AAV2 (SEQ ID NO:8 of WO2016134375; herein SEQ ID NO: 1716), or AAV9 (SEQ ID NO: 11 of WO2016134375; herein SEQ ID NO: 1717). In some embodiments, modifications, such as insertions are made in AAV2 proteins at P34-A35, T138-A139, A139-P140, G453- T454, N587-R588, and/or R588-Q589. In certain embodiments, insertions are made at D384, G385, 1560, T561, N562, E563, E564, E565, N704, and/or Y705 of AAV9. The ocular cell targeting peptide may be, but is not limited to, any of the following amino acid sequences, GSTPPPM (SEQ ID NO: 1 of WO2016134375; herein SEQ ID NO: 1718), or GETRAPL (SEQ ID NO: 4 of WO2016134375; herein SEQ ID NO: 1719).

[0083] In some embodiments, the AAV serotype may be modified as described in the U.S. Patent Application Publication No. US20170145405 the contents of which are herein incorporated by reference in their entirety. AAV serotypes may include, modified AAV2 (e.g., modifications at Y444F, Y500F, Y730F and/or S662V), modified AAV3 (e.g., modifications at Y705F, Y731F and/or T492V), and modified AAV6 (e.g., modifications at S663V and/or T492V).

[0084] In some embodiments, the AAV serotype may be modified as described in the International Publication No. WO2017083722; the contents of which are herein incorporated by reference in their entirety. AAV serotypes may include, AAV1 (Y705+731F+T492V), AAV2 (Y444+500+730F+T491V), AAV3 (Y705+731F), AAV5, AAV 5(Y436+693+719F), AAV6 (VP3 variant Y705F/Y731F/T492V), AAV8 (Y733F), AAV9, AAV9 (VP3 variant Y731F), and AAV10 (Y733F).

[0085] In some embodiments, the AAV serotype may comprise, as described in International Patent Publication WO2017015102; the contents of which are herein incorporated by reference in their entirety, an engineered epitope comprising the amino acids SPAKFA (SEQ ID NO: 24 of WO2017015102; herein SEQ ID NO: 1720) or NKDKLN (SEQ ID NO:2 of WO2017015102; herein SEQ ID NO: 1721). The epitope may be inserted

in the region of amino acids 665 to 670 based on the numbering of the VP1 capsid of AAV8 (SEQ ID NO: 3 of WO2017015102) and/or residues 664 to 668 of AAV3B (SEQ ID NO: 3).

[0086] In one embodiment, the AAV serotype may be, or may have a sequence as described in International Patent Publication WO2017058892 (the contents of which are herein incorporated by reference in their entirety), such as, but not limited to, AAV variants with capsid proteins that may comprise a substitution at one or more (e.g., 2, 3, 4, 5, 6, or 7) of amino acid residues 262-268, 370- 379, 451 -459, 472-473, 493-500, 528-534, 547-552, 588- 597, 709-710, 716-722 of AAV1, in any combination, or the equivalent amino acid residues in AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAVrh8, AAVrh10, AAVrh32.33, bovine AAV or avian AAV. The amino acid substitution may be, but is not limited to, any of the amino acid sequences described in WO2017058892. In one embodiment, the AAV may comprise an amino acid substitution at residues 256L, 258K, 259Q, 261S, 263A, 264S, 265T, 266G, 272H, 385S, 386Q, S472R, V473D, N500E 547S, 709A, 710N, 716D, 717N, 718N, 720L, A456T, Q457T, N458Q, K459S, T492S, K493A, S586R, S587G, S588N, T589R and/or 722T of AAV1 (SEQ ID NO: l of WO2017058892) in any combination, 244N, 246Q, 248R, 249E, 250I, 251K, 252S, 253G, 254S, 255V, 256D, 263Y, 377E, 378N, 453L, 456R, 532Q, 533P, 535N, 536P, 537G, 538T, 539T, 540A, 541T, 542Y, 543L, 546N, 653V, 654P, 656S, 697Q, 698F, 704D, 705S, 706T, 707G, 708E, 709Y and/or 710R of AAV5 (SEQ ID NO:5 of WO2017058892) in any combination, 248R, 316V, 317Q, 318D, 319S, 443N, 530N, 531S, 532Q 533P, 534A, 535N, 540A, 541 T, 542Y, 543L, 545G, 546N, 697Q, 704D, 706T, 708E, 709Yand/or 710R of AAV5 (SEQ ID NO: 5 of WO2017058892) in any combination, 264S, 266G, 269N, 272H, 457Q, 588S and/or 589I of AAV6 (SEQ ID NO:6 WO2017058892) in any combination, 457T, 459N, 496G, 499N, 500N, 589Q, 590N and/or 592A of AAV8 (SEQ ID NO: 8 WO2017058892) in any combination,451I, 452N, 453G, 454S, 455G, 456Q, 457N and/or 458Q of AAV9 (SEQ ID NO: 9 WO2017058892) in any combination.

[0087] In some embodiments, the AAV may include a sequence of amino acids at positions 155, 156 and 157 of VP1 or at positions 17, 18, 19 and 20 of VP2, as described in International Publication No. WO 2017066764, the contents of which are herein incorporated by reference in their entirety. The sequences of amino acid may be, but not limited to, N-S-S, S-X-S, S-S-Y, N-X-S, N-S-Y, S-X-Y and N-X-Y, where N, X and Y are, but not limited to, independently non-serine, or non-threonine amino acids, wherein the AAV may be, but not limited to AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10,

AAV11 and AAV12. In some embodiments, the AAV may include a deletion of at least one amino acid at positions 156, 157 or 158 of VP1 or at positions 19, 20 or 21 of VP2, wherein the AAV may be, but not limited to AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11 and AAV12.

[0088] In one embodiment, the AAV may be a serotype generated by Cre-recombination-based AAV targeted evolution (CREATE) as described by Deverman et al., (Nature Biotechnology 34(2):204-209 (2016)), the contents of which are herein incorporated by reference in their entirety. In one embodiment, AAV serotypes generated in this manner have improved CNS transduction and/or neuronal and astrocytic tropism, as compared to other AAV serotypes. As non-limiting examples, the AAV serotype may include a peptide such as, but not limited to, PHP.B, PHP.B2, PHP.B3, PHP.A, PHP.S, G2A12, G2A15, G2A3, G2B4, and G2B5. In one embodiment, these AAV serotypes may be AAV9 (SEQ ID NO: 9 or 136) derivatives with a 7-amino acid insert between amino acids 588-589. Non-limiting examples of these 7-amino acid inserts include TLAVPFK (PHP.B; SEQ ID NO: 1260), SVSKPFL (PHP.B2; SEQ ID NO: 1268), FTLTTPK (PHP.B3; SEQ ID NO: 1269), YTLSQGW (PHP.A; SEQ ID NO: 1275), QAVRTSL (PHP.S; SEQ ID NO: 1319), LAKERLS (G2A3; SEQ ID NO: 1320), MNSTKNV (G2B4; SEQ ID NO: 1321), and/or VSGGHHS (G2B5; SEQ ID NO: 1322).

[0089] In one embodiment, the AAV serotype may be as described in Jackson et al (Frontiers in Molecular Neuroscience 9:154 (2016)), the contents of which are herein incorporated by reference in their entirety.

[0090] In the DNA and RNA sequences referenced and/or described herein, the single letter symbol has the following description: A for adenine; C for cytosine; G for guanine; T for thymine; U for Uracil; W for weak bases such as adenine or thymine; S for strong nucleotides such as cytosine and guanine; M for amino nucleotides such as adenine and cytosine; K for keto nucleotides such as guanine and thymine; R for purines adenine and guanine; Y for pyrimidine cytosine and thymine; B for any base that is not A (e.g., cytosine, guanine, and thymine); D for any base that is not C (e.g., adenine, guanine, and thymine); H for any base that is not G (e.g., adenine, cytosine, and thymine); V for any base that is not T (e.g., adenine, cytosine, and guanine); N for any nucleotide (which is not a gap); and Z is for zero.

[0091] In any of the amino acid sequences referenced and/or described herein, the single letter symbol has the following description: G (Gly) for Glycine; A (Ala) for Alanine; L

(Leu) for Leucine; M (Met) for Methionine; F (Phe) for Phenylalanine; W (Trp) for Tryptophan; K (Lys) for Lysine; Q (Gln) for Glutamine; E (Glu) for Glutamic Acid; S (Ser) for Serine; P (Pro) for Proline; V (Val) for Valine; I (Ile) for Isoleucine; C (Cys) for Cysteine; Y (Tyr) for Tyrosine; H (His) for Histidine; R (Arg) for Arginine; N (Asn) for Asparagine; D (Asp) for Aspartic Acid; T (Thr) for Threonine; B (Asx) for Aspartic acid or Asparagine; J (Xle) for Leucine or Isoleucine; O (Pyl) for Pyrrolysine; U (Sec) for Selenocysteine; X (Xaa) for any amino acid; and Z (Glx) for Glutamine or Glutamic acid.

[0092] In some embodiments, the AAV serotype is PHP.B or AAV9. In some embodiments, the AAV serotype is paired with a synapsin promoter to enhance neuronal transduction, as compared to when more ubiquitous promoters are used (i.e., CBA or CMV).

[0093] In one embodiment, the AAV serotype is a serotype comprising the AAVPHP.N (PHP.N) peptide, or a variant thereof.

[0094] In one embodiment the AAV serotypes is a serotype comprising the AAVPHP.B (PHP.B) peptide, or a variant thereof.

[0095] In one embodiment, the AAV serotype is a serotype comprising the AAVPHP.A (PHP.A) peptide, or a variant thereof.

[0096] In one embodiment, the AAV serotype is a serotype comprising the PHP.S peptide, or a variant thereof.

[0097] In one embodiment, the AAV serotype is a serotype comprising the PHP.B2 peptide, or a variant thereof.

[0098] In one embodiment, the AAV serotype is a serotype comprising the PHP.B3 peptide, or a variant thereof.

[0099] In one embodiment, the AAV serotype is a serotype comprising the G2B4 peptide, or a variant thereof.

[0100] In one embodiment, the AAV serotype is a serotype comprising the G2B5 peptide, or a variant thereof.

[0101] In one embodiment, the AAV serotype is VOY101, or a variant thereof. In one preferred embodiment, the VOY101 comprises an amino acid sequence of SEQ ID NO. 1. In another embodiment, the capsid sequence comprises a nucleic acid sequence of SEQ ID NO. 1809.

[0102] In one embodiment, the AAV serotype is VOY201, or a variant thereof. In one preferred embodiment, the VOY201 comprises a nucleic acid sequence of SEQ ID NO. 1810.

[0103] In one embodiment the AAV capsid is one that allows for blood brain barrier penetration following intravenous administration. Non-limiting examples of such AAV capsids include VOY101, VOY201 or AAV capsids comprising a peptide insert such as, but not limited to, AAVPHP.N (PHP.N), AAVPHP.B (PHP.B), PHP.S, G2A3, G2B4, G2B5, G2A12, G2A15, PHP.B2, PHP.B3, and AAVPHP.A (PHP.A). In one embodiment, the blood brain barrier penetrating capsid is VOY101. In one embodiment, the blood brain barrier penetrating capsid is VOY201. In one embodiment, the blood brain barrier penetrating capsid comprises the PHP.A peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the PHP.B peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the PHP.B2 peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the PHP.B3 peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the G2A3 peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the G2B4 peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the G2B5 peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the PHP.N peptide insert. In one embodiment, the blood brain barrier penetrating capsid comprises the PHP.S peptide insert.

Viral Genome Component: Inverted Terminal Repeats (ITRs)

[0104] The AAV particles of the present invention comprise a viral genome with at least one ITR region and a payload region. In one embodiment, the viral genome has two ITRs. These two ITRs flank the payload region at the 5' and 3' ends. The ITRs function as origins of replication comprising recognition sites for replication. ITRs comprise sequence regions which can be complementary and symmetrically arranged. ITRs incorporated into viral genomes of the invention may be comprised of naturally occurring polynucleotide sequences or recombinantly derived polynucleotide sequences.

[0105] The ITRs may be derived from the same serotype as the capsid, selected from any of the serotypes listed in Table 1, or a derivative thereof. The ITR may be of a different serotype than the capsid. In one embodiment, the AAV particle has more than one ITR. In a non-limiting example, the AAV particle has a viral genome comprising two ITRs. In one embodiment, the ITRs are of the same serotype as one another. In another embodiment, the ITRs are of different serotypes. Non-limiting examples include zero, one or both of the ITRs having the same serotype as the capsid. In one embodiment both ITRs of the viral genome of the AAV particle are AAV2 ITRs.

[0106] Independently, each ITR may be about 100 to about 150 nucleotides in length. An ITR may be about 100-105 nucleotides in length, 106-110 nucleotides in length, 111-115 nucleotides in length, 116-120 nucleotides in length, 121-125 nucleotides in length, 126-130 nucleotides in length, 131-135 nucleotides in length, 136-140 nucleotides in length, 141-145 nucleotides in length or 146-150 nucleotides in length. In one embodiment, the ITRs are 140-142 nucleotides in length. Non-limiting examples of ITR length are 102, 105, 130, 140, 141, 142, 145 nucleotides in length, and those having at least 90% identity thereto, or at least 95% identity thereto, or at least 98% identity thereto, or at least 99% identity thereto.

Viral Genome Component: Promoters

[0107] In one embodiment, the payload region of the viral genome comprises at least one element to enhance the transgene target specificity and expression (See e.g., Powell et al. Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy, 2015; the contents of which are herein incorporated by reference in their entirety). Non-limiting examples of elements to enhance the transgene target specificity and expression include promoters, endogenous miRNAs, post-transcriptional regulatory elements (PREs), polyadenylation (PolyA) signal sequences and upstream enhancers (USEs), CMV enhancers and introns.

[0108] A person skilled in the art may recognize that expression of the polypeptides of the invention in a target cell may require a specific promoter, including but not limited to, a promoter that is species specific, inducible, tissue-specific, or cell cycle-specific (Parr et al., *Nat. Med.*3:1145-9 (1997); the contents of which are herein incorporated by reference in their entirety).

[0109] In one embodiment, the promoter is deemed to be efficient when it drives expression of the polypeptide(s) encoded in the payload region of the viral genome of the AAV particle.

[0110] In one embodiment, the promoter is a promoter deemed to be efficient when it drives expression in the cell being targeted.

[0111] In one embodiment, the promoter is a promoter having a tropism for the cell being targeted.

[0112] In one embodiment, the promoter drives expression of the payload for a period of time in targeted tissues. Expression driven by a promoter may be for a period of 1 hour, 2, hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21

hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 2 weeks, 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 3 weeks, 22 days, 23 days, 24 days, 25 days, 26 days, 27 days, 28 days, 29 days, 30 days, 31 days, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more than 10 years. Expression may be for 1-5 hours, 1-12 hours, 1-2 days, 1-5 days, 1-2 weeks, 1-3 weeks, 1-4 weeks, 1-2 months, 1-4 months, 1-6 months, 2-6 months, 3-6 months, 3-9 months, 4-8 months, 6-12 months, 1-2 years, 1-5 years, 2-5 years, 3-6 years, 3-8 years, 4-8 years or 5-10 years. As a non-limiting example, the promoter is a weak promoter for sustained expression of a payload in nervous tissues.

[0113] In one embodiment, the promoter drives expression of the polypeptides of the invention for at least 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, 11 years, 12 years, 13 years, 14 years, 15 years, 16 years, 17 years, 18 years, 19 years, 20 years, 21 years, 22 years, 23 years, 24 years, 25 years, 26 years, 27 years, 28 years, 29 years, 30 years, 31 years, 32 years, 33 years, 34 years, 35 years, 36 years, 37 years, 38 years, 39 years, 40 years, 41 years, 42 years, 43 years, 44 years, 45 years, 46 years, 47 years, 48 years, 49 years, 50 years, 55 years, 60 years, 65 years, or more than 65 years.

[0114] Promoters may be naturally occurring or non-naturally occurring. Non-limiting examples of promoters include viral promoters, plant promoters and mammalian promoters. In some embodiments, the promoters may be human promoters. In some embodiments, the promoter may be truncated or mutated.

[0115] Promoters which drive or promote expression in most tissues include, but are not limited to, human elongation factor 1α-subunit (EF1α), cytomegalovirus (CMV) immediate-early enhancer and/or promoter, chicken β-actin (CBA) and its derivative CAG, β glucuronidase (GUSB), or ubiquitin C (UBC). Tissue-specific expression elements can be used to restrict expression to certain cell types such as, but not limited to, muscle specific promoters, B cell promoters, monocyte promoters, leukocyte promoters, macrophage promoters, pancreatic acinar cell promoters, endothelial cell promoters, lung tissue

promoters, astrocyte promoters, or nervous system promoters which can be used to restrict expression to neurons or subtypes of neurons, astrocytes, or oligodendrocytes.

[0116] Non-limiting examples of muscle-specific promoters include mammalian muscle creatine kinase (MCK) promoter, mammalian desmin (DES) promoter, mammalian troponin I (TNNI2) promoter, and mammalian skeletal alpha-actin (ASKA) promoter (see, e.g. U.S. Patent Application Publication No. US 20110212529, the contents of which are herein incorporated by reference in their entirety).

[0117] Non-limiting examples of tissue-specific expression elements for neurons include neuron-specific enolase (NSE), platelet-derived growth factor (PDGF), platelet-derived growth factor B-chain (PDGF-β), synapsin (Syn), methyl-CpG binding protein 2 (MeCP2), Ca^{2+}/calmodulin-dependent protein kinase II (CaMKII), metabotropic glutamate receptor 2 (mGluR2), neurofilament light (NFL) or heavy (NFH), β-globin minigene nβ2, preproenkephalin (PPE), enkephalin (Enk) and excitatory amino acid transporter 2 (EAAT2) promoters. Non-limiting examples of tissue-specific expression elements for astrocytes include glial fibrillary acidic protein (GFAP) and EAAT2 promoters. A non-limiting example of a tissue-specific expression element for oligodendrocytes includes the myelin basic protein (MBP) promoter.

[0118] In one embodiment, the promoter may be less than 1 kb. The promoter may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800 nucleotides. The promoter may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800.

[0119] In one embodiment, the promoter may be a combination of two or more components of the same or different starting or parental promoters such as, but not limited to, CMV and CBA. Each component may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800. Each component may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500,

300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800. In one embodiment, the promoter is a combination of a 382 nucleotide CMV-enhancer sequence and a 260 nucleotide CBA-promoter sequence.

[0120] In one embodiment, the viral genome comprises a ubiquitous promoter. Non-limiting examples of ubiquitous promoters include CMV, CBA (including derivatives CAG, CBh, etc.), EF-1α, PGK, UBC, GUSB (hGBp), and UCOE (promoter of HNRPA2B1-CBX3).

[0121] Yu et al. (Molecular Pain 2011, 7:63; the contents of which are herein incorporated by reference in their entirety) evaluated the expression of eGFP under the CAG, EFIα, PGK and UBC promoters in rat DRG cells and primary DRG cells using lentiviral vectors and found that UBC showed weaker expression than the other 3 promoters and only 10-12% glial expression was seen for all promoters. Soderblom et al. (E. Neuro 2015, 2(2): ENEURO.0001-15; the contents of which are herein incorporated by reference in their entirety) evaluated the expression of eGFP in AAV8 with CMV and UBC promoters and AAV2 with the CMV promoter after injection in the motor cortex. Intranasal administration of a plasmid containing a UBC or EFIα promoter showed a sustained airway expression greater than the expression with the CMV promoter (See e.g., Gill et al., Gene Therapy 2001, Vol. 8, 1539-1546; the contents of which are herein incorporated by reference in their entirety). Husain et al. (Gene Therapy 2009, 16(7): 927-932; the contents of which are herein incorporated by reference in their entirety) evaluated an HβH construct with a hGUSB promoter, a HSV-1LAT promoter and an NSE promoter and found that the HβH construct showed weaker expression than NSE in mouse brain. Passini and Wolfe (J. Virol. 2001, 12382-12392, the contents of which are herein incorporated by reference in their entirety) evaluated the long term effects of the HβH vector following an intraventricular injection in neonatal mice and found that there was sustained expression for at least 1 year. Low expression in all brain regions was found by Xu et al. (Gene Therapy 2001, 8, 1323-1332; the contents of which are herein incorporated by reference in their entirety) when NFL and NFH promoters were used as compared to the CMV-lacZ, CMV-luc, EF, GFAP, hENK, nAChR, PPE, PPE + wpre, NSE (0.3 kb), NSE (1.8 kb) and NSE (1.8 kb + wpre). Xu et al. found that the promoter activity in descending order was NSE (1.8 kb), EF, NSE (0.3 kb), GFAP, CMV, hENK, PPE, NFL and NFH. NFL is a 650-nucleotide promoter and NFH is a 920 nucleotide promoter which are both absent in the liver but NFH is abundant in the sensory proprioceptive neurons, brain and spinal cord and NFH is present in the heart. SCN8A is a

470 nucleotide promoter which expresses throughout the DRG, spinal cord and brain with particularly high expression seen in the hippocampal neurons and cerebellar Purkinje cells, cortex, thalamus and hypothalamus (See e.g., Drews et al. *Identification of evolutionary conserved, functional noncoding elements in the promoter region of the sodium channel gene SCN8A,* Mamm Genome (2007) 18:723-731; and Raymond et al. *Expression of Alternatively Spliced Sodium Channel α-subunit genes,* Journal of Biological Chemistry (2004) 279(44) 46234-46241; the contents of each of which are herein incorporated by reference in their entireties).

[0122] Any of the promoters taught by the aforementioned Yu, Soderblom, Gill, Husain, Passini, Xu, Drews or Raymond may be used in the present inventions.

[0123] In one embodiment, the promoter is not cell specific.

[0124] In one embodiment, the promoter is a ubiquitin c (UBC) promoter. The UBC promoter may have a size of 300-350 nucleotides. As a non-limiting example, the UBC promoter is 332 nucleotides in length.

[0125] In one embodiment, the promoter is a β-glucuronidase (GUSB) promoter. The GUSB promoter may have a size of 350-400 nucleotides. As a non-limiting example, the GUSB promoter is 378 nucleotides in length.

[0126] In one embodiment, the promoter is a neurofilament light (NFL) promoter. The NFL promoter may have a size of 600-700 nucleotides. As a non-limiting example, the NFL promoter is 650 nucleotides in length.

[0127] In one embodiment, the promoter is a neurofilament heavy (NFH) promoter. The NFH promoter may have a size of 900-950 nucleotides. As a non-limiting example, the NFH promoter is 920 nucleotides in length.

[0128] In one embodiment, the promoter is a SCN8A promoter. The SCN8A promoter may have a size of 450-500 nucleotides. As a non-limiting example, the SCN8A promoter is 470 nucleotides in length.

[0129] In one embodiment, the promoter is a frataxin (FXN) promoter.

[0130] In one embodiment, the promoter is a phosphoglycerate kinase 1 (PGK) promoter.

[0131] In one embodiment, the promoter is a chicken β-actin (CBA) promoter.

[0132] In one embodiment, the promoter is a cytomegalovirus (CMV) promoter.

[0133] In one embodiment, the promoter is a H1 promoter.

[0134] In one embodiment, the promoter is an engineered promoter.

[0135] In one embodiment, the promoter is a liver or a skeletal muscle promoter. Non-limiting examples of liver promoters include human α-1-antitrypsin (hAAT) and thyroxine binding globulin (TBG). Non-limiting examples of skeletal muscle promoters include Desmin, MCK or synthetic C5-12.

[0136] In one embodiment, the promoter is a RNA pol III promoter. As a non-limiting example, the RNA pol III promoter is U6. As a non-limiting example, the RNA pol III promoter is H1.

[0137] In one embodiment, the promoter is a cardiomyocyte-specific promoter. Non-limiting examples of cardiomyocyte-specific promoters include αMHC, cTnT, and CMV-MLC2k.

[0138] In one embodiment, the viral genome comprises two promoters. As a non-limiting example, the promoters are an EF1α promoter and a CMV promoter.

[0139] In one embodiment, the viral genome comprises an enhancer element, a promoter and/or a 5'UTR intron. The enhancer element, also referred to herein as an "enhancer," may be, but is not limited to, a CMV enhancer, the promoter may be, but is not limited to, a CMV, CBA, UBC, GUSB, NSE, Synapsin, MeCP2, and GFAP promoter and the 5'UTR/intron may be, but is not limited to, SV40, and CBA-MVM. As a non-limiting example, the enhancer, promoter and/or intron used in combination may be: (1) CMV enhancer, CMV promoter, SV40 5'UTR intron; (2) CMV enhancer, CBA promoter, SV 40 5'UTR intron; (3) CMV enhancer, CBA promoter, CBA-MVM 5'UTR intron; (4) UBC promoter; (5) GUSB promoter; (6) NSE promoter; (7) Synapsin promoter; (8) MeCP2 promoter and (9) GFAP promoter.

[0140] In one embodiment, the viral genome comprises an engineered promoter.

[0141] In another embodiment, the viral genome comprises a promoter from a naturally expressed protein.

[0142] Viral Genome Component: Untranslated Regions (UTRs)

[0143] By definition, wild type untranslated regions (UTRs) of a gene are transcribed but not translated. Generally, the 5' UTR starts at the transcription start site and ends at the start codon and the 3' UTR starts immediately following the stop codon and continues until the termination signal for transcription.

[0144] Features typically found in abundantly expressed genes of specific target organs may be engineered into UTRs to enhance the stability and protein production. As a non-limiting example, a 5' UTR from mRNA normally expressed in the liver (e.g., albumin,

serum amyloid A, Apolipoprotein A/B/E, transferrin, alpha fetoprotein, erythropoietin, or Factor VIII) may be used in the viral genomes of the AAV particles of the invention to enhance expression in hepatic cell lines or liver.

[0145] While not wishing to be bound by theory, wild-type 5′ untranslated regions (UTRs) include features which play roles in translation initiation. Kozak sequences, which are commonly known to be involved in the process by which the ribosome initiates translation of many genes, are usually included in 5' UTRs. Kozak sequences have the consensus CCR(A/G)CCAUGG, where R is a purine (adenine or guanine) three bases upstream of the start codon (ATG), which is followed by another 'G'.

[0146] In one embodiment, the 5'UTR in the viral genome includes a Kozak sequence.

[0147] In one embodiment, the 5'UTR in the viral genome does not include a Kozak sequence.

[0148] While not wishing to be bound by theory, wild-type 3′ UTRs are known to have stretches of Adenosines and Uridines embedded therein. These AU rich signatures are particularly prevalent in genes with high rates of turnover. Based on their sequence features and functional properties, the AU rich elements (AREs) can be separated into three classes (Chen et al, 1995, the contents of which are herein incorporated by reference in its entirety): Class I AREs, such as, but not limited to, c-Myc and MyoD, contain several dispersed copies of an AUUUA motif within U-rich regions. Class II AREs, such as, but not limited to, GM-CSF and TNF-a, possess two or more overlapping UUAUUUA(U/A)(U/A) nonamers. Class III ARES, such as, but not limited to, c-Jun and Myogenin, are less well defined. These U rich regions do not contain an AUUUA motif. Most proteins binding to the AREs are known to destabilize the messenger, whereas members of the ELAV family, most notably HuR, have been documented to increase the stability of mRNA. HuR binds to AREs of all the three classes. Engineering the HuR specific binding sites into the 3′ UTR of nucleic acid molecules will lead to HuR binding and thus, stabilization of the message *in vivo*.

[0149] Introduction, removal or modification of 3′ UTR AU rich elements (AREs) can be used to modulate the stability of polynucleotides. When engineering specific polynucleotides, e.g., payload regions of viral genomes, one or more copies of an ARE can be introduced to make polynucleotides less stable and thereby curtail translation and decrease production of the resultant protein. Likewise, AREs can be identified and removed or mutated to increase the intracellular stability and thus increase translation and production of the resultant protein.

[0150] In one embodiment, the 3' UTR of the viral genome may include an oligo(dT) sequence for templated addition of a poly-A tail.

[0151] In one embodiment, the viral genome may include at least one miRNA seed, binding site or full sequence. microRNAs (or miRNA or miR) are 19-25 nucleotide noncoding RNAs that bind to the sites of nucleic acid targets and down-regulate gene expression either by reducing nucleic acid molecule stability or by inhibiting translation. A microRNA sequence comprises a "seed" region, i.e., a sequence in the region of positions 2-8 of the mature microRNA, which sequence has perfect Watson-Crick complementarity to the miRNA target sequence of the nucleic acid.

[0152] In one embodiment, the viral genome may be engineered to include, alter or remove at least one miRNA binding site, full sequence or seed region.

[0153] Any UTR from any gene known in the art may be incorporated into the viral genome of the AAV particle. These UTRs, or portions thereof, may be placed in the same orientation as in the gene from which they were selected or they may be altered in orientation or location. In one embodiment, the UTR used in the viral genome of the AAV particle may be inverted, shortened, lengthened, made with one or more other 5′ UTRs or 3′ UTRs known in the art. As used herein, the term "altered" as it relates to a UTR, means that the UTR has been changed in some way in relation to a reference sequence. For example, a 3′ or 5′ UTR may be altered relative to a wild type or native UTR by the change in orientation or location as taught above or may be altered by the inclusion of additional nucleotides, deletion of nucleotides, swapping or transposition of nucleotides.

[0154] In one embodiment, the viral genome of the AAV particle comprises at least one artificial UTR which is not a variant of a wild type UTR.

[0155] In one embodiment, the viral genome of the AAV particle comprises UTRs which have been selected from a family of transcripts whose proteins share a common function, structure, feature or property.

[0156] Viral Genome Component: Polyadenylation Sequence

[0157] In one embodiment, the viral genome of the AAV particles of the present invention comprise at least one polyadenylation sequence. The viral genome of the AAV particle may comprise a polyadenylation sequence between the 3' end of the payload coding sequence and the 5' end of the 3'ITR.

[0158] In one embodiment, the polyadenylation sequence or "polyA sequence" may range from absent to about 500 nucleotides in length. The polyadenylation sequence may be, but is

not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, and 500 nucleotides in length.

[0159] In one embodiment, the polyadenylation sequence is 50-100 nucleotides in length.

[0160] In one embodiment, the polyadenylation sequence is 50-150 nucleotides in length.

[0161] In one embodiment, the polyadenylation sequence is 50-160 nucleotides in length.

[0162] In one embodiment, the polyadenylation sequence is 50-200 nucleotides in length.

[0163] In one embodiment, the polyadenylation sequence is 60-100 nucleotides in length.

[0164] In one embodiment, the polyadenylation sequence is 60-150 nucleotides in length.

[0165] In one embodiment, the polyadenylation sequence is 60-160 nucleotides in length.

[0166] In one embodiment, the polyadenylation sequence is 60-200 nucleotides in length.

[0167] In one embodiment, the polyadenylation sequence is 70-100 nucleotides in length.

[0168] In one embodiment, the polyadenylation sequence is 70-150 nucleotides in length.

[0169] In one embodiment, the polyadenylation sequence is 70-160 nucleotides in length.

[0170] In one embodiment, the polyadenylation sequence is 70-200 nucleotides in length.

[0171] In one embodiment, the polyadenylation sequence is 80-100 nucleotides in length.

[0172] In one embodiment, the polyadenylation sequence is 80-150 nucleotides in length.

[0173] In one embodiment, the polyadenylation sequence is 80-160 nucleotides in length.

[0174] In one embodiment, the polyadenylation sequence is 80-200 nucleotides in length.

[0175] In one embodiment, the polyadenylation sequence is 90-100 nucleotides in length.

[0176] In one embodiment, the polyadenylation sequence is 90-150 nucleotides in length.

[0177] In one embodiment, the polyadenylation sequence is 90-160 nucleotides in length.

[0178] In one embodiment, the polyadenylation sequence is 90-200 nucleotides in length.

[0179] Viral Genome Component: Introns

[0180] In one embodiment, the viral genome of the AAV particles of the present invention comprises at least one element to enhance the transgene target specificity and expression (See e.g., Powell et al. *Viral Expression Cassette Elements to Enhance Transgene Target Specificity and Expression in Gene Therapy*, Discov. Med, 2015, 19(102): 49-57; the contents of which are herein incorporated by reference in their entirety) such as an intron. Non-limiting examples of introns include, MVM (67-97 bps), F.IX truncated intron 1 (300 bps), β-globin SD/immunoglobulin heavy chain splice acceptor (250 bps), adenovirus splice donor/immunoglobin splice acceptor (500 bps), SV40 late splice donor/splice acceptor (19S/16S) (180 bps) and hybrid adenovirus splice donor/IgG splice acceptor (230 bps).

[0181] In one embodiment, the intron or intron portion may be 100-500 nucleotides in length. The intron may have a length of 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490 or 500 nucleotides. The intron may have a length between 80-100, 80-120, 80-140, 80-160, 80-180, 80-200, 80-250, 80-300, 80-350, 80-400, 80-450, 80-500, 200-300, 200-400, 200-500, 300-400, 300-500, or 400-500 nucleotides.

Viral Genome Component: Stuffer sequences

[0182] In one embodiment, the viral genome of the AAV particles of the present invention comprises at least one element to improve packaging efficiency and expression, such as a stuffer or filler sequence. Non-limiting examples of stuffer sequences include albumin and/or alpha-1 antitrypsin. Any known viral, mammalian, or plant sequence may be manipulated for use as a stuffer sequence.

[0183] In one embodiment, the stuffer or filler sequence may be from about 100-3500 nucleotides in length. The stuffer sequence may have a length of about 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900 or 3000 nucleotides.

Viral Genome Component: miRNA

[0184] In one embodiment, the viral genome comprises at least one sequence encoding a miRNA to reduce the expression of the transgene is a specific tissue. miRNAs and their targeted tissues are well known in the art. As a non-limiting example, a miR-122 miRNA may be encoded in the viral genome to reduce the expression of the viral genome in the liver.

AAV Production

[0185] The present invention provides methods for the generation of parvoviral particles, *e.g.* AAV particles, by viral genome replication in a viral replication cell.

[0186] In accordance with the invention, the viral genome comprising a payload region will be incorporated into the AAV particle produced in the viral replication cell. Methods of making AAV particles are well known in the art and are described in e.g., U.S. Patent Nos. US6204059, US5756283, US6258595, US6261551, US6270996, US6281010, US6365394, US6475769, US6482634, US6485966, US6943019, US6953690, US7022519, US7238526, US7291498 and US7491508, US5064764, US6194191, US6566118, US8137948; or International Publication Nos. WO1996039530, WO1998010088, WO1999014354, WO1999015685, WO1999047691, WO2000055342, WO2000075353 and WO2001023597; Methods In Molecular Biology, ed. Richard, Humana Press, NJ (1995); O'Reilly et al., Baculovirus Expression Vectors, A Laboratory Manual, Oxford Univ. Press (1994); Samulski et al.,*J. Vir.*63:3822-8 (1989); Kajigaya et al., *Proc. Nat'l. Acad. Sci. USA* 88: 4646-50 (1991); Ruffing et al., *J. Vir.* 66:6922-30 (1992); Kimbauer et al., *Vir.*, 219:37-44 (1996); Zhao et al., *Vir.*272:382-93 (2000); the contents of each of which are herein incorporated by reference in their entirety. In one embodiment, the AAV particles are made using the methods described in International Patent Publication WO2015191508, the contents of which are herein incorporated by reference in their entirety.

[0187] Viral replication cells commonly used for production of recombinant AAV viral particles include but are not limited to HEK293 cells, COS cells, HeLa cells, KB cells, and other mammalian cell lines as described in U.S. Patent. Nos. US6156303, US5387484, US5741683, US5691176, and US5688676; U.S. Patent Application Publication No. 2002/0081721, and International Patent Publication Nos. WO 2000047757, WO 2000024916, and WO 1996017947, the contents of each of which are herein incorporated by reference in their entirety.

[0188] In some embodiments, the present invention provides a method for producing an AAV particle having enhanced (increased, improved) transduction efficiency comprising the steps of: 1) co-transfecting competent bacterial cells with a bacmid vector and either a viral construct vector and/or AAV payload construct vector, 2) isolating the resultant viral construct expression vector and AAV payload construct expression vector and separately transfecting viral replication cells, 3) isolating and purifying resultant payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, 4) co-infecting a viral replication cell with both the AAV payload and viral construct particles comprising viral construct expression vector or AAV payload construct expression vector, and 5) harvesting and purifying the AAV particle comprising a viral genome.

[0189] In some embodiments, the present invention provides a method for producing an AAV particle comprising the steps of 1) simultaneously co-transfecting mammalian cells, such as, but not limited to HEK293 cells, with a payload region, a construct expressing rep and cap genes and a helper construct, 2) harvesting and purifying the AAV particle comprising a viral genome.

[0190] In some embodiments, the viral genome of the AAV particle of the invention optionally encodes a selectable marker. The selectable marker may comprise a cell-surface marker, such as any protein expressed on the surface of the cell including, but not limited to receptors, CD markers, lectins, integrins, or truncated versions thereof.

[0191] In some embodiments, selectable marker reporter genes are described in International Publication Nos. WO 1996023810 and WO 1996030540; Heim et al., Current Biology 2:178-182 (1996); Heim et al., Proc. Natl. Acad. Sci. USA (1995); or Heim et al., Science 373:663-664 (1995);, the contents of each of which are incorporated herein by reference in their entirety.

Genome Size

[0192] In one embodiment, the AAV particle which comprises a payload described herein may be single stranded or double stranded viral genome. The size of the viral genome may be small, medium, large or the maximum size. Additionally, the viral genome may comprise a promoter and a polyA tail.

[0193] In one embodiment, the viral genome which comprises a payload described herein may be a small single stranded viral genome. A small single stranded viral genome may be 2.1 to 3.5 kb in size such as about 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, and 3.5 kb in size. As a non-limiting example, the small single stranded viral genome may be 3.2 kb in size. As another non-limiting example, the small single stranded viral genome may be 2.2 kb in size. Additionally, the viral genome may comprise a promoter and a polyA tail.

[0194] In one embodiment, the viral genome which comprises a payload described herein may be a small double stranded viral genome. A small double stranded viral genome may be 1.3 to 1.7 kb in size such as about 1.3, 1.4, 1.5, 1.6, and 1.7 kb in size. As a non-limiting example, the small double stranded viral genome may be 1.6 kb in size. Additionally, the viral genome may comprise a promoter and a polyA tail.

[0195] In one embodiment, the viral genome which comprises a payload described herein e.g., polynucleotide, siRNA or dsRNA, or miRNA may be a medium single stranded viral genome. A medium single stranded viral genome may be 3.6 to 4.3 kb in size such as about 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2 and 4.3 kb in size. As a non-limiting example, the medium single stranded viral genome may be 4.0 kb in size. Additionally, the viral genome may comprise a promoter and a polyA tail.

[0196] In one embodiment, the viral genome which comprises a payload described herein may be a medium double stranded viral genome. A medium double stranded viral genome may be 1.8 to 2.1 kb in size such as about 1.8, 1.9, 2.0, and 2.1 kb in size. As a non-limiting example, the medium double stranded viral genome may be 2.0 kb in size. Additionally, the viral genome may comprise a promoter and a polyA tail.

[0197] In one embodiment, the viral genome which comprises a payload described herein may be a large single stranded viral genome. A large single stranded viral genome may be 4.4 to 6.0 kb in size such as about 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9 and 6.0 kb in size. As a non-limiting example, the large single stranded viral genome may be 4.7 kb in size. As another non-limiting example, the large single stranded viral genome may be 4.8 kb in size. As yet another non-limiting example, the large single

stranded viral genome may be 6.0 kb in size. Additionally, the viral genome may comprise a promoter and a polyA tail.

[0198] In one embodiment, the viral genome which comprises a payload described herein may be a large double stranded viral genome. A large double stranded viral genome may be 2.2 to 3.0 kb in size such as about 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9 and 3.0 kb in size. As a non-limiting example, the large double stranded viral genome may be 2.4 kb in size. Additionally, the viral genome may comprise a promoter and a polyA tail.

Payloads of the Invention

[0199] The AAV particles of the present disclosure comprise at least one payload region. As used herein, "payload" or "payload region" refers to one or more polynucleotides or polynucleotide regions encoded by or within a viral genome or an expression product of such polynucleotide or polynucleotide region, e.g., a transgene, a polynucleotide encoding a polypeptide or multi-polypeptide or a modulatory nucleic acid or regulatory nucleic acid. Payloads of the present invention typically encode polypeptides or fragments or variants thereof.

[0200] The payload region may be constructed in such a way as to reflect a region similar to or mirroring the natural organization of an mRNA.

[0201] The payload region may comprise a combination of coding and non-coding nucleic acid sequences.

[0202] In some embodiments, the AAV payload region may encode a coding or non-coding RNA.

[0203] In one embodiment, the AAV particle comprises a viral genome with a payload region comprising nucleic acid sequences encoding more than one polypeptide of interest. In such an embodiment, a viral genome encoding more than one polypeptide may be replicated and packaged into a viral particle. A target cell transduced with a viral particle comprising more than one polypeptide may express each of the polypeptides in a single cell.

[0204] In one embodiment, the AAV payload region may comprise the components as shown in FIG. 1. The payload region **110** is located within the viral genome **100**. At the 5' and/or the 3' end of the payload region **110** there may be at least one inverted terminal repeat (ITR) **120**. In one embodiment, within the payload region, there is a promoter region **130**, an intron region **140** and a coding region **150**.

[0205] Where the AAV particle payload region encodes a polypeptide, the polypeptide may be a peptide or protein. As a non-limiting example, the payload region may encode at

least one allele of apolipoprotein E (APOE) such as, but not limited to ApoE2, ApoE3 and/or ApoE4. As a second non-limiting example, the payload region may encode a human or a primate frataxin protein, or fragment or variant thereof. As another non-limiting example, the payload region may encode an antibody, or a fragment thereof. As another non-limiting example, the payload region may encode human AADC, or fragment or variant thereof. As another non-limiting example, the payload region may encode human ATP2A2, or fragment or variant thereof. As further another example, the payload region may encode human S100A1, or fragment or variant thereof. The AAV viral genomes encoding polypeptides described herein may be useful in the fields of human disease, viruses, infections veterinary applications and a variety of *in vivo* and *in vitro* settings.

[0206] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of neurological diseases and/or disorders.

[0207] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of tauopathy.

[0208] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Alzheimer's Disease.

[0209] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Friedreich's ataxia, or any disease stemming from a loss or partial loss of frataxin protein.

[0210] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Parkinson's Disease.

[0211] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Amyotrophic lateral sclerosis.

[0212] In some embodiments, the AAV particles are useful in the field of medicine for the treatment, prophylaxis, palliation or amelioration of Huntington's Disease.

[0213] In some embodiments, the AAV particles are useful in the field of medicine for treatment, prophylaxis, palliation or amelioration of cardiovascular diseases.

The nature of the polypeptides and variants

[0214] Amino acid sequences encoded by payload regions of the viral genomes of the invention may be translated as a whole polypeptide, a plurality of polypeptides or fragments of polypeptides, which independently may be encoded by one or more nucleic acids, fragments of nucleic acids or variants of any of the aforementioned. As used herein, "polypeptide" means a polymer of amino acid residues (natural or unnatural) linked together

most often by peptide bonds. The term, as used herein, refers to proteins, polypeptides, and peptides of any size, structure, or function. In some instances, the polypeptide encoded is smaller than about 50 amino acids and the polypeptide is then termed a peptide. If the polypeptide is a peptide, it will be at least about 2, 3, 4, or at least 5 amino acid residues long. Thus, polypeptides include gene products, naturally occurring polypeptides, synthetic polypeptides, homologs, orthologs, paralogs, fragments and other equivalents, variants, and analogs of the foregoing. A polypeptide may be a single molecule or may be a multi-molecular complex such as a dimer, trimer or tetramer. They may also comprise single chain or multichain polypeptides and may be associated or linked. The term polypeptide may also apply to amino acid polymers in which one or more amino acid residues are an artificial chemical analogue of a corresponding naturally occurring amino acid.

[0215] The term “polypeptide variant” refers to molecules which differ in their amino acid sequence from a native or reference sequence. The amino acid sequence variants may possess substitutions, deletions, and/or insertions at certain positions within the amino acid sequence, as compared to a native or reference sequence. Ordinarily, variants will possess at least about 50% identity (homology) to a native or reference sequence, and preferably, they will be at least about 80%, more preferably at least about 90% identical (homologous) to a native or reference sequence.

[0216] In some embodiments “variant mimics” are provided. As used herein, the term “variant mimic” is one which contains one or more amino acids which would mimic an activated sequence. For example, glutamate may serve as a mimic for phosphoro-threonine and/or phosphoro-serine. Alternatively, variant mimics may result in deactivation or in an inactivated product containing the mimic, e.g., phenylalanine may act as an inactivating substitution for tyrosine; or alanine may act as an inactivating substitution for serine.

[0217] The term "amino acid sequence variant" refers to molecules with some differences in their amino acid sequences as compared to a native or starting sequence. The amino acid sequence variants may possess substitutions, deletions, and/or insertions at certain positions within the amino acid sequence. “Native” or “starting” sequence should not be confused with a wild type sequence. As used herein, a native or starting sequence is a relative term referring to an original molecule against which a comparison may be made. “Native” or “starting” sequences or molecules may represent the wild-type (that sequence found in nature) but do not have to be the wild-type sequence.

[0218] Ordinarily, variants will possess at least about 70% homology to a native sequence, and preferably, they will be at least about 80%, more preferably at least about 90% homologous to a native sequence. "Homology" as it applies to amino acid sequences is defined as the percentage of residues in the candidate amino acid sequence that are identical with the residues in the amino acid sequence of a second sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology. Methods and computer programs for the alignment are well known in the art. It is understood that homology depends on a calculation of percent identity but may differ in value due to gaps and penalties introduced in the calculation.

[0219] By "homologs" as it applies to amino acid sequences is meant the corresponding sequence of other species having substantial identity to a second sequence of a second species.

[0220] "Analogs" is meant to include polypeptide variants which differ by one or more amino acid alterations, e.g., substitutions, additions or deletions of amino acid residues that still maintain the properties of the parent polypeptide.

[0221] Sequence tags or amino acids, such as one or more lysines, can be added to the peptide sequences of the invention (e.g., at the N-terminal or C-terminal ends). Sequence tags can be used for peptide purification or localization. Lysines can be used to increase peptide solubility or to allow for biotinylation. Alternatively, amino acid residues located at the carboxy and amino terminal regions of the amino acid sequence of a peptide or protein may optionally be deleted providing for truncated sequences. Certain amino acids (e.g., C-terminal or N-terminal residues) may alternatively be deleted depending on the use of the sequence, as for example, expression of the sequence as part of a larger sequence which is soluble, or linked to a solid support.

[0222] "Substitutional variants" when referring to proteins are those that have at least one amino acid residue in a native or starting sequence removed and a different amino acid inserted in its place at the same position. The substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more amino acids have been substituted in the same molecule.

[0223] As used herein the term "conservative amino acid substitution" refers to the substitution of an amino acid that is normally present in the sequence with a different amino acid of similar size, charge, or polarity. Examples of conservative substitutions include the substitution of a non-polar (hydrophobic) residue such as isoleucine, valine and leucine for

another non-polar residue. Likewise, examples of conservative substitutions include the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, and between glycine and serine. Additionally, the substitution of a basic residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue such as aspartic acid or glutamic acid for another acidic residue are additional examples of conservative substitutions. Examples of non-conservative substitutions include the substitution of a non-polar (hydrophobic) amino acid residue such as isoleucine, valine, leucine, alanine, methionine for a polar (hydrophilic) residue such as cysteine, glutamine, glutamic acid or lysine and/or a polar residue for a non-polar residue.

[0224] "Insertional variants" when referring to proteins are those with one or more amino acids inserted immediately adjacent to an amino acid at a particular position in a native or starting sequence. "Immediately adjacent" to an amino acid means connected to either the alpha-carboxy or alpha-amino functional group of the amino acid.

[0225] "Deletional variants" when referring to proteins, are those with one or more amino acids in the native or starting amino acid sequence removed. Ordinarily, deletional variants will have one or more amino acids deleted in a particular region of the molecule.

[0226] As used herein, the term "derivative" is used synonymously with the term "variant" and refers to a molecule that has been modified or changed in any way relative to a reference molecule or starting molecule. In some embodiments, derivatives include native or starting proteins that have been modified with an organic proteinaceous or non-proteinaceous derivatizing agent, and post-translational modifications. Covalent modifications are traditionally introduced by reacting targeted amino acid residues of the protein with an organic derivatizing agent that is capable of reacting with selected side-chains or terminal residues, or by harnessing mechanisms of post-translational modifications that function in selected recombinant host cells. The resultant covalent derivatives are useful in programs directed at identifying residues important for biological activity, for immunoassays, or for the preparation of anti-protein antibodies for immunoaffinity purification of the recombinant glycoprotein. Such modifications are within the ordinary skill in the art and are performed without undue experimentation.

[0227] Certain post-translational modifications are the result of the action of recombinant host cells on the expressed polypeptide. Glutaminyl and asparaginyl residues are frequently post-translationally deamidated to the corresponding glutamyl and aspartyl residues.

Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues may be present in the proteins used in accordance with the present invention.

[0228] Other post-translational modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)).

[0229] "Features" when referring to proteins are defined as distinct amino acid sequence-based components of a molecule. Features of the proteins of the present invention include surface manifestations, local conformational shape, folds, loops, half-loops, domains, half-domains, sites, termini or any combination thereof.

[0230] As used herein when referring to proteins the term "surface manifestation" refers to a polypeptide based component of a protein appearing on an outermost surface.

[0231] As used herein when referring to proteins the term "local conformational shape" means a polypeptide based structural manifestation of a protein which is located within a definable space of the protein.

[0232] As used herein when referring to proteins the term "fold" means the resultant conformation of an amino acid sequence upon energy minimization. A fold may occur at the secondary or tertiary level of the folding process. Examples of secondary level folds include beta sheets and alpha helices. Examples of tertiary folds include domains and regions formed due to aggregation or separation of energetic forces. Regions formed in this way include hydrophobic and hydrophilic pockets, and the like.

[0233] As used herein the term "turn" as it relates to protein conformation means a bend which alters the direction of the backbone of a peptide or polypeptide and may involve one, two, three or more amino acid residues.

[0234] As used herein when referring to proteins the term "loop" refers to a structural feature of a peptide or polypeptide which reverses the direction of the backbone of a peptide or polypeptide and comprises four or more amino acid residues. Oliva et al. have identified at least 5 classes of protein loops (J. Mol Biol, 266 (4): 814-830; 1997).

[0235] As used herein when referring to proteins the term "half-loop" refers to a portion of an identified loop having at least half the number of amino acid residues as the loop from which it is derived. It is understood that loops may not always contain an even number of amino acid residues. Therefore, in those cases where a loop contains or is identified to comprise an odd number of amino acids, a half-loop of the odd-numbered loop will comprise

the whole number portion or next whole number portion of the loop (number of amino acids of the loop/2+/-0.5 amino acids). For example, a loop identified as a 7 amino acid loop could produce half-loops of 3 amino acids or 4 amino acids (7/2=3.5+/-0.5 being 3 or 4).

[0236] As used herein when referring to proteins the term "domain" refers to a motif of a polypeptide having one or more identifiable structural or functional characteristics or properties (e.g., binding capacity, serving as a site for protein-protein interactions).

[0237] As used herein when referring to proteins the term "half-domain" means portion of an identified domain having at least half the number of amino acid residues as the domain from which it is derived. It is understood that domains may not always contain an even number of amino acid residues. Therefore, in those cases where a domain contains or is identified to comprise an odd number of amino acids, a half-domain of the odd-numbered domain will comprise the whole number portion or next whole number portion of the domain (number of amino acids of the domain/2+/-0.5 amino acids). For example, a domain identified as a 7 amino acid domain could produce half-domains of 3 amino acids or 4 amino acids (7/2=3.5+/-0.5 being 3 or 4). It is also understood that sub-domains may be identified within domains or half-domains, these subdomains possessing less than all of the structural or functional properties identified in the domains or half domains from which they were derived. It is also understood that the amino acids that comprise any of the domain types herein need not be contiguous along the backbone of the polypeptide (i.e., nonadjacent amino acids may fold structurally to produce a domain, half-domain or subdomain).

[0238] As used herein when referring to proteins the terms "site" as it pertains to amino acid based embodiments is used synonymous with "amino acid residue" and "amino acid side chain". A site represents a position within a peptide or polypeptide that may be modified, manipulated, altered, derivatized or varied within the polypeptide based molecules of the present invention.

[0239] As used herein the terms "termini or terminus" when referring to proteins refers to an extremity of a peptide or polypeptide. Such extremity is not limited only to the first or final site of the peptide or polypeptide but may include additional amino acids in the terminal regions. The polypeptide based molecules of the present invention may be characterized as having both an N-terminus (terminated by an amino acid with a free amino group (NH2)) and a C-terminus (terminated by an amino acid with a free carboxyl group (COOH)). Proteins of the invention are in some cases made up of multiple polypeptide chains brought together by disulfide bonds or by non-covalent forces (multimers, oligomers). These sorts of proteins will

have multiple N- and C-termini. Alternatively, the termini of the polypeptides may be modified such that they begin or end, as the case may be, with a non-polypeptide based moiety such as an organic conjugate.

[0240] Once any of the features have been identified or defined as a component of a molecule of the invention, any of several manipulations and/or modifications of these features may be performed by moving, swapping, inverting, deleting, randomizing or duplicating. Furthermore, it is understood that manipulation of features may result in the same outcome as a modification to the molecules of the invention. For example, a manipulation which involves deleting a domain would result in the alteration of the length of a molecule just as modification of a nucleic acid to encode less than a full length molecule would.

[0241] Modifications and manipulations can be accomplished by methods known in the art such as site directed mutagenesis. The resulting modified molecules may then be tested for activity using in vitro or in vivo assays such as those described herein or any other suitable screening assay known in the art.

Payloads: Nucleic Acids Encoding a Protein of Interest

[0242] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding a protein of interest.

[0243] Apolipoprotein E (APOE)

[0244] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding an allele of the apolipoprotein E (APOE) gene (e.g., ApoE2, ApoE3, and/or ApoE4).

[0245] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid signal peptide with the sequence MKVLWAALLVTFLAGCQA (SEQ ID NO: 1722).

[0246] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid signal peptide with the sequence MSSGASRKSWDPGNPWPPDWPITGRKMKVLWAALLVTFLAGCQA (SEQ ID NO: 1723).

[0247] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid sequence, or fragment thereof, or variant thereof, described in Table 2.

[0248] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence, or fragment thereof, or variant thereof, described in Table 2.

Table 2. Apolipoprotein E Sequences

Identification	Reference	SEQ ID NO
APOE SEQ-001	ENSP00000252486; NP_000032.1; NP_001289618.1; NP_001289619.1; NP_001289620.1	1724
APOE SEQ-002	ENSP00000252486; NP_000032.1; NP_001289618.1; NP_001289619.1; NP_001289620.1; Mature peptide	1725
APOE SEQ-003	ENSP00000413135	1726
APOE SEQ-004	ENSP00000413135; Mature peptide	1727
APOE SEQ-005	ENSP00000413653	1728
APOE SEQ-006	ENSP00000413653; Mature peptide	1729
APOE SEQ-007	ENSP00000410423	1730
APOE SEQ-008	ENSP00000410423; Mature peptide	1731
APOE SEQ-009	NP_001289617.1	1732
APOE SEQ-010	NP_001289617.1; Mature peptide	1733
APOE SEQ-011	ENST00000252486.8	1734
APOE SEQ-012	CCDS12647.1 for ENST00000252486.8	1735
APOE SEQ-013	ENST00000446996.5	1736
APOE SEQ-014	ENST00000485628.2	1737
APOE SEQ-015	ENST00000434152.5	1738
APOE SEQ-016	ENST00000425718.1	1739
APOE SEQ-017	NM_000041.3	1740
APOE SEQ-018	NM_001302689.1	1741
APOE SEQ-019	NM_001302690.1	1742
APOE SEQ-020	NM_001302691.1	1743
APOE SEQ-021	NM_001302688.1	1744

[0249] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding one or more variants of SEQ ID NO: 1724. The variant may include, but is not limited to, one or more of the variants: E21K (the amino acid E (Glu) at position 21 in SEQ ID NO: 1724 is changed to K (Lys)), E31K (the amino acid E (Glu) at position 31 in SEQ ID NO: 1724 is changed to K (Lys)), R43C (the amino acid R (Arg) at position 43 in SEQ ID NO: 1724 is changed to C (Cys)), L46P (the amino acid L (Leu) at position 46 in SEQ ID NO: 1724 is changed to P (Pro)), T60A (the amino acid T (Thr) at position 60 in SEQ ID NO: 1724 is changed to A (Ala)), Q64H (the amino acid Q (Gln) at position 64 in SEQ ID NO: 1724 is changed to H (His)), Q99K (the amino acid Q (Gln) at position 99 in SEQ ID NO: 1724 is changed to K (Lys)), P102R (the amino acid P (Pro) at position 102 in SEQ ID NO: 1724 is changed to R (Arg)), A117T (the amino acid A (Ala) at position 117 in SEQ ID NO: 1724 is changed to T (Thr)), A124V (the amino acid A (Ala) at

position 124 in SEQ ID NO: 1724 is changed to V (Val)), C130R (the amino acid C (Cys) at position 130 in SEQ ID NO: 1724 is changed to R (Arg)), G145D (the amino acid G (Gly) at position 145 in SEQ ID NO: 1724 is changed to D (Asp)), G145GEVQAMLG (the amino acid G (Gly) at position 145 in SEQ ID NO: 1724 is changed to be GEVQAMLG (Gly-Glu-Val-Gln-Ala-Met-Leu-Gly)), R152Q (the amino acid R (Arg) at position 152 in SEQ ID NO: 1724 is changed to Q (Gln)), R154C (the amino acid R (Arg) at position 154 in SEQ ID NO: 1724 is changed to C (Cys)), R154S (the amino acid R (Arg) at position 154 in SEQ ID NO: 1724 is changed to S (Ser)), R160C (the amino acid R (Arg) at position 160 in SEQ ID NO: 1724 is changed to C (Cys)), R163H (the amino acid R (Arg) at position 163 in SEQ ID NO: 1724 is changed to H (His)), R163P (the amino acid R (Arg) at position 163 in SEQ ID NO: 1724 is changed to P (Pro)), K164E (the amino acid K (Lys) at position 164 in SEQ ID NO: 1724 is changed to E (Glu)), K164Q (the amino acid K (Lys) at position 164 in SEQ ID NO: 1724 is changed to Q (Gln)), A170P (the amino acid A (Ala) at position 170 in SEQ ID NO: 1724 is changed to P (Pro)), R176C (the amino acid R (Arg) at position 176 in SEQ ID NO: 1724 is changed to C (Cys)), R242Q (the amino acid R (Arg) at position 242 in SEQ ID NO: 1724 is changed to Q (Gln)), R246C (the amino acid R (Arg) at position 246 in SEQ ID NO: 1724 is changed to C (Cys)), V254E (the amino acid V (Val) at position 254 in SEQ ID NO: 1724 is changed to E (Glu)), EE262-263KK (the amino acids EE (Glu-Glu) at positions 262-263 in SEQ ID NO: 1724 are changed to KK (Lys-Lys)), R269G (the amino acid R (Arg) at position 269 in SEQ ID NO: 1724 is changed to G (Gly)), L270E (the amino acid L (Leu) at position 270 in SEQ ID NO: 1724 is changed to E (Glu)), R292H (the amino acid R (Arg) at position 292 in SEQ ID NO: 1724 is changed to H (His)), S314R (the amino acid S (Ser) at position 314 in SEQ ID NO: 1724 is changed to R (Arg)), the removal of amino acid 167, or a combination thereof. As a non-limiting example, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding an amino acid sequence where the amino acid C (Cys) at position 130 in SEQ ID NO: 1724 is changed to R (Arg). As a non-limiting example, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding an amino acid sequence where the amino acid R (Arg) at position 176 in SEQ ID NO: 1724 is changed to C (Cys). As a non-limiting example, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding an amino acid sequence where the amino acid C (Cys) at position 130 in SEQ ID NO: 1724 is changed to R and the amino acid R (Arg) at position 176 in SEQ ID NO: 1724 is changed to C (Cys).

[0250] In some embodiments, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding an ApoE molecule comprising a signal peptide sequence as given in SEQ ID NO: 1722 or 1723. As a non-limiting example, the signal peptide may be cleaved during cellular processing to yield a mature peptide as given in SEQ ID NOs: 1725, 1727, 1729, 1731, and 1733. Alternatively, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding an ApoE molecule that lacks a signal peptide sequences, as given in SEQ ID NOs: 1725, 1727, 1729, 1731, and 1733.

[0251] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding one or more variants of SEQ ID NO: 1725. The variant may include, but is not limited to, one or more of the variants: C112R (the amino acid C (Cys) at position 112 in SEQ ID NO: 1725 is changed to R (Arg)), or R158C (the amino acid R (Arg) at position 158 in SEQ ID NO: 1725 is changed to C (Cys).

[0252] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences that encode ApoE2 (cys112, cys158).

[0253] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences that encode ApoE3 (cys112, arg158).

[0254] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences that encode ApoE4 (arg112, arg158).

[0255] Frataxin (FXN)

[0256] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding frataxin (FXN).

[0257] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid sequence, or fragment thereof, or variant thereof, described in Table 3.

[0258] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence, or fragment thereof, or variant thereof, described in Table 3.

Table 3. Frataxin Sequences

Identification	Reference	SEQ ID NO
FXN SEQ-001	NP_000135.2	1745
FXN SEQ-002	NP_852090.1	1746
FXN SEQ-003	NP_001155178.1	1747
FXN SEQ-004	NM_000144.4	1748
FXN SEQ-005	NM_181425.2	1749
FXN SEQ-006	NM_001161706.1	1750

Aromatic L-Amino Acid Decarboxylase (AADC)

[0259] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding Aromatic L-Amino Acid Decarboxylase (AADC).

[0260] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid sequence, or fragment thereof, or variant thereof, described in Table 4.

[0261] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence, or fragment thereof, or variant thereof, described in Table 4.

Table 4. Aromatic L-Amino Acid Decarboxylase Sequences

Identification	Reference	SEQ ID NO
AADC SEQ-001	NP_000781.1	1751
AADC SEQ-002	NM_000790.3	1752

ATPase Sarcoplasmic/Endoplasmic Reticulum Ca2+ Transporting 2 (ATP2A2)

[0262] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding ATPase Sarcoplasmic/Endoplasmic Reticulum Ca2+ Transporting 2 (ATP2A2).

[0263] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid sequence, or fragment thereof, or variant thereof, described in Table 5.

[0264] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence, or fragment thereof, or variant thereof, described in Table 5.

Table 5. ATPase Sarcoplasmic/Endoplasmic Reticulum Ca2+ Transporting 2

Identification	Reference	SEQ ID NO
ATP2A2 SEQ-001	NP_001672.1	1803
ATP2A2 SEQ-002	NP_733765.1	1804
ATP2A2 SEQ-003	NM_001681.3	1805
ATP2A2 SEQ-004	NM_170665.3	1806

S100 Calcium Binding Protein A1 (S100A1)

[0265] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding S100 Calcium Binding Protein A1 (S100A1).

[0266] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid sequence, or fragment thereof, or variant thereof, described in Table 6.

[0267] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence, or fragment thereof, or variant thereof, described in Table 6.

Table 6. S100 Calcium Binding Protein A1

Identification	Reference	SEQ ID NO
S100A1 SEQ-001	NP_006262.1	1807
S100A1 SEQ-002	NM_006271.1	1808

Anti Tau Paired Helical Filaments (Tau-PHFs) antibodies

[0268] In one embodiment, the payload region of the AAV particle comprises one or more nucleic acid sequences encoding the heavy chain and/or light chain of an antibody specific to Paired Helical Filaments (PHF) formed by abnormally folded Tau proteins (Tau-PHFs). The payload region may also comprise one or more nucleic acid sequences encoding a linker region between the nucleic acid sequences encoding the heavy and light chain. As a non-limiting example, the linker region comprises a furin cleavage recognition sequence (nucleic acid sequence shown as SEQ ID NO: 1811) and/or a 2A *cis*-acting hydrolase element (nucleic acid sequence shown as SEQ ID NO: 1812). As a non-limiting example, the nucleic acid sequence of the linker region is SEQ ID NO: 1813. As a non-limiting example, the antibody that specifically binds to Tau paired helical filaments is PHF-1. The PHF-1 antibody may comprise heavy chains and light chains as taught in this disclosure.

[0269] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence encoding an amino acid sequence, or fragment thereof, or variant thereof, described in Table 7.

[0270] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence, or fragment thereof, or variant thereof, described in Table 7.

Table 7. Anti Tau Paired Helical Filament Antibodies

Identification	Reference	SEQ ID NO
PHF-1 SEQ-001	Heavy Chain	1814
PHF-1 SEQ-002	Light Chain	1815

[0271] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence SEQ ID NO: 1816 which comprises (5' to 3') the kozak (SEQ ID NO: 1817), heavy chain (SEQ ID NO: 1814), linker region (which includes the furin cleavage recognition sequence (SEQ ID NO: 1811) and the 2A *cis*-acting hydrolase element sequence (SEQ ID NO: 1812)), light chain sequence (SEQ ID NO: 1812) of PHF-1, and the stop codon TAG described in Figure 5A of WO2015035190, the contents of which are herein incorporated by reference in their entirety.

[0272] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence SEQ ID NO: 1818, which comprises (5' to 3') the kozak (SEQ ID NO: 1817), light chain (SEQ ID NO: 1815), linker region (which includes the furin cleavage recognition sequence (SEQ ID NO: 1811) and the 2A *cis*-acting hydrolase element sequence (SEQ ID NO: 1812)), heavy chain (SEQ ID NO: 1814) of PHF-1, and the stop codon TAG.

[0273] In one embodiment, the payload region of the AAV particle comprises a nucleic acid encoding the heavy chain and/or light chain of PHF-1 as taught in Figure 5A of WO2015035190, the contents of which are herein incorporated by reference in their entirety, wherein the heavy chain and/or light chain of PHF-1 in WO2015035190 has been altered (e.g., modified and/or mutated). The sequence may be mutated or modified to change the state or structure of a molecule. As a non-limiting example, the sequence may include an addition of an amino acid, an amino acid substitution, and/or a deletion of an amino acid.

[0274] In one embodiment, the payload region of the AAV particle comprises a nucleic acid encoding the light chain of PHF-1 where the light chain sequence has been altered to remove the second methionine at the beginning of the light chain amino acid sequence. As a non-limiting example, the payload region of the AAV particle comprises a nucleic acid encoding an amino acid sequence encoding a light chain of PHF-1 as shown in Table 8.

Table 8. Anti Tau Paired Helical Filament Antibodies

Identification	Reference	SEQ ID NO
PHF-1 SEQ-003	Light Chain	1819

[0275] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence SEQ ID NO: 1820, which comprises (5' to 3') the kozak (SEQ ID NO: 1817), heavy chain (SEQ ID NO: 1814), linker region (which includes the furin cleavage recognition sequence (SEQ ID NO: 1811) and the 2A *cis*-acting hydrolase element sequence (SEQ ID NO: 1812)), light chain sequence (SEQ ID NO: 1819) with one codon of "ATG" at the 5' end of the light chain sequence of PHF-1, and the stop codon TAG.

[0276] In one embodiment, the payload region of the AAV particle comprises a nucleic acid sequence SEQ ID NO: 1821, which comprises (5' to 3') the kozak (SEQ ID NO: 1817), light chain sequence with one codon of "ATG" at the 5' end of the light chain sequence (SEQ ID NO: 1819), linker region (which includes the furin cleavage recognition sequence (SEQ ID NO: 1811) and the 2A *cis*-acting hydrolase element sequence (SEQ ID NO: 1812)), heavy chain of PHF-1 (SEQ ID NO: 1814), and the stop codon TAG.

Payloads: Modulatory Polynucleotides as Payloads

[0277] The AAV particles of the present disclosure comprise at least one payload region comprising one or more modulatory polynucleotides, e.g., RNA or DNA molecules as therapeutic agents. Exemplary modulatory polynucleotides may be miRNAs, dsRNA and siRNA duplexes. RNA interference mediated gene silencing can specifically inhibit targeted gene expression. The present invention then provides small double stranded RNA (dsRNA) molecules (small interfering RNA, siRNA) targeting a gene of interest, pharmaceutical compositions comprising such siRNAs, as well as processes of their design. The present invention also provides methods of their use for inhibiting gene expression and protein production of gene of interest, for treating a neurological disease.

[0278] The present invention provides small interfering RNA (siRNA) duplexes (and modulatory polynucleotides encoding them) that target the mRNA of a gene of interest to interfere with the gene expression and/or protein production.

[0279] In one embodiment, the siRNA duplexes of the present invention may target the gene of interest along any segment of their respective nucleotide sequence.

[0280] In one embodiment, the siRNA duplexes of the present invention may target the gene of interest at the location of a single-nucleotide polymorphism (SNP) or variant within the nucleotide sequence.

[0281] In some embodiments, a nucleic acid sequence encoding such siRNA molecules, or a single strand of the siRNA molecules, is inserted into the viral genome of the AAV particle and introduced into cells, specifically cells in the central nervous system.

[0282] AAV particles have been investigated for siRNA delivery because of several unique features. Non-limiting examples of the features include (i) the ability to infect both dividing and non-dividing cells; (ii) a broad host range for infectivity, including human cells; (iii) wild-type AAV has not been associated with any disease and has not been shown to replicate in infected cells; (iv) the lack of cell-mediated immune response against the vector and (v) the non-integrative nature in a host chromosome thereby reducing potential for long-term expression. Moreover, infection with AAV particles has minimal influence on changing the pattern of cellular gene expression (Stilwell and Samulski et al., *Biotechniques*, 2003, 34, 148-150; the contents of which are incorporated herein by reference in their entirety).

[0283] The encoded siRNA duplex of the present invention contains an antisense strand and a sense strand hybridized together forming a duplex structure, wherein the antisense strand is complementary to the nucleic acid sequence of the targeted gene, and wherein the sense strand is homologous to the nucleic acid sequence of the targeted gene. In some

aspects, the 5'end of the antisense strand has a 5' phosphate group and the 3'end of the sense strand contains a 3'hydroxyl group. In other aspects, there are none, one or 2 nucleotide overhangs at the 3'end of each strand.

[0284] According to the present invention, each strand of the siRNA duplex targeting a gene of interest is about 19 to 25, 19 to 24 or 19 to 21 nucleotides in length, preferably about 19 nucleotides, 20 nucleotides, 21 nucleotides, 22 nucleotides, 23 nucleotides, 24 nucleotides, or 25 nucleotides in length. In some aspects, the siRNAs may be unmodified RNA molecules.

[0285] In other aspects, the siRNAs may contain at least one modified nucleotide, such as base, sugar or backbone modification.

[0286] In one embodiment, an siRNA or dsRNA includes at least two sequences that are complementary to each other. The dsRNA includes a sense strand having a first sequence and an antisense strand having a second sequence. The antisense strand includes a nucleotide sequence that is substantially complementary to at least part of an mRNA encoding the target gene, and the region of complementarity is 30 nucleotides or less, and at least 15 nucleotides in length. Generally, the dsRNA is 19 to 25, 19 to 24 or 19 to 21 nucleotides in length. In some embodiments, the dsRNA is from about 15 to about 25 nucleotides in length, and in other embodiments the dsRNA is from about 25 to about 30 nucleotides in length. In some embodiments, the dsRNA is about 15 nucleotides in length, 16 nucleotides in length, 17 nucleotides in length, 18 nucleotides in length, 19 nucleotides, 20 nucleotides, 21 nucleotides, 22 nucleotides, 23 nucleotides, 24 nucleotides in length, 25 nucleotides in length, 26 nucleotides in length, 27 nucleotides in length, 28 nucleotides in length, 29 nucleotides in length, or 30 nucleotides in length.

[0287] The dsRNA, whether directly administered or encoded in an expression vector upon contacting with a cell expressing the target protein, inhibits the expression of the protein by at least 10%, at least 20%, at least 25%, at least 30%, at least 35% or at least 40% or more, such as when assayed by a method as described herein.

[0288] According to the present invention, the siRNA duplexes or dsRNA molecules s are designed and tested for their ability in reducing expression of the target gene (e.g., mRNA levels of the target gene) in cultured cells. siRNA design tools are available in the art. Any commercial softwares may be used to design the siRNA duplexes against a gene of interest.

[0289] According to the present invention, AAV particles comprising a payload region having the nucleic acids of the siRNA duplexes, one strand of the siRNA duplex or the dsRNA targeting a gene of interest are produced, the AAV particle serotypes may be or may

include a capsid and/or a peptide insert such as, but not limited to VOY101, VOY201, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5 (G2B5), PHP.S, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21,

AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3,

AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, and/or AAVF9/HSC9 and variants thereof.

[0290] In one embodiment, the siRNA duplexes or encoded dsRNA molecules may be used to reduce the expression of target protein by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of target protein expression may be reduced 50-90%.

[0291] In one embodiment, the siRNA duplexes or encoded dsRNA molecules may be used to reduce the expression of target mRNA by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. As a non-limiting example, the expression of target mRNA expression may be reduced 50-90%.

[0292] In one embodiment, the siRNA duplexes or encoded dsRNA molecules may be used to reduce the expression of target protein and/or mRNA in at least one region of the CNS. The expression of target protein and/or mRNA is reduced by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in at least one region of the CNS. As a non-limiting example, the expression of target protein and mRNA in the neurons (e.g., cortical neurons) is reduced by 50-90%. As a non-limiting example, the expression of target protein and mRNA in the neurons (e.g., cortical neurons) is reduced by 40-50%.

[0293] In some embodiments, the AAV particle of the present invention comprising the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest is administered to the subject in need for treating and/or ameliorating a disease, e.g., a neurological disorder or a cardiovascular disease. The AAV particle serotype may be or include a peptide such as but is not limited to VOY101, VOY201, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP,

AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5, PHP.S, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17,

AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10,

AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, and/or AAVF9/HSC9 and variants thereof.

[0294] In some embodiments, an AAVPHP.B particle (an AAV particle comprising a PHP.B peptide insert) comprising the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest is administered to the subject in need for treating and/or ameliorating a neurological disease.

[0295] In some embodiments, an AAVPHP.A particle (an AAV particle comprising a PHP.A peptide insert) comprising the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest is administered to the subject in need for treating and/or ameliorating a neurological disease.

[0296] In some embodiments, an AAVPHP.N particle (an AAV particle comprising a PHP.N peptide insert) comprising the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest is administered to the subject in need for treating and/or ameliorating a neurological disease.

[0297] In some embodiments, an AAV particle comprising a PHP.S peptide insert, comprises the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest, and the AAV particle may be administered to the subject in need for treating and/or ameliorating a neurological disease.

[0298] In some embodiments, an AAV particle that has a serotype of VOY101 comprising the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest is

administered to the subject in need for treating and/or ameliorating a neurological disease. In one embodiment, the VOY101 capsid comprises an amino acid sequence of SEQ ID NO. 1. In one embodiment, the VOY101 capsid comprises a nucleic acid sequence of SEQ ID NO. 1809.

[0299] In some embodiments, an AAV particle that has the serotype of VOY201 comprising the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest is administered to the subject in need for treating and/or ameliorating a neurological disease. In one embodiment, the VOY201 capsid comprises a nucleic acid sequence of SEQ ID NO. 1810.

[0300] In some embodiments, an AAV particle that has a serotype of a variant of the AAV9 comprising the nucleic acid sequence of at least one siRNA duplex targeting a gene of interest is administered to the subject in need for treating and/or ameliorating a neurological disease.

[0301] In some embodiments, a first AAV particle comprising the nucleic acid sequence of at least one siRNA duplex (e.g., payload) targeting a gene of interest may be selected for administration to a subject, where the first AAV particle provides a higher level of viral genome to cells (e.g., astrocytes) as compared to a second AAV particle comprising the same payload. In one embodiment, the level of the first viral genome may provide 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9 or more than 9 times higher in cells (e.g., astrocytes) as compared to the level in cells of a subject of the second AAV particle. In one embodiment, the level of the first viral genome may be 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99% higher than the level of the second viral genome in cells (e.g., astrocytes). In one embodiment, the level of the first viral genome may be 1-10%, 5-10%, 10-15%, 10-20%, 15-20%, 20-30%, 25-30%, 25-35%, 30-35%, 30-40%, 35-40%, 35-45%, 40-45%, 40-50%, 45-50%, 45-55%, 50-55%, 50-60%, 55-60%, 55-65%, 60-65%, 60-70%, 65-70%, 65-75%, 70-75%, 70-80%, 75-80%, 75-85%, 80-85%, 80-90%, 85-90%, 85-95%, 90-95%, 90-99%, or 95-99% higher than the level of the second viral genome in cells (e.g., astrocytes).

[0302] In some embodiments, a first AAV particle comprising the nucleic acid sequence of at least one siRNA duplex targeting the gene of interest may be selected for administration to a subject, where the first particle provides a higher viral genome to the astrocytes as compared to the amount seen in the liver of the subject. The first particle may provide 1, 2,

3, 4, 5, 6, 7, 8, 9 or more than 9 times more viral genome to the astrocytes as compared to the amount in the liver.

[0303] In some embodiments, the siRNA molecules or the AAV particles comprising such siRNA molecules may be introduced directly into the central nervous system of the subject, for example, by infusion into the putamen.

[0304] In some embodiments, the siRNA molecules or the AAV particles comprising such siRNA molecules may be introduced directly into the central nervous system of the subject, for example, by infusion to the thalamus a subject.

[0305] In some embodiments, the siRNA molecules or the AAV particles comprising such siRNA molecules may be introduced directly into the central nervous system of the subject, for example, by infusion to the white matter a subject.

[0306] In some embodiments, the siRNA molecules or the AAV particles comprising such siRNA molecules may be introduced to the central nervous system of the subject, for example, by intravenous administration to a subject.

[0307] In some embodiments, the AAV particles comprising at least one siRNA duplex targeting a gene of interest may be used as a solo therapy or in combination therapy for treatment of a disease, for example, in combination with one or more neuroprotective agents for treatment of neuronal degeneration.

siRNA Molecules

[0308] The present invention relates to RNA interference (RNAi) induced inhibition of gene expression for treating neurological disorders. Provided herein are siRNA duplexes or encoded dsRNA that target a gene of interest (referred to herein collectively as "siRNA molecules"). Such siRNA duplexes or encoded dsRNA can reduce or silence target gene expression in cells, for example, astrocytes or microglia, cortical, hippocampal, entorhinal, thalamic, sensory or motor neurons, thereby, ameliorating symptoms of neurological disease.

[0309] RNAi (also known as post-transcriptional gene silencing (PTGS), quelling, or co-suppression) is a post-transcriptional gene silencing process in which RNA molecules, in a sequence specific manner, inhibit gene expression, typically by causing the destruction of specific mRNA molecules. The active components of RNAi are short/small double stranded RNAs (dsRNAs), called small interfering RNAs (siRNAs), that typically contain 15-30 nucleotides (e.g., 19 to 25, 19 to 24 or 19-21 nucleotides) and 2 nucleotide 3' overhangs and that match the nucleic acid sequence of the target gene. These short RNA species may be

naturally produced *in vivo* by Dicer-mediated cleavage of larger dsRNAs and they are functional in mammalian cells.

[0310] Naturally expressed small RNA molecules, named microRNAs (miRNAs), elicit gene silencing by regulating the expression of mRNAs. The miRNAs containing RNA Induced Silencing Complex (RISC) targets mRNAs presenting a perfect sequence complementarity with nucleotides 2-7 in the 5' region of the miRNA which is called the seed region, and other base pairs with its 3' region. miRNA mediated down regulation of gene expression may be caused by cleavage of the target mRNAs, translational inhibition of the target mRNAs, or mRNA decay. miRNA targeting sequences are usually located in the 3'-UTR of the target mRNAs. A single miRNA may target more than 100 transcripts from various genes, and one mRNA may be targeted by different miRNAs.

[0311] siRNA duplexes or dsRNA targeting a specific mRNA may be designed and synthesized *in vitro* and introduced into cells for activating RNAi processes. Elbashir et al. demonstrated that 21-nucleotide siRNA duplexes (termed small interfering RNAs) were capable of effecting potent and specific gene knockdown without inducing immune response in mammalian cells (Elbashir SM et al., *Nature*, 2001, 411, 494-498). Since this initial report, post-transcriptional gene silencing by siRNAs quickly emerged as a powerful tool for genetic analysis in mammalian cells and has the potential to produce novel therapeutics.

[0312] *In vitro* synthetized siRNA molecules may be introduced into cells in order to activate RNAi. An exogenous siRNA duplex, when it is introduced into cells, similar to the endogenous dsRNAs, can be assembled to form the RNA Induced Silencing Complex (RISC), a multiunit complex that facilitates searching through the genome for RNA sequences that are complementary to one of the two strands of the siRNA duplex (i.e., the antisense strand). During the process, the sense strand (or passenger strand) of the siRNA is lost from the complex, while the antisense strand (or guide strand) of the siRNA is matched with its complementary RNA. In particular, the targets of siRNA containing RISC complex are mRNAs presenting a perfect sequence complementarity. Then, siRNA mediated gene silencing occurs, cleaving, releasing and degrading the target.

[0313] The siRNA duplex comprised of a sense strand homologous to the target mRNA and an antisense strand that is complementary to the target mRNA offers much more advantage in terms of efficiency for target RNA destruction compared to the use of the single strand (ss)-siRNAs (e.g. antisense strand RNA or antisense oligonucleotides). In many cases

it requires higher concentration of the ss-siRNA to achieve the effective gene silencing potency of the corresponding duplex.

[0314] Any of the foregoing molecules may be encoded by an AAV particle or viral genome.

Target Genes

[0315] Non-limiting examples of the neurological diseases which may be treated with the modulatory polynucleotides of the invention include tauopathies, Alzheimer Disease, Huntington's Disease, and/or Amyotrophic Lateral Sclerosis. Target genes may be any of the genes associated with any neurological disease such as, but not limited to, those listed herein.

[0316] In one embodiment, the target gene is an allele of the apolipoprotein E (APOE) gene (e.g., ApoE2, ApoE3, and/or ApoE4). As a non-limiting example, the target gene is APOE and the target gene has one of the sequences taught in Table 2, a fragment or variant thereof.

[0317] In another embodiment, the target gene is superoxide dismutase (SOD1). As a non-limiting example, the target gene is SOD1 and the target gene has a sequence of SEQ ID NO: 1753 (NCBI reference number NM_000454.4), a fragment or variant thereof.

[0318] In another embodiment, the target gene is huntingtin (HTT). As a non-limiting example, the target gene is HTT having a nucleotide sequence of SEQ ID NO: 1754 (NCBI reference number NM_002111.7), a fragment or variant thereof. As a non-limiting example, the target gene is HTT and the target gene encodes an amino acid sequence of SEQ ID NO: 1755 (NCBI reference number NP_002102.4), a fragment or variant thereof.

[0319] In yet another embodiment, the target gene is microtubule-associated protein tau (MAPT). As a non-limiting example, the target gene is MAPT having a nucleotide sequence of any of the nucleic acid sequences shown in Table 9, a fragment or variant thereof. As a non-limiting example, the target gene is MAPT and the target gene encodes an amino acid sequence of any of the amino acid sequences shown in Table 9, a fragment or variant thereof.

Table 9. Microtubule-Associated Protein Tau Sequences

Identification	Reference	SEQ ID NO
MAPT SEQ-001	NP_058519.3	1756
MAPT SEQ-002	NP_005901.2	1757
MAPT SEQ-003	NP_058518.1	1758
MAPT SEQ-004	NP_058525.1	1759
MAPT SEQ-005	NP_001116539.1	1760
MAPT SEQ-006	NP_001116538.2	1761
MAPT SEQ-007	NP_001190180.1	1762

MAPT SEQ-008	NP_001190181.1	1763
MAPT SEQ-009	NM_016835.4	1764
MAPT SEQ-010	NM_005910.5	1765
MAPT SEQ-011	NM_016834.4	1766
MAPT SEQ-012	NM_016841.4	1767
MAPT SEQ-013	NM_001123067.3	1768
MAPT SEQ-014	NM_001123066.3	1769
MAPT SEQ-015	NM_001203251.1	1770
MAPT SEQ-016	NM_001203252.1	1771

Design and Sequences of siRNA duplexes

[0320] Some guidelines for designing siRNAs have been proposed in the art. These guidelines generally recommend generating a 19-nucleotide duplexed region, symmetric 2-3 nucleotide 3'overhangs, 5-phosphate and 3-hydroxyl groups targeting a region in the gene to be silenced. Other rules that may govern siRNA sequence preference include, but are not limited to, (i) A/U at the 5′ end of the antisense strand; (ii) G/C at the 5′ end of the sense strand; (iii) at least five A/U residues in the 5′ terminal one-third of the antisense strand; and (iv) the absence of any GC stretch of more than 9 nucleotides in length. In accordance with such consideration, together with the specific sequence of a target gene, highly effective siRNA molecules essential for suppressing mammalian target gene expression may be readily designed.

[0321] According to the present invention, siRNA molecules (e.g., siRNA duplexes or encoded dsRNA) that target a gene of interest are designed. Such siRNA molecules can specifically, suppress target gene expression and protein production. In some aspects, the siRNA molecules are designed and used to selectively "knock out" target gene variants in cells, i.e., transcripts that are identified in neurological disease. In some aspects, the siRNA molecules are designed and used to selectively "knock down" target gene variants in cells.

[0322] In one embodiment, an siRNA molecule of the present invention comprises a sense strand and a complementary antisense strand in which both strands are hybridized together to form a duplex structure. The antisense strand has sufficient complementarity to the target mRNA sequence to direct target-specific RNAi, i.e., the siRNA molecule has a sequence sufficient to trigger the destruction of the target mRNA by the RNAi machinery or process.

[0323] In some embodiments, the antisense strand and target mRNA sequences have 100% complementarity. The antisense strand may be complementary to any part of the target mRNA sequence.

[0324] In other embodiments, the antisense strand and target mRNA sequences comprise at least one mismatch. As a non-limiting example, the antisense strand and the target mRNA sequence have at least 30%, 40%, 50%, 60%, 70%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-99%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-99%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-99%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-99%, 60-70%, 60-80%, 60-90%, 60-95%, 60-99%, 70-80%, 70-90%, 70-95%, 70-99%, 80-90%, 80-95%, 80-99%, 90-95%, 90-99% or 95-99% complementary.

[0325] According to the present invention, the siRNA molecule has a length from about 10-50 or more nucleotides, i.e., each strand comprising 10-50 nucleotides (or nucleotide analogs). Preferably, the siRNA molecule has a length from about 15-30, e.g., 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in each strand, wherein one of the strands is sufficiently complementary to a target region. In one embodiment, the siRNA molecule has a length from about 19 to 25, 19 to 24 or 19 to 21 nucleotides.

[0326] In some embodiments, the siRNA molecules of the present invention can be synthetic RNA duplexes comprising about 19 nucleotides to about 25 nucleotides, and two overhanging nucleotides at the 3'-end. In some aspects, the siRNA molecules may be unmodified RNA molecules. In other aspects, the siRNA molecules may contain at least one modified nucleotide, such as base, sugar or backbone modifications.

[0327] In one embodiment, the siRNA molecules of the present invention may comprise an antisense sequence and a sense sequence, or a fragment or variant thereof. As a non-limiting example, the antisense sequence and the sense sequence have at least 30%, 40%, 50%, 60%, 70%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-99%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-99%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-99%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-99%, 60-70%, 60-80%, 60-90%, 60-95%, 60-99%, 70-80%, 70-90%, 70-95%, 70-99%, 80-90%, 80-95%, 80-99%, 90-95%, 90-99% or 95-99% complementary.

[0328] DNA expression plasmids can be used to stably express the siRNA duplexes or dsRNA of the present invention in cells and achieve long-term inhibition of the target gene. In one aspect, the sense and antisense strands of a siRNA duplex are typically linked by a

short spacer sequence leading to the expression of a stem-loop structure termed short hairpin RNA (shRNA). The hairpin is recognized and cleaved by Dicer, thus generating mature siRNA molecules.

[0329] In other embodiments, the siRNA molecules of the present invention can be encoded in AAV particles for delivery to a cell. In one embodiment, the siRNA may be inserted to an AAV viral genome, flanked by the ITRs.

[0330] According to the present invention, the AAV particles comprising the nucleic acids encoding the siRNA molecules targeting mRNA of a gene of interest may include AAV particle serotypes, and/or may include a peptide insertion such as, but are not limited to, VOY101, VOY201, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5, PHP.S, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5,

AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM

10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3, AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, and/or AAVF9/HSC9 and variants thereof.

[0331] In some embodiments, the siRNA duplexes or encoded dsRNA of the present invention suppress (or degrade) target mRNA. Accordingly, the siRNA duplexes or encoded

dsRNA can be used to substantially inhibit target gene expression in a cell, for example a neuron or astrocyte. In some aspects, the inhibition of target gene expression refers to an inhibition by at least about 20%, preferably by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. Accordingly, the protein product of the targeted gene may be inhibited by at least about 20%, preferably by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[0332] In some embodiments, siRNA molecules targeting a gene of interest may be designed using any available design tools. According to the present invention, the siRNA molecules are designed and tested for their ability in reducing target gene mRNA levels in cultured cells.

[0333] In one embodiment, the siRNA molecules are designed and tested for their ability in reducing ApoE2 levels in cultured cells.

[0334] In one embodiment, the siRNA molecules are designed and tested for their ability in reducing ApoE3 levels in cultured cells.

[0335] In one embodiment, the siRNA molecules are designed and tested for their ability in reducing ApoE4 levels in cultured cells.

[0336] In one embodiment, the siRNA molecules are designed and tested for their ability in reducing SOD1 levels in cultured cells.

[0337] In one embodiment, the siRNA molecules are designed and tested for their ability in reducing HTT levels in cultured cells.

[0338] In one embodiment, the siRNA molecules are designed and tested for their ability in reducing Tau levels in cultured cells.

[0339] In one embodiment, the siRNA molecules comprise a miRNA seed match for the guide strand. In another embodiment, the siRNA molecules comprise a miRNA seed match

for the passenger strand. In yet another embodiment, the siRNA duplexes or encoded dsRNA targeting a gene of interest do not comprise a seed match for the guide or passenger strand.

[0340] In one embodiment, the siRNA duplexes or encoded dsRNA targeting a gene of interest may have almost no significant full-length off targets for the guide strand. In another embodiment, the siRNA duplexes or encoded dsRNA targeting a gene of interest may have almost no significant full-length off targets for the passenger strand. The siRNA duplexes or encoded dsRNA targeting a gene of interest may have less than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%,11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 1-5%, 2-6%, 3-7%, 4-8%, 5-9%, 5-10%, 6-10%, 5-15%, 5-20%, 5-25% 5-30%, 10-20%, 10-30%, 10-40%, 10-50%, 15-30%, 15-40%, 15-45%, 20-40%, 20-50%, 25-50%, 30-40%, 30-50%, 35-50%, 40-50%, 45-50% full-length off targets for the passenger strand. In yet another embodiment, the siRNA duplexes or encoded dsRNA targeting a gene of interest may have almost no significant full-length off targets for the guide strand or the passenger strand. The siRNA duplexes or encoded dsRNA targeting a gene of interest may have less than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%,11%, 12%, 13%, 14%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 1-5%, 2-6%, 3-7%, 4-8%, 5-9%, 5-10%, 6-10%, 5-15%, 5-20%, 5-25% 5-30%, 10-20%, 10-30%, 10-40%, 10-50%, 15-30%, 15-40%, 15-45%, 20-40%, 20-50%, 25-50%, 30-40%, 30-50%, 35-50%, 40-50%, 45-50% full-length off targets for the guide or passenger strand.

[0341] In one embodiment, the siRNA duplexes or encoded dsRNA targeting a gene of interest may have high activity *in vitro*. In another embodiment, the siRNA molecules may have low activity *in vitro*. In yet another embodiment, the siRNA duplexes or dsRNA targeting the gene of interest may have high guide strand activity and low passenger strand activity *in vitro*.

[0342] In one embodiment, the siRNA molecules have a high guide strand activity and low passenger strand activity *in vitro*. The target knock-down (KD) by the guide strand may be at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99%, 99.5% or 100%. The target knock-down by the guide strand may be 60-65%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 60-99%, 60-99.5%, 60-100%, 65-70%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 65-99%, 65-99.5%, 65-100%, 70-75%, 70-80%, 70-85%, 70-90%, 70-95%, 70-99%, 70-99.5%, 70-100%, 75-80%, 75-85%, 75-90%, 75-95%, 75-99%, 75-99.5%, 75-100%, 80-85%, 80-90%, 80-95%, 80-99%, 80-99.5%, 80-100%, 85-90%, 85-95%, 85-99%, 85-99.5%, 85-100%, 90-95%, 90-99%, 90-99.5%, 90-100%, 95-99%, 95-99.5%, 95-100%, 99-

99.5%, 99-100% or 99.5-100%. As a non-limiting example, the target knock-down (KD) by the guide strand is greater than 70%.

[0343] In one embodiment, the IC_{50} of the passenger strand for the nearest off target is greater than 100 multiplied by the IC_{50} of the guide strand for the target. As a non-limiting example, if the IC_{50} of the passenger strand for the nearest off target is greater than 100 multiplied by the IC_{50} of the guide strand for the target then the siRNA molecules are said to have high guide strand activity and a low passenger strand activity *in vitro*.

[0344] In one embodiment, the 5' processing of the guide strand has a correct start (n) at the 5' end at least 75%, 80%, 85%, 90%, 95%, 99% or 100% of the time *in vitro* or *in vivo*. As a non-limiting example, the 5' processing of the guide strand is precise and has a correct start (n) at the 5' end at least 99% of the time *in vitro*. As a non-limiting example, the 5' processing of the guide strand is precise and has a correct start (n) at the 5' end at least 99% of the time *in vivo*.

[0345] In one embodiment, the guide to passenger (G:P) (also referred to as the antisense to sense) strand ratio expressed is 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1;1, 2:10, 2:9, 2:8, 2:7, 2:6, 2:5, 2:4, 2:3, 2:2, 2:1, 3:10, 3:9, 3:8, 3:7, 3:6, 3:5, 3:4, 3:3, 3:2, 3:1, 4:10, 4:9, 4:8, 4:7, 4:6, 4:5, 4:4, 4:3, 4:2, 4:1, 5:10, 5:9, 5:8, 5:7, 5:6, 5:5, 5:4, 5:3, 5:2, 5:1, 6:10, 6:9, 6:8, 6:7, 6:6, 6:5, 6:4, 6:3, 6:2, 6:1, 7:10, 7:9, 7:8, 7:7, 7:6, 7:5, 7:4, 7:3, 7:2, 7:1, 8:10, 8:9, 8:8, 8:7, 8:6, 8:5, 8:4, 8:3, 8:2, 8:1, 9:10, 9:9, 9:8, 9:7, 9:6, 9:5, 9:4, 9:3, 9:2, 9:1, 10:10, 10:9, 10:8, 10:7, 10:6, 10:5, 10:4, 10:3, 10:2, 10:1, 1:99, 5:95, 10:90, 15:85, 20:80, 25:75, 30:70, 35:65, 40:60, 45:55, 50:50, 55:45, 60:40, 65:35, 70:30, 75:25, 80:20, 85:15, 90:10, 95:5, or 99:1 *in vitro* or *in vivo*. The guide to passenger ratio refers to the ratio of the guide strands to the passenger strands after the excision of the guide strand. For example, an 80:20 guide to passenger ratio would have 8 guide strands to every 2 passenger strands clipped out of the precursor. As a non-limiting example, the guide-to-passenger strand ratio is 80:20 *in vitro*. As a non-limiting example, the guide-to-passenger strand ratio is 80:20 *in vivo*. As a non-limiting example, the guide-to-passenger strand ratio is 8:2 *in vitro*. As a non-limiting example, the guide-to-passenger strand ratio is 8:2 *in vivo*. As a non-limiting example, the guide-to-passenger strand ratio is 9:1 *in vitro*. As a non-limiting example, the guide-to-passenger strand ratio is 9:1 *in vivo*.

[0346] In one embodiment, the passenger to guide (P:G) (also referred to as the sense to antisense) strand ratio expressed is 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1;1, 2:10, 2:9, 2:8, 2:7, 2:6, 2:5, 2:4, 2:3, 2:2, 2:1, 3:10, 3:9, 3:8, 3:7, 3:6, 3:5, 3:4, 3:3, 3:2, 3:1, 4:10, 4:9,

4:8, 4:7, 4:6, 4:5, 4:4, 4:3, 4:2, 4:1, 5:10, 5:9, 5:8, 5:7, 5:6, 5:5, 5:4, 5:3, 5:2, 5:1, 6:10, 6:9, 6:8, 6:7, 6:6, 6:5, 6:4, 6:3, 6:2, 6:1, 7:10, 7:9, 7:8, 7:7, 7:6, 7:5, 7:4, 7:3, 7:2, 7:1, 8:10, 8:9, 8:8, 8:7, 8:6, 8:5, 8:4, 8:3, 8:2, 8:1, 9:10, 9:9, 9:8, 9:7, 9:6, 9:5, 9:4, 9:3, 9:2, 9:1, 10:10, 10:9, 10:8, 10:7, 10:6, 10:5, 10:4, 10:3, 10:2, 10:1, 1:99, 5:95, 10:90, 15:85, 20:80, 25:75, 30:70, 35:65, 40:60, 45:55, 50:50, 55:45, 60:40, 65:35, 70:30, 75:25, 80:20, 85:15, 90:10, 95:5, or 99:1 *in vitro* or *in vivo*. The passenger to guide ratio refers to the ratio of the passenger strands to the guide strands after the excision of the guide strand. For example, an 80:20 passenger to guide ratio would have 8 passenger strands to every 2 guide strands clipped out of the precursor. As a non-limiting example, the passenger-to-guide strand ratio is 80:20 *in vitro*. As a non-limiting example, the passenger-to-guide strand ratio is 80:20 *in vivo*. As a non-limiting example, the passenger-to-guide strand ratio is 8:2 *in vitro*. As a non-limiting example, the passenger-to-guide strand ratio is 8:2 *in vivo*. As a non-limiting example, the passenger-to-guide strand ratio is 9:1 *in vitro*. As a non-limiting example, the passenger-to-guide strand ratio is 9:1 *in vivo*.

[0347] In one embodiment, the integrity of the viral genome encoding the dsRNA is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99% of the full length of the construct. As a non-limiting example, the integrity of the viral genome is 80% of the full length of the construct.

[0348] In one embodiment, the passenger and/or guide strand is designed based on the method and rules outlined in European Patent Publication No. EP1752536, the contents of which are herein incorporated by reference in their entirety. As a non-limiting example, the 3'-terminal base of the sequence is adenine, thymine or uracil. As a non-limiting example, the 5'-terminal base of the sequence is guanine or cytosine. As a non-limiting example, the 3'-terminal sequence comprises seven bases rich in one or more bases of adenine, thymine and uracil. As a non-limiting example, the base number is at such a level as causing RNA interference without expressing cytotoxicity.

Molecular Scaffold

[0349] In one embodiment, the siRNA molecules may be encoded in a modulatory polynucleotide which also comprises a molecular scaffold. As used herein a "molecular scaffold" is a framework or starting molecule that forms the sequence or structural basis against which to design or make a subsequent molecule.

[0350] In one embodiment, the modulatory polynucleotide which comprises the payload (e.g., siRNA, miRNA or other RNAi agent described herein) includes a molecular scaffold

which comprises at least one 5' flanking sequence which may be of any length and may be derived in whole or in part from wild type microRNA sequence or be completely artificial. A 3' flanking sequence may mirror the 5' flanking sequence in size and origin. Either flanking sequence may be absent. In one embodiment, both the 5' and 3' flanking sequences are absent. The 3' flanking sequence may optionally contain one or more CNNC motifs, where "N" represents any nucleotide.

[0351] In some embodiments the 5' and 3' flanking sequences are the same length.

[0352] In some embodiments the 5' flanking sequence is from 1-10 nucleotides in length, from 5-15 nucleotides in length, from 10-30 nucleotides in length, from 20-50 nucleotides in length, greater than 40 nucleotides in length, greater than 50 nucleotides in length, greater than 100 nucleotides in length or greater than 200 nucleotides in length.

[0353] In some embodiments, the 5' flanking sequence may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413,

414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, or 500 nucleotides in length.

[0354] In some embodiments the 3' flanking sequence is from 1-10 nucleotides in length, from 5-15 nucleotides in length, from 10-30 nucleotides in length, from 20-50 nucleotides in length, greater than 40 nucleotides in length, greater than 50 nucleotides in length, greater than 100 nucleotides in length or greater than 200 nucleotides in length.

[0355] In some embodiments, the 3' flanking sequence may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431,

432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, or 500 nucleotides in length.

[0356] In some embodiments the 5' and 3' flanking sequences are the same sequence. In some embodiments they differ by 2%, 3%, 4%, 5%, 10%, 20% or more than 30% when aligned to each other.

[0357] In one embodiment, the molecular scaffold comprises at least one 3' flanking region. As a non-limiting example, the 3' flanking region may comprise a 3' flanking sequence which may be of any length and may be derived in whole or in part from wild type microRNA sequence or be a completely artificial sequence.

[0358] Forming the stem of a stem loop structure is a minimum of at least one payload sequence. In some embodiments, the payload sequence comprises at least one nucleic acid sequence which is in part complementary or will hybridize to the target sequence. In some embodiments, the payload is an siRNA molecule or fragment of an siRNA molecule.

[0359] In some embodiments, the 5' arm of the stem loop comprises a sense sequence.

[0360] In some embodiments, the 3' arm of the stem loop comprises an antisense sequence. The antisense sequence, in some instances, comprises a "G" nucleotide at the 5' most end.

[0361] In other embodiments, the sense sequence may reside on the 3' arm while the antisense sequence resides on the 5' arm of the stem of the stem loop structure.

[0362] The sense and antisense sequences may be completely complementary across a substantial portion of their length. In other embodiments, the sense sequence and antisense sequence may be at least 70, 80, 90, 95 or 99% complementary across independently at least 50, 60, 70, 80, 85, 90, 95, or 99% of the length of the strands.

[0363] Neither the identity of the sense sequence nor the homology of the antisense sequence need be 100% complementary to the target.

[0364] Separating the sense and antisense sequence of the stem loop structure is a loop (also known as a loop motif). The loop may be of any length, between 4-30 nucleotides, between 4-20 nucleotides, between 4-15 nucleotides, between 5-15 nucleotides, between 6-12 nucleotides, 6 nucleotides, 7, nucleotides, 8 nucleotides, 9 nucleotides, 10 nucleotides, 11 nucleotides, and/or 12 nucleotides.

[0365] In some embodiments, the loop comprises at least one UGUG motif. In some embodiments, the UGUG motif is located at the 5' terminus of the loop.

[0366] Spacer regions may be present in the modulatory polynucleotide to separate one or more modules from one another. There may be one or more such spacer regions present.

[0367] In one embodiment, a spacer region of between 8-20, i.e., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides may be present between the sense sequence and a flanking sequence.

[0368] In one embodiment, the spacer is 13 nucleotides and is located between the 5' terminus of the sense sequence and a flanking sequence. In one embodiment, a spacer is of sufficient length to form approximately one helical turn of the sequence.

[0369] In one embodiment, a spacer region of between 8-20, i.e., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides may be present between the antisense sequence and a flanking sequence.

[0370] In one embodiment, the spacer sequence is between 10-13, i.e., 10, 11, 12 or 13 nucleotides and is located between the 3' terminus of the antisense sequence and a flanking sequence. In one embodiment, a spacer is of sufficient length to form approximately one helical turn of the sequence.

[0371] In one embodiment, the modulatory polynucleotide comprises in the 5' to 3' direction, a 5' flanking sequence, a 5' arm, a loop motif, a 3' arm and a 3' flanking sequence. As a non-limiting example, the 5' arm may comprise a sense sequence and the 3' arm comprises the antisense sequence. In another non-limiting example, the 5' arm comprises the antisense sequence and the 3' arm comprises the sense sequence.

[0372] In one embodiment, the 5' arm, payload (e.g., sense and/or antisense sequence), loop motif and/or 3' arm sequence may be altered (e.g., substituting 1 or more nucleotides, adding nucleotides and/or deleting nucleotides). The alteration may cause a beneficial change in the function of the construct (e.g., increase knock-down of the target sequence, reduce degradation of the construct, reduce off target effect, increase efficiency of the payload, and reduce degradation of the payload).

[0373] In one embodiment, the molecular scaffold of the modulatory polynucleotides is aligned in order to have the rate of excision of the guide strand be greater than the rate of excision of the passenger strand. The rate of excision of the guide or passenger strand may be, independently, 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99%. As a non-

limiting example, the rate of excision of the guide strand is at least 80%. As another non-limiting example, the rate of excision of the guide strand is at least 90%.

[0374] In one embodiment, the rate of excision of the guide strand is greater than the rate of excision of the passenger strand. In one aspect, the rate of excision of the guide strand may be at least 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99% greater than the passenger strand.

[0375] In one embodiment, the efficiency of excision of the guide strand is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 99% or more than 99%. As a non-limiting example, the efficiency of the excision of the guide strand is greater than 80%.

[0376] In one embodiment, the efficiency of the excision of the guide strand is greater than the excision of the passenger strand from the molecular scaffold. The excision of the guide strand may be 2, 3, 4, 5, 6, 7, 8, 9, 10 or more than 10 times more efficient than the excision of the passenger strand from the molecular scaffold.

[0377] In one embodiment, the molecular scaffold comprises a dual-function targeting modulatory polynucleotide. As used herein, a "dual-function targeting" modulatory polynucleotide is a polynucleotide where both the guide and passenger strands knock down the same target or the guide and passenger strands knock down different targets.

[0378] In one embodiment, the molecular scaffold of the modulatory polynucleotides described herein comprise a 5' flanking region, a loop region and a 3' flanking region. Non-limiting examples of the sequences for the 5' flanking region, loop region and the 3' flanking region which may be used in the molecular scaffolds described herein are shown in Tables 10-12.

Table 10. 5' Flanking Regions for Molecular Scaffold

5' Flanking Region Name	5' Flanking Region Sequence	5' Flanking Region SEQ ID NO
5F1	UUUAUGCCUCAUCCUCUGAGUGCUGAAGGCUUGCUGUAGGCU GUAUGCUG	1772
5F2	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGC GCUCUUCGGAA	1773
5F3	GAAGCAAAGAAGGGGCAGAGGGAGCCCGUGAGCUGAGUGGGC CAGGGACUGGGAGAAGGAGUGAGGAGGCAGGGCCGGCAUGCC UCUGCUGCUGGCCAGA	1774
5F4	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGC GCUCUUCGGGA	1775
5F5	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGC GCUCCACGGAA	1776
5F6	GGGCCCUCCCGCAGAACACCAUGCGCUCCACGGAA	1777

5F7	CUCCCGCAGAACACCAUGCGCUCCACGGAA	1778
5F8	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGC GCUCCACGGAAG	1779
5F9	GUGCUGGGCGGGGGGCGGCGGGCCCUCCCGCAGAACACCAUGC GCUCCUCGGAA	1780

Table 11. Loop Motif

Loop Motif Region Name	Loop Motif Region Sequence	Loop Motif Region SEQ ID NO
L1	UGUGACCUGG	1781
L2	UGUGAUUUGG	1782
L3	UAUAAUUUGG	1783
L4	CCUGACCCAGU	1784
L5	GUCUGCACCUGUCACUAG	1785
L6	GUGACCCAAG	1786
L7	GUGGCCACUGAGAAG	1787
L8	GUGACCCAAU	1788
L9	GUGACCCAAC	1789

Table 12. 3'Flanking Regions for Molecular Scaffold

3' Flanking Region Name	3' Flanking Region Sequence	3' Flanking Region SEQ ID NO
3F1	AGUGUAUGAUGCCUGUUACUAGCAUUCACAUGGAACA AAUUGCUGCCGUG	1791
3F2	CUGAGGAGCGCCUUGACAGCAGCCAUGGGAGGGCCGCC CCCUACCUCAGUGA	1792
3F3	CUGUGGAGCGCCUUGACAGCAGCCAUGGGAGGGCCGCC CCCUACCUCAGUGA	1793
3F4	UGGCCGUGUAGUGCUACCCAGCGCUGGCUGCCUCCUCA GCAUUGCAAUUCCUCUCCCAUCUGGGCACCAGUCAGCU ACCCUGGUGGGAAUCUGGGUAGCC	1794
3F5	GGCCGUGUAGUGCUACCCAGCGCUGGCUGCCUCCUCAG CAUUGCAAUUCCUCUCCCAUCUGGGCACCAGUCAGCUA CCCUGGUGGGAAUCUGGGUAGCC	1795
3F6	UCCUGAGGAGCGCCUUGACAGCAGCCAUGGGAGGGCC GCCCCCUACCUCAGUGA	1796
3F7	CUGAGGAGCGCCUUGACAGCAGCCAUGGGAGGGCC	1797
3F8	CUGCGGAGCGCCUUGACAGCAGCCAUGGGAGGGCCGCC CCCUACCUCAGUGA	1798

[0379] Any of the regions described in Tables 8-10 may be used in the molecular scaffolds described herein.

[0380] In one embodiment, the molecular scaffold may comprise one 5' flanking region listed in Table 10. As a non-limiting example, the molecular scaffold may comprise the 5' flanking region 5F1, 5F2, 5F3, 5F4, 5F5, 5F6, 5F7, 5F8 or 5F9.

[0381] In one embodiment, the molecular scaffold may comprise one loop motif region listed in Table 11. As a non-limiting example, the molecular scaffold may comprise the loop motif region L1, L2, L3, L4, L5, L6, L7, L8, L9, or L10.

[0382] In one embodiment, the molecular scaffold may comprise one 3' flanking region listed in Table 12. As a non-limiting example, the molecular scaffold may comprise the 3' flanking region 3F1, 3F2, 3F3, 3F4, 3F5, 3F6, 3F7 or 3F8.

[0383] In one embodiment, the molecular scaffold may comprise at least one 5' flanking region and at least one loop motif region as described in Tables 10 and 11. As a non-limiting example, the molecular scaffold may comprise 5F1 and L1, 5F1 and L2, 5F1 and L3, 5F1 and L4, 5F1 and L5, 5F1 and L6, 5F1 and L7, 5F1 and L8, 5F1 and L9, 5F1 and L10, 5F2 and L1, 5F2 and L2, 5F2 and L3, 5F2 and L4, 5F2 and L5, 5F2 and L6, 5F2 and L7, 5F2 and L8, 5F2 and L9, 5F2 and L10, 5F3 and L1, 5F3 and L2, 5F3 and L3, 5F3 and L4, 5F3 and L5, 5F3 and L6, 5F3 and L7, 5F3 and L8, 5F3 and L9, 5F3 and L10, 5F4 and L1, 5F4 and L2, 5F4 and L3, 5F4 and L4, 5F4 and L5, 5F4 and L6, 5F4 and L7, 5F4 and L8, 5F4 and L9, 5F4 and L10, 5F5 and L1, 5F5 and L2, 5F5 and L3, 5F5 and L4, 5F5 and L5, 5F5 and L6, 5F5 and L7, 5F5 and L8, 5F5 and L9, 5F5 and L10, 5F6 and L1, 5F6 and L2, 5F6 and L3, 5F6 and L4, 5F6 and L5, 5F6 and L6, 5F6 and L7, 5F6 and L8, 5F6 and L9, 5F6 and L10, 5F7 and L1, 5F7 and L2, 5F7 and L3, 5F7 and L4, 5F7 and L5, 5F7 and L6, 5F7 and L7, 5F7 and L8, 5F7 and L9, 5F7 and L10, 5F8 and L1, 5F8 and L2, 5F8 and L3, 5F8 and L4, 5F8 and L5, 5F8 and L6, 5F8 and L7, 5F8 and L8, 5F8 and L9, 5F8 and L10, 5F9 and L1, 5F9 and L2, 5F9 and L3, 5F9 and L4, 5F9 and L5, 5F9 and L6, 5F9 and L7, 5F9 and L8, 5F9 and L9, or 5F9 and L10.

[0384] In one embodiment, the molecular scaffold may comprise at least one 3' flanking region and at least one loop motif region as described in Tables 11 and 12. As a non-limiting example, the molecular scaffold may comprise 3F1 and L1, 3F1 and L2, 3F1 and L3, 3F1 and L4, 3F1 and L5, 3F1 and L6, 3F1 and L7, 3F1 and L8, 3F1 and L9, 3F1 and L10, 3F2 and L1, 3F2 and L2, 3F2 and L3, 3F2 and L4, 3F2 and L5, 3F2 and L6, 3F2 and L7, 3F2 and L8, 3F2 and L9, 3F2 and L10, 3F3 and L1, 3F3 and L2, 3F3 and L3, 3F3 and L4, 3F3 and L5, 3F3 and L6, 3F3 and L7, 3F3 and L8, 3F3 and L9, 3F3 and L10, 3F4 and L1, 3F4 and L2, 3F4 and L3, 3F4 and L4, 3F4 and L5, 3F4 and L6, 3F4 and L7, 3F4 and L8, 3F4 and L9, 3F4 and L10, 3F5 and L1, 3F5 and L2, 3F5 and L3, 3F5 and L4, 3F5 and L5, 3F5 and L6, 3F5 and L7, 3F5 and L8, 3F5 and L9, 3F5 and L10, 3F6 and L1, 3F6 and L2, 3F6 and L3, 3F6 and L4, 3F6 and L5, 3F6 and L6, 3F6 and L7, 3F6 and L8, 3F6 and L9, 3F6 and L10, 3F7

and L1, 3F7 and L2, 3F7 and L3, 3F7 and L4, 3F7 and L5, 3F7 and L6, 3F7 and L7, 3F7 and L8, 3F7 and L9, 3F7 and L10, 3F8 and L1, 3F8 and L2, 3F8 and L3, 3F8 and L4, 3F8 and L5, 3F8 and L6, 3F8 and L7, 3F8 and L8, 3F8 and L9, or 3F8 and L10.

[0385] In one embodiment, the molecular scaffold may comprise at least one 5' flanking region and at least 3' flanking region as described in Tables 10 and 12. As a non-limiting example, the molecular scaffold may comprise 5F1 and 3F1, 5F1 and 3F2, 5F1 and 3F3, 5F1 and 3F4, 5F1 and 3F5, 5F1 and 3F6, 5F1 and 3F7, 5F1 and 3F8, 5F2 and 3F1, 5F2 and 3F2, 5F2 and 3F3, 5F2 and 3F4, 5F2 and 3F5, 5F2 and 3F6, 5F2 and 3F7, 5F2 and 3F8, 5F3 and 3F1, 5F3 and 3F2, 5F3 and 3F3, 5F3 and 3F4, 5F3 and 3F5, 5F3 and 3F6, 5F3 and 3F7, 5F3 and 3F8, 5F4 and 3F1, 5F4 and 3F2, 5F4 and 3F3, 5F4 and 3F4, 5F4 and 3F5, 5F4 and 3F6, 5F4 and 3F7, 5F4 and 3F8, 5F5 and 3F1, 5F5 and 3F2, 5F5 and 3F3, 5F5 and 3F4, 5F5 and 3F5, 5F5 and 3F6, 5F5 and 3F7, 5F5 and 3F8, 5F6 and 3F1, 5F6 and 3F2, 5F6 and 3F3, 5F6 and 3F4, 5F6 and 3F5, 5F6 and 3F6, 5F6 and 3F7, 5F6 and 3F8, 5F7 and 3F1, 5F7 and 3F2, 5F7 and 3F3, 5F7 and 3F4, 5F7 and 3F5, 5F7 and 3F6, 5F7 and 3F7, 5F7 and 3F8, 5F8 and 3F1, 5F8 and 3F2, 5F8 and 3F3, 5F8 and 3F4, 5F8 and 3F5, 5F8 and 3F6, 5F8 and 3F7, 5F8 and 3F8, 5F9 and 3F1, 5F9 and 3F2, 5F9 and 3F3, 5F9 and 3F4, 5F9 and 3F5, 5F9 and 3F6, 5F9 and 3F7, or 5F9 and 3F8.

[0386] In one embodiment, the molecular scaffold may comprise at least one 5' flanking region, at least one loop motif region and at least one 3' flanking region as described in Tables 10-12. As a non-limiting example, the molecular scaffold may comprise 5F1, L1 and 3F1; 5F1, L1 and 3F2; 5F1, L1 and 3F3; 5F1, L1 and 3F4; 5F1, L1 and 3F5; 5F1, L1 and 3F6; 5F1, L1 and 3F7; 5F1, L1 and 3F8; 5F2, L1 and 3F1; 5F2, L1 and 3F2; 5F2, L1 and 3F3; 5F2, L1 and 3F4; 5F2, L1 and 3F5; 5F2, L1 and 3F6; 5F2, L1 and 3F7; 5F2, L1 and 3F8; 5F3, L1 and 3F1; 5F3, L1 and 3F2; 5F3, L1 and 3F3; 5F3, L1 and 3F4; 5F3, L1 and 3F5; 5F3, L1 and 3F6; 5F3, L1 and 3F7; 5F3, L1 and 3F8; 5F4, L1 and 3F1; 5F4, L1 and 3F2; 5F4, L1 and 3F3; 5F4, L1 and 3F4; 5F4, L1 and 3F5; 5F4, L1 and 3F6; 5F4, L1 and 3F7; 5F4, L1 and 3F8; 5F5, L1 and 3F1; 5F5, L1 and 3F2; 5F5, L1 and 3F3; 5F5, L1 and 3F4; 5F5, L1 and 3F5; 5F5, L1 and 3F6; 5F5, L1 and 3F7; 5F5, L1 and 3F8; 5F6, L1 and 3F1; 5F6, L1 and 3F2; 5F6, L1 and 3F3; 5F6, L1 and 3F4; 5F6, L1 and 3F5; 5F6, L1 and 3F6; 5F6, L1 and 3F7; 5F6, L1 and 3F8; 5F7, L1 and 3F1; 5F7, L1 and 3F2; 5F7, L1 and 3F3; 5F7, L1 and 3F4; 5F7, L1 and 3F5; 5F7, L1 and 3F6; 5F7, L1 and 3F7; 5F7, L1 and 3F8; 5F8, L1 and 3F1; 5F8, L1 and 3F2; 5F8, L1 and 3F3; 5F8, L1 and 3F4; 5F8, L1 and 3F5; 5F8, L1 and 3F6; 5F8, L1 and 3F7; 5F8, L1 and 3F8; 5F9, L1 and 3F1; 5F9, L1 and

3F2; 5F9, L1 and 3F3; 5F9, L1 and 3F4; 5F9, L1 and 3F5; 5F9, L1 and 3F6; 5F9, L1 and 3F7; 5F9, L1 and 3F8; 5F1, L2 and 3F1; 5F1, L2 and 3F2; 5F1, L2 and 3F3; 5F1, L2 and 3F4; 5F1, L2 and 3F5; 5F1, L2 and 3F6; 5F1, L2 and 3F7; 5F1, L2 and 3F8; 5F2, L2 and 3F1; 5F2, L2 and 3F2; 5F2, L2 and 3F3; 5F2, L2 and 3F4; 5F2, L2 and 3F5; 5F2, L2 and 3F6; 5F2, L2 and 3F7; 5F2, L2 and 3F8; 5F3, L2 and 3F1; 5F3, L2 and 3F2; 5F3, L2 and 3F3; 5F3, L2 and 3F4; 5F3, L2 and 3F5; 5F3, L2 and 3F6; 5F3, L2 and 3F7; 5F3, L2 and 3F8; 5F4, L2 and 3F1; 5F4, L2 and 3F2; 5F4, L2 and 3F3; 5F4, L2 and 3F4; 5F4, L2 and 3F5; 5F4, L2 and 3F6; 5F4, L2 and 3F7; 5F4, L2 and 3F8; 5F5, L2 and 3F1; 5F5, L2 and 3F2; 5F5, L2 and 3F3; 5F5, L2 and 3F4; 5F5, L2 and 3F5; 5F5, L2 and 3F6; 5F5, L2 and 3F7; 5F5, L2 and 3F8; 5F6, L2 and 3F1; 5F6, L2 and 3F2; 5F6, L2 and 3F3; 5F6, L2 and 3F4; 5F6, L2 and 3F5; 5F6, L2 and 3F6; 5F6, L2 and 3F7; 5F6, L2 and 3F8; 5F7, L2 and 3F1; 5F7, L2 and 3F2; 5F7, L2 and 3F3; 5F7, L2 and 3F4; 5F7, L2 and 3F5; 5F7, L2 and 3F6; 5F7, L2 and 3F7; 5F7, L2 and 3F8; 5F8, L2 and 3F1; 5F8, L2 and 3F2; 5F8, L2 and 3F3; 5F8, L2 and 3F4; 5F8, L2 and 3F5; 5F8, L2 and 3F6; 5F8, L2 and 3F7; 5F8, L2 and 3F8; 5F9, L2 and 3F1; 5F9, L2 and 3F2; 5F9, L2 and 3F3; 5F9, L2 and 3F4; 5F9, L2 and 3F5; 5F9, L2 and 3F6; 5F9, L2 and 3F7; 5F9, L2 and 3F8; 5F1, L3 and 3F1; 5F1, L3 and 3F2; 5F1, L3 and 3F3; 5F1, L3 and 3F4; 5F1, L3 and 3F5; 5F1, L3 and 3F6; 5F1, L3 and 3F7; 5F1, L3 and 3F8; 5F2, L3 and 3F1; 5F2, L3 and 3F2; 5F2, L3 and 3F3; 5F2, L3 and 3F4; 5F2, L3 and 3F5; 5F2, L3 and 3F6; 5F2, L3 and 3F7; 5F2, L3 and 3F8; 5F3, L3 and 3F1; 5F3, L3 and 3F2; 5F3, L3 and 3F3; 5F3, L3 and 3F4; 5F3, L3 and 3F5; 5F3, L3 and 3F6; 5F3, L3 and 3F7; 5F3, L3 and 3F8; 5F4, L3 and 3F1; 5F4, L3 and 3F2; 5F4, L3 and 3F3; 5F4, L3 and 3F4; 5F4, L3 and 3F5; 5F4, L3 and 3F6; 5F4, L3 and 3F7; 5F4, L3 and 3F8; 5F5, L3 and 3F1; 5F5, L3 and 3F2; 5F5, L3 and 3F3; 5F5, L3 and 3F4; 5F5, L3 and 3F5; 5F5, L3 and 3F6; 5F5, L3 and 3F7; 5F5, L3 and 3F8; 5F6, L3 and 3F1; 5F6, L3 and 3F2; 5F6, L3 and 3F3; 5F6, L3 and 3F4; 5F6, L3 and 3F5; 5F6, L3 and 3F6; 5F6, L3 and 3F7; 5F6, L3 and 3F8; 5F7, L3 and 3F1; 5F7, L3 and 3F2; 5F7, L3 and 3F3; 5F7, L3 and 3F4; 5F7, L3 and 3F5; 5F7, L3 and 3F6; 5F7, L3 and 3F7; 5F7, L3 and 3F8; 5F8, L3 and 3F1; 5F8, L3 and 3F2; 5F8, L3 and 3F3; 5F8, L3 and 3F4; 5F8, L3 and 3F5; 5F8, L3 and 3F6; 5F8, L3 and 3F7; 5F8, L3 and 3F8; 5F9, L3 and 3F1; 5F9, L3 and 3F2; 5F9, L3 and 3F3; 5F9, L3 and 3F4; 5F9, L3 and 3F5; 5F9, L3 and 3F6; 5F9, L3 and 3F7; 5F9, L3 and 3F8; 5F1, L4 and 3F1; 5F1, L4 and 3F2; 5F1, L4 and 3F3; 5F1, L4 and 3F4; 5F1, L4 and 3F5; 5F1, L4 and 3F6; 5F1, L4 and 3F7; 5F1, L4 and 3F8; 5F2, L4 and 3F1; 5F2, L4 and 3F2; 5F2, L4 and 3F3; 5F2, L4 and 3F4; 5F2, L4 and 3F5; 5F2, L4 and 3F6; 5F2, L4 and

3F7; 5F2, L4 and 3F8; 5F3, L4 and 3F1; 5F3, L4 and 3F2; 5F3, L4 and 3F3; 5F3, L4 and 3F4; 5F3, L4 and 3F5; 5F3, L4 and 3F6; 5F3, L4 and 3F7; 5F3, L4 and 3F8; 5F4, L4 and 3F1; 5F4, L4 and 3F2; 5F4, L4 and 3F3; 5F4, L4 and 3F4; 5F4, L4 and 3F5; 5F4, L4 and 3F6; 5F4, L4 and 3F7; 5F4, L4 and 3F8; 5F5, L4 and 3F1; 5F5, L4 and 3F2; 5F5, L4 and 3F3; 5F5, L4 and 3F4; 5F5, L4 and 3F5; 5F5, L4 and 3F6; 5F5, L4 and 3F7; 5F5, L4 and 3F8; 5F6, L4 and 3F1; 5F6, L4 and 3F2; 5F6, L4 and 3F3; 5F6, L4 and 3F4; 5F6, L4 and 3F5; 5F6, L4 and 3F6; 5F6, L4 and 3F7; 5F6, L4 and 3F8; 5F7, L4 and 3F1; 5F7, L4 and 3F2; 5F7, L4 and 3F3; 5F7, L4 and 3F4; 5F7, L4 and 3F5; 5F7, L4 and 3F6; 5F7, L4 and 3F7; 5F7, L4 and 3F8; 5F8, L4 and 3F1; 5F8, L4 and 3F2; 5F8, L4 and 3F3; 5F8, L4 and 3F4; 5F8, L4 and 3F5; 5F8, L4 and 3F6; 5F8, L4 and 3F7; 5F8, L4 and 3F8; 5F9, L4 and 3F1; 5F9, L4 and 3F2; 5F9, L4 and 3F3; 5F9, L4 and 3F4; 5F9, L4 and 3F5; 5F9, L4 and 3F6; 5F9, L4 and 3F7; 5F9, L4 and 3F8; 5F1, L5 and 3F1; 5F1, L5 and 3F2; 5F1, L5 and 3F3; 5F1, L5 and 3F4; 5F1, L5 and 3F5; 5F1, L5 and 3F6; 5F1, L5 and 3F7; 5F1, L5 and 3F8; 5F2, L5 and 3F1; 5F2, L5 and 3F2; 5F2, L5 and 3F3; 5F2, L5 and 3F4; 5F2, L5 and 3F5; 5F2, L5 and 3F6; 5F2, L5 and 3F7; 5F2, L5 and 3F8; 5F3, L5 and 3F1; 5F3, L5 and 3F2; 5F3, L5 and 3F3; 5F3, L5 and 3F4; 5F3, L5 and 3F5; 5F3, L5 and 3F6; 5F3, L5 and 3F7; 5F3, L5 and 3F8; 5F4, L5 and 3F1; 5F4, L5 and 3F2; 5F4, L5 and 3F3; 5F4, L5 and 3F4; 5F4, L5 and 3F5; 5F4, L5 and 3F6; 5F4, L5 and 3F7; 5F4, L5 and 3F8; 5F5, L5 and 3F1; 5F5, L5 and 3F2; 5F5, L5 and 3F3; 5F5, L5 and 3F4; 5F5, L5 and 3F5; 5F5, L5 and 3F6; 5F5, L5 and 3F7; 5F5, L5 and 3F8; 5F6, L5 and 3F1; 5F6, L5 and 3F2; 5F6, L5 and 3F3; 5F6, L5 and 3F4; 5F6, L5 and 3F5; 5F6, L5 and 3F6; 5F6, L5 and 3F7; 5F6, L5 and 3F8; 5F7, L5 and 3F1; 5F7, L5 and 3F2; 5F7, L5 and 3F3; 5F7, L5 and 3F4; 5F7, L5 and 3F5; 5F7, L5 and 3F6; 5F7, L5 and 3F7; 5F7, L5 and 3F8; 5F8, L5 and 3F1; 5F8, L5 and 3F2; 5F8, L5 and 3F3; 5F8, L5 and 3F4; 5F8, L5 and 3F5; 5F8, L5 and 3F6; 5F8, L5 and 3F7; 5F8, L5 and 3F8; 5F9, L5 and 3F1; 5F9, L5 and 3F2; 5F9, L5 and 3F3; 5F9, L5 and 3F4; 5F9, L5 and 3F5; 5F9, L5 and 3F6; 5F9, L5 and 3F7; or 5F9, L5 and 3F8.

[0387] In one embodiment, the molecular scaffold may comprise one or more linkers known in the art. The linkers may separate regions or one molecular scaffold from another. As a non-limiting example, the molecular scaffold may be polycistronic.

[0388] In one embodiment, the modulatory polynucleotide is designed using at least one of the following properties: loop variant, seed mismatch/bulge/wobble variant, stem mismatch, loop variant and basal stem mismatch variant, seed mismatch and basal stem

mismatch variant, stem mismatch and basal stem mismatch variant, seed wobble and basal stem wobble variant, or a stem sequence variant.

Introduction into cells

[0389] siRNA molecules may be delivered to target cells for targeting the gene of interest inside the target cells. In some embodiments, the cells may include, but are not limited to, cells of mammalian origin, cells of human origins, embryonic stem cells, induced pluripotent stem cells, neural stem cells, neural progenitor cells, and differentiated neural cells.

[0390] In some embodiments, the siRNA molecules (e.g., siRNA duplexes) of may be introduced into target cells using viral vectors such as AAV particles. These AAV particles are engineered and optimized to facilitate the entry of siRNA molecule into cells that are not readily amendable to transfection, e.g., neurons. Also, some synthetic viral vectors possess an ability to integrate the shRNA into the cell genome, thereby leading to stable siRNA expression and long-term knockdown of a target gene. In this manner, viral vectors are engineered as vehicles for specific delivery while lacking the deleterious replication and/or integration features found in wild-type virus.

[0391] In some embodiments, the siRNA molecules are introduced into a cell by contacting the cell with a composition comprising a lipophilic carrier and an AAV particle comprising a nucleic acid sequence encoding the siRNA molecules. In other embodiments, the siRNA molecule is introduced into a cell by transfecting or infecting the cell with an AAV particle comprising nucleic acid sequences capable of producing the siRNA molecule when transcribed in the cell. In some embodiments, the siRNA molecule is introduced into a cell by injecting into the cell an AAV particle comprising a nucleic acid sequence capable of producing the siRNA molecule when transcribed in the cell.

[0392] In some embodiments, an AAV particle comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be transduced into cells.

[0393] In other embodiments, the AAV particles comprising the nucleic acid sequence encoding the siRNA molecules may be delivered into cells by electroporation (e.g. U.S. Patent Application Publication No. 20050014264; the contents of which are herein incorporated by reference in their entirety).

[0394] Other methods for introducing AAV particles comprising the nucleic acid sequence for the siRNA molecules described herein may include photochemical

internalization as described in U. S. Patent Application Publication No. 20120264807; the contents of which are herein incorporated by reference in their entirety.

[0395] In one embodiment, the AAV particles from any relevant species, such as, but not limited to, human, dog, mouse, rat or monkey may be introduced into cells.

[0396] In one embodiment, the AAV particles may be introduced into cells which are relevant to the disease to be treated. As a non-limiting example, the disease is a tauopathy and/or Alzheimer's Disease and the target cells are entorhinal cortex, hippocampal or cortical neurons.

[0397] In one embodiment, the AAV particles may be introduced into cells which have a high level of endogenous expression of the target sequence.

[0398] In another embodiment, the AAV particles may be introduced into cells which have a low level of endogenous expression of the target sequence.

[0399] In one embodiment, the cells may be those which have a high efficiency of AAV transduction.

[0400] In other embodiments, AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to deliver siRNA molecules to the central nervous system (e.g., U.S. Pat. No. 6,180,613; the contents of which are herein incorporated by reference in their entirety).

[0401] In some aspects, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may further comprise a modified capsid including peptides from non-viral origin. In other aspects, the AAV particle may contain a CNS specific (e.g., tropism for CNS or CNS tissues) chimeric capsid to facilitate the delivery of encoded siRNA duplexes into the brain and the spinal cord. For example, an alignment of cap nucleotide sequences from AAV variants exhibiting CNS tropism may be constructed to identify variable region (VR) sequence and structure.

[0402] In one embodiment, the AAV particle comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may encode siRNA molecules which are polycistronic molecules. The siRNA molecules may additionally comprise one or more linkers between regions of the siRNA molecules.

[0403] In one embodiment, an AAV particle may comprise at least one of the modulatory polynucleotides encoding at least one of the siRNA sequences or duplexes described herein.

[0404] In one embodiment, an expression vector or viral genome may comprise, from ITR to ITR recited 5' to 3', an ITR, a promoter, an intron, a modulatory polynucleotide, a polyA sequence and an ITR.

[0405] In one embodiment, the encoded siRNA molecule may be located downstream of a promoter in an expression vector such as, but not limited to, CMV, U6, H1, CBA or a CBA promoter with a SV40 intron. Further, the encoded siRNA molecule may also be located upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector.

[0406] In one embodiment, the encoded siRNA molecule may be located upstream of the polyadenylation sequence in an expression vector. Further, the encoded siRNA molecule may be located downstream of a promoter such as, but not limited to, CMV, U6, CBA or a CBA promoter with a SV40 intron in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within the first 1%, 2%, 3%, 4%, 5%,

6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the promoter and/or upstream of the polyadenylation sequence in an expression vector.

[0407] In one embodiment, the encoded siRNA molecule may be located in a scAAV.

[0408] In one embodiment, the encoded siRNA molecule may be located in an ssAAV.

[0409] In one embodiment, the encoded siRNA molecule may be located near the 5' end of the flip ITR in an expression vector. In another embodiment, the encoded siRNA molecule may be located near the 3' end of the flip ITR in an expression vector. In yet another embodiment, the encoded siRNA molecule may be located near the 5' end of the flop ITR in an expression vector. In yet another embodiment, the encoded siRNA molecule may be located near the 3' end of the flop ITR in an expression vector. In one embodiment, the encoded siRNA molecule may be located between the 5' end of the flip ITR and the 3' end of the flop ITR in an expression vector. In one embodiment, the encoded siRNA molecule may be located between (e.g., half-way between the 5' end of the flip ITR and 3' end of the flop ITR or the 3' end of the flop ITR and the 5' end of the flip ITR), the 3' end of the flip ITR and the 5' end of the flip ITR in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more than 30 nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 nucleotides downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located within 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 5-10, 5-15, 5-20, 5-25, 5-30, 10-15, 10-20, 10-25, 10-30, 15-20, 15-25, 15-30, 20-25, 20-30 or 25-30 upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As a non-limiting example, the encoded siRNA molecule may be located

within the first 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25% or more than 25% of the nucleotides upstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector. As another non-limiting example, the encoded siRNA molecule may be located with the first 1-5%, 1-10%, 1-15%, 1-20%, 1-25%, 5-10%, 5-15%, 5-20%, 5-25%, 10-15%, 10-20%, 10-25%, 15-20%, 15-25%, or 20-25% downstream from the 5' or 3' end of an ITR (e.g., Flip or Flop ITR) in an expression vector.

[0410] In one embodiment, AAV particle comprising the nucleic acid sequence for the siRNA molecules may be formulated for CNS delivery. Agents that cross the brain blood barrier may be used. Capsids engineered for efficient crossing of the blood brain barrier may be used. Non-limiting examples of such capsids or peptide inserts include VOY101, VOY201, AAVPHP.N, AAVPHP.A, AAVPHP.B, PHP.B2, PHP.B3, G2A3, G2B4, G2B5, PHP.S, and variants thereof. For example, some cell penetrating peptides that can target siRNA molecules to the brain blood barrier endothelium may be used to formulate the siRNA duplexes targeting the gene of interest.

[0411] In one embodiment, AAV particle comprising the nucleic acid sequence for the payloads of interest (e.g., Frataxin, APOE, Tau) of the present invention may be formulated for CNS delivery. Agents that cross the brain blood barrier may be used. Capsids engineered for efficient crossing of the blood brain barrier may be used. Non-limiting examples of such capsids or peptide inserts include VOY101, VOY201, AAVPHP.N, AAVPHP.A, AAVPHP.B, PHP.B2, PHP.B3, G2A3, G2B4, G2B5, PHP.S, and variants thereof. For example, some cell penetrating peptides that deliver the payload to the brain blood barrier endothelium may be used to formulate the payload of the gene of interest.

[0412] In one embodiment, the AAV particle comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be administered directly to the CNS. As a non-limiting example, the vector comprises a nucleic acid sequence encoding the siRNA molecules targeting ApoE2. As a non-limiting example, the vector comprises a nucleic acid sequence encoding the siRNA molecules targeting ApoE3. As a non-limiting example, the vector comprises a nucleic acid sequence encoding the siRNA molecules targeting ApoE4. As a non-limiting example, the vector comprises a nucleic acid sequence encoding the siRNA molecules targeting SOD1. As a non-limiting example, the vector comprises a nucleic acid sequence encoding the siRNA molecules targeting HTT. As a non-limiting example, the vector comprises a nucleic acid sequence encoding the siRNA molecules targeting Tau.

[0413] In specific embodiments, compositions of AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be administered in a way which facilitates the vectors or siRNA molecule to enter the central nervous system and penetrate into CNS tissues and/or cells.

[0414] In one embodiment, the AAV particle may be administered to a subject (e.g., to the CNS of a subject via intrathecal administration) in a therapeutically effective amount for the siRNA duplexes or dsRNA to target the motor neurons and astrocytes in the spinal cord and/or brain stem. As a non-limiting example, the siRNA duplexes or dsRNA may reduce the expression of a target protein or mRNA. As another non-limiting example, the siRNA duplexes or dsRNA can suppress a target gene or protein and reduce target gene or protein mediated toxicity. The reduction of target protein and/or mRNA as well as target gene and/or protein mediated toxicity may be accomplished with almost no enhanced inflammation.

II. FORMULATION AND DELIVERY

Pharmaceutical Compositions

[0415] According to the present invention the AAV particles may be prepared as pharmaceutical compositions. It will be understood that such compositions necessarily comprise one or more active ingredients and, most often, a pharmaceutically acceptable excipient.

[0416] Relative amounts of the active ingredient (e.g. AAV particle), a pharmaceutically acceptable excipient, and/or any additional ingredients in a pharmaceutical composition in accordance with the present disclosure may vary, depending upon the identity, size, and/or condition of the subject being treated and further depending upon the route by which the composition is to be administered. For example, the composition may comprise between 0.1% and 99% (w/w) of the active ingredient. By way of example, the composition may comprise between 0.1% and 100%, e.g., between .5 and 50%, between 1-30%, between 5-80%, at least 80% (w/w) active ingredient.

[0417] In some embodiments, the AAV particle pharmaceutical compositions described herein may comprise at least one payload. As a non-limiting example, the pharmaceutical compositions may contain an AAV particle with 1, 2, 3, 4 or 5 payloads.

[0418] Although the descriptions of pharmaceutical compositions provided herein are principally directed to pharmaceutical compositions which are suitable for administration to humans, it will be understood by the skilled artisan that such compositions are generally suitable for administration to any other animal, e.g., to non-human animals, e.g. non-human

mammals. Modification of pharmaceutical compositions suitable for administration to humans in order to render the compositions suitable for administration to various animals is well understood, and the ordinarily skilled veterinary pharmacologist can design and/or perform such modification with merely ordinary, if any, experimentation. Subjects to which administration of the pharmaceutical compositions is contemplated include, but are not limited to, humans and/or other primates; mammals, including commercially relevant mammals such as cattle, pigs, horses, sheep, cats, dogs, mice, rats, birds, including commercially relevant birds such as poultry, chickens, ducks, geese, and/or turkeys.

[0419] In some embodiments, compositions are administered to humans, human patients or subjects.

Formulations

[0420] Formulations of the present invention can include, without limitation, saline, liposomes, such preparatory methods include the step of associating the active ingredient with an lipid nanoparticles, polymers, peptides, proteins, cells transfected with viral vectors (e.g., for transfer or transplantation into a subject) and combinations thereof.

[0421] Formulations of the pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. As used herein the term "pharmaceutical composition" refers to compositions comprising at least one active ingredient and optionally one or more pharmaceutically acceptable excipients.

[0422] In generalexcipient and/or one or more other accessory ingredients. As used herein, the phrase "active ingredient" generally refers either to an AAV particle carrying a payload region encoding the polypeptides of the invention or to the end product encoded by a viral genome of an AAV particle as described herein.

[0423] Formulations of the AAV particles and pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient into association with an excipient and/or one or more other accessory ingredients, and then, if necessary and/or desirable, dividing, shaping and/or packaging the product into a desired single- or multi-dose unit.

[0424] A pharmaceutical composition in accordance with the present disclosure may be prepared, packaged, and/or sold in bulk, as a single unit dose, and/or as a plurality of single unit doses. As used herein, a "unit dose" refers to a discrete amount of the pharmaceutical composition comprising a predetermined amount of the active ingredient. The amount of the

active ingredient is generally equal to the dosage of the active ingredient which would be administered to a subject and/or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

[0425] In one embodiment, the AAV particles of the invention may be formulated in PBS with 0.001% of pluronic acid (F-68) at a pH of about 7.0.

[0426] In some embodiments, the AAV formulations described herein may contain sufficient AAV particles for expression of at least one expressed functional payload. As a non-limiting example, the AAV particles may contain viral genomes encoding 1, 2, 3, 4 or 5 functional payloads.

[0427] In some embodiments, the formulations described herein may contain at least one AAV particle comprising the nucleic acid sequence encoding a protein of interest. The protein of interest may include but are not limited to an antibody, AADC, APOE2, Frataxin, ATP2A2, and/or S100A1.

[0428] In some embodiments, the formulations described herein may contain at least one AAV particle comprising the nucleic acid sequence encoding the siRNA molecules described herein. In one embodiment, the siRNA molecules may target gene of interest at one target site. In another embodiment, the formulation comprises a plurality of AAV particles, each AAV particle comprising a nucleic acid sequence encoding a siRNA molecule targeting the gene of interest at a different target site. The target gene may be targeted at 2, 3, 4, 5 or more than 5 sites. In one embodiment, the target gene may include but is not limited to SOD1, HTT, APOE, and MAPT.

[0429] According to the present invention AAV particles may be formulated for CNS delivery. Agents that cross the brain blood barrier may be used. For example, some cell penetrating peptides that can target molecules to the brain blood barrier endothelium may be used for formulation (e.g., Mathupala, *Expert Opin Ther Pat.*, 2009, 19, 137-140; the contents of which are incorporated herein by reference in their entirety).

[0430] In other embodiments, the AAV particles of the present invention may be formulated for delivery to other tissues and organs, e.g., cardiovascular tissues.

Excipients and Diluents

[0431] The AAV particles of the invention can be formulated using one or more excipients or diluents to (1) increase stability; (2) increase cell transfection or transduction; (3) permit the sustained or delayed release of the payload; (4) alter the biodistribution (e.g., target the viral particle to specific tissues or cell types); (5) increase the translation of

encoded protein; (6) alter the release profile of encoded protein and/or (7) allow for regulatable expression of the payload of the invention.

[0432] In some embodiments, a pharmaceutically acceptable excipient may be at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% pure. In some embodiments, an excipient is approved for use for humans and for veterinary use. In some embodiments, an excipient may be approved by United States Food and Drug Administration. In some embodiments, an excipient may be of pharmaceutical grade. In some embodiments, an excipient may meet the standards of the United States Pharmacopoeia (USP), the European Pharmacopoeia (EP), the British Pharmacopoeia, and/or the International Pharmacopoeia.

[0433] Excipients, as used herein, include, but are not limited to, any and all solvents, dispersion media, diluents, or other liquid vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, and the like, as suited to the particular dosage form desired. Various excipients for formulating pharmaceutical compositions and techniques for preparing the composition are known in the art (see Remington: The Science and Practice of Pharmacy, 21st Edition, A. R. Gennaro, Lippincott, Williams & Wilkins, Baltimore, MD, 2006; incorporated herein by reference in its entirety). The use of a conventional excipient medium may be contemplated within the scope of the present disclosure, except insofar as any conventional excipient medium may be incompatible with a substance or its derivatives, such as by producing any undesirable biological effect or otherwise interacting in a deleterious manner with any other component(s) of the pharmaceutical composition.

[0434] Exemplary diluents include, but are not limited to, calcium carbonate, sodium carbonate, calcium phosphate, dicalcium phosphate, calcium sulfate, calcium hydrogen phosphate, sodium phosphate lactose, sucrose, cellulose, microcrystalline cellulose, kaolin, mannitol, sorbitol, inositol, sodium chloride, dry starch, cornstarch, powdered sugar, *etc.*, and/or combinations thereof.

Inactive Ingredients

[0435] In some embodiments, AAV particle formulations may comprise at least one inactive ingredient. As used herein, the term "inactive ingredient" refers to one or more agents that do not contribute to the activity of the active ingredient of the pharmaceutical composition included in formulations. In some embodiments, all, none or some of the

inactive ingredients which may be used in the formulations of the present invention may be approved by the US Food and Drug Administration (FDA).

[0436] In one embodiment, the AAV particle pharmaceutical compositions comprise at least one inactive ingredient such as, but not limited to, 1,2,6-Hexanetriol; 1,2-Dimyristoyl-Sn-Glycero-3-(Phospho-S-(1-Glycerol)); 1,2-Dimyristoyl-Sn-Glycero-3-Phosphocholine; 1,2-Dioleoyl-Sn-Glycero-3-Phosphocholine; 1,2-Dipalmitoyl-Sn-Glycero-3-(Phospho-Rac-(1-Glycerol)); 1,2-Distearoyl-Sn-Glycero-3-(Phospho-Rac-(1-Glycerol)); 1,2-Distearoyl-Sn-Glycero-3-Phosphocholine; 1-O-Tolylbiguanide; 2-Ethyl-1,6-Hexanediol; Acetic Acid; Acetic Acid, Glacial; Acetic Anhydride; Acetone; Acetone Sodium Bisulfite; Acetylated Lanolin Alcohols; Acetylated Monoglycerides; Acetylcysteine; Acetyltryptophan, DL-; Acrylates Copolymer; Acrylic Acid-Isooctyl Acrylate Copolymer; Acrylic Adhesive 788; Activated Charcoal; Adcote 72A103; Adhesive Tape; Adipic Acid; Aerotex Resin 3730; Alanine; Albumin Aggregated; Albumin Colloidal; Albumin Human; Alcohol; Alcohol, Dehydrated; Alcohol, Denatured; Alcohol, Diluted; Alfadex; Alginic Acid; Alkyl Ammonium Sulfonic Acid Betaine; Alkyl Aryl Sodium Sulfonate; Allantoin; Allyl .Alpha.-Ionone; Almond Oil; Alpha-Terpineol; Alpha-Tocopherol; Alpha-Tocopherol Acetate, Dl-; Alpha-Tocopherol, Dl-; Aluminum Acetate; Aluminum Chlorhydroxy Allantoinate; Aluminum Hydroxide; Aluminum Hydroxide - Sucrose, Hydrated; Aluminum Hydroxide Gel; Aluminum Hydroxide Gel F 500; Aluminum Hydroxide Gel F 5000; Aluminum Monostearate; Aluminum Oxide; Aluminum Polyester; Aluminum Silicate; Aluminum Starch Octenylsuccinate; Aluminum Stearate; Aluminum Subacetate; Aluminum Sulfate Anhydrous; Amerchol C; Amerchol-Cab; Aminomethylpropanol; Ammonia; Ammonia Solution; Ammonia Solution, Strong; Ammonium Acetate; Ammonium Hydroxide; Ammonium Lauryl Sulfate; Ammonium Nonoxynol-4 Sulfate; Ammonium Salt Of C-12-C-15 Linear Primary Alcohol Ethoxylate; Ammonium Sulfate; Ammonyx; Amphoteric-2; Amphoteric-9; Anethole; Anhydrous Citric Acid; Anhydrous Dextrose; Anhydrous Lactose; Anhydrous Trisodium Citrate; Aniseed Oil; Anoxid Sbn; Antifoam; Antipyrine; Apaflurane; Apricot Kernel Oil Peg-6 Esters; Aquaphor; Arginine; Arlacel; Ascorbic Acid; Ascorbyl Palmitate; Aspartic Acid; Balsam Peru; Barium Sulfate; Beeswax; Beeswax, Synthetic; Beheneth-10; Bentonite; Benzalkonium Chloride; Benzenesulfonic Acid; Benzethonium Chloride; Benzododecinium Bromide; Benzoic Acid; Benzyl Alcohol; Benzyl Benzoate; Benzyl Chloride; Betadex; Bibapcitide; Bismuth Subgallate; Boric Acid; Brocrinat; Butane; Butyl Alcohol; Butyl Ester Of Vinyl Methyl Ether/Maleic Anhydride Copolymer (125000 Mw);

Butyl Stearate; Butylated Hydroxyanisole; Butylated Hydroxytoluene; Butylene Glycol; Butylparaben; Butyric Acid; C20-40 Pareth-24; Caffeine; Calcium; Calcium Carbonate; Calcium Chloride; Calcium Gluceptate; Calcium Hydroxide; Calcium Lactate; Calcobutrol; Caldiamide Sodium; Caloxetate Trisodium; Calteridol Calcium; Canada Balsam; Caprylic/Capric Triglyceride; Caprylic/Capric/Stearic Triglyceride; Captan; Captisol; Caramel; Carbomer 1342; Carbomer 1382; Carbomer 934; Carbomer 934p; Carbomer 940; Carbomer 941; Carbomer 980; Carbomer 981; Carbomer Homopolymer Type B (Allyl Pentaerythritol Crosslinked); Carbomer Homopolymer Type C (Allyl Pentaerythritol Crosslinked); Carbon Dioxide; Carboxy Vinyl Copolymer; Carboxymethylcellulose; Carboxymethylcellulose Sodium; Carboxypolymethylene; Carrageenan; Carrageenan Salt; Castor Oil; Cedar Leaf Oil; Cellulose; Cellulose, Microcrystalline; Cerasynt-Se; Ceresin; Ceteareth-12; Ceteareth-15; Ceteareth-30; Cetearyl Alcohol/Ceteareth-20; Cetearyl Ethylhexanoate; Ceteth-10; Ceteth-2; Ceteth-20; Ceteth-23; Cetostearyl Alcohol; Cetrimonium Chloride; Cetyl Alcohol; Cetyl Esters Wax; Cetyl Palmitate; Cetylpyridinium Chloride; Chlorobutanol; Chlorobutanol Hemihydrate; Chlorobutanol, Anhydrous; Chlorocresol; Chloroxylenol; Cholesterol; Choleth; Choleth-24; Citrate; Citric Acid; Citric Acid Monohydrate; Citric Acid, Hydrous; Cocamide Ether Sulfate; Cocamine Oxide; Coco Betaine; Coco Diethanolamide; Coco Monoethanolamide; Cocoa Butter; Coco-Glycerides; Coconut Oil; Coconut Oil, Hydrogenated; Coconut Oil/Palm Kernel Oil Glycerides, Hydrogenated; Cocoyl Caprylocaprate; Cola Nitida Seed Extract; Collagen; Coloring Suspension; Corn Oil; Cottonseed Oil; Cream Base; Creatine; Creatinine; Cresol; Croscarmellose Sodium; Crospovidone; Cupric Sulfate; Cupric Sulfate Anhydrous; Cyclomethicone; Cyclomethicone/Dimethicone Copolyol; Cysteine; Cysteine Hydrochloride; Cysteine Hydrochloride Anhydrous; Cysteine, Dl-; D&C Red No. 28; D&C Red No. 33; D&C Red No. 36; D&C Red No. 39; D&C Yellow No. 10; Dalfampridine; Daubert 1-5 Pestr (Matte) 164z; Decyl Methyl Sulfoxide; Dehydag Wax Sx; Dehydroacetic Acid; Dehymuls E; Denatonium Benzoate; Deoxycholic Acid; Dextran; Dextran 40; Dextrin; Dextrose; Dextrose Monohydrate; Dextrose Solution; Diatrizoic Acid; Diazolidinyl Urea; Dichlorobenzyl Alcohol; Dichlorodifluoromethane; Dichlorotetrafluoroethane; Diethanolamine; Diethyl Pyrocarbonate; Diethyl Sebacate; Diethylene Glycol Monoethyl Ether; Diethylhexyl Phthalate; Dihydroxyaluminum Aminoacetate; Diisopropanolamine; Diisopropyl Adipate; Diisopropyl Dilinoleate; Dimethicone 350; Dimethicone Copolyol; Dimethicone Mdx4-4210; Dimethicone Medical Fluid 360; Dimethyl Isosorbide; Dimethyl Sulfoxide;

Dimethylaminoethyl Methacrylate - Butyl Methacrylate - Methyl Methacrylate Copolymer; Dimethyldioctadecylammonium Bentonite; Dimethylsiloxane/Methylvinylsiloxane Copolymer; Dinoseb Ammonium Salt; Dipalmitoylphosphatidylglycerol, Dl-; Dipropylene Glycol; Disodium Cocoamphodiacetate; Disodium Laureth Sulfosuccinate; Disodium Lauryl Sulfosuccinate; Disodium Sulfosalicylate; Disofenin; Divinylbenzene Styrene Copolymer; Dmdm Hydantoin; Docosanol; Docusate Sodium; Duro-Tak 280-2516; Duro-Tak 387-2516; Duro-Tak 80-1196; Duro-Tak 87-2070; Duro-Tak 87-2194; Duro-Tak 87-2287; Duro-Tak 87-2296; Duro-Tak 87-2888; Duro-Tak 87-2979; Edetate Calcium Disodium; Edetate Disodium; Edetate Disodium Anhydrous; Edetate Sodium; Edetic Acid; Egg Phospholipids; Entsufon; Entsufon Sodium; Epilactose; Epitetracycline Hydrochloride; Essence Bouquet 9200; Ethanolamine Hydrochloride; Ethyl Acetate; Ethyl Oleate; Ethylcelluloses; Ethylene Glycol; Ethylene Vinyl Acetate Copolymer; Ethylenediamine; Ethylenediamine Dihydrochloride; Ethylene-Propylene Copolymer; Ethylene-Vinyl Acetate Copolymer (28% Vinyl Acetate); Ethylene-Vinyl Acetate Copolymer (9% Vinylacetate); Ethylhexyl Hydroxystearate; Ethylparaben; Eucalyptol; Exametazime; Fat, Edible; Fat, Hard; Fatty Acid Esters; Fatty Acid Pentaerythriol Ester; Fatty Acids; Fatty Alcohol Citrate; Fatty Alcohols; Fd&C Blue No. 1; Fd&C Green No. 3; Fd&C Red No. 4; Fd&C Red No. 40; Fd&C Yellow No. 10 (Delisted); Fd&C Yellow No. 5; Fd&C Yellow No. 6; Ferric Chloride; Ferric Oxide; Flavor 89-186; Flavor 89-259; Flavor Df-119; Flavor Df-1530; Flavor Enhancer; Flavor Fig 827118; Flavor Raspberry Pfc-8407; Flavor Rhodia Pharmaceutical No. Rf 451; Fluorochlorohydrocarbons; Formaldehyde; Formaldehyde Solution; Fractionated Coconut Oil; Fragrance 3949-5; Fragrance 520a; Fragrance 6.007; Fragrance 91-122; Fragrance 9128-Y; Fragrance 93498g; Fragrance Balsam Pine No. 5124; Fragrance Bouquet 10328; Fragrance Chemoderm 6401-B; Fragrance Chemoderm 6411; Fragrance Cream No. 73457; Fragrance Cs-28197; Fragrance Felton 066m; Fragrance Firmenich 47373; Fragrance Givaudan Ess 9090/1c; Fragrance H-6540; Fragrance Herbal 10396; Fragrance Nj-1085; Fragrance P O Fl-147; Fragrance Pa 52805; Fragrance Pera Derm D; Fragrance Rbd-9819; Fragrance Shaw Mudge U-7776; Fragrance Tf 044078; Fragrance Ungerer Honeysuckle K 2771; Fragrance Ungerer N5195; Fructose; Gadolinium Oxide; Galactose; Gamma Cyclodextrin; Gelatin; Gelatin, Crosslinked; Gelfoam Sponge; Gellan Gum (Low Acyl); Gelva 737; Gentisic Acid; Gentisic Acid Ethanolamide; Gluceptate Sodium; Gluceptate Sodium Dihydrate; Gluconolactone; Glucuronic Acid; Glutamic Acid, Dl-; Glutathione; Glycerin; Glycerol Ester Of Hydrogenated Rosin; Glyceryl Citrate; Glyceryl Isostearate;

Glyceryl Laurate; Glyceryl Monostearate; Glyceryl Oleate; Glyceryl Oleate/Propylene Glycol; Glyceryl Palmitate; Glyceryl Ricinoleate; Glyceryl Stearate; Glyceryl Stearate - Laureth-23; Glyceryl Stearate/Peg Stearate; Glyceryl Stearate/Peg-100 Stearate; Glyceryl Stearate/Peg-40 Stearate; Glyceryl Stearate-Stearamidoethyl Diethylamine; Glyceryl Trioleate; Glycine; Glycine Hydrochloride; Glycol Distearate; Glycol Stearate; Guanidine Hydrochloride; Guar Gum; Hair Conditioner (18n195-1m); Heptane; Hetastarch; Hexylene Glycol; High Density Polyethylene; Histidine; Human Albumin Microspheres; Hyaluronate Sodium; Hydrocarbon; Hydrocarbon Gel, Plasticized; Hydrochloric Acid; Hydrochloric Acid, Diluted; Hydrocortisone; Hydrogel Polymer; Hydrogen Peroxide; Hydrogenated Castor Oil; Hydrogenated Palm Oil; Hydrogenated Palm/Palm Kernel Oil Peg-6 Esters; Hydrogenated Polybutene 635-690; Hydroxide Ion; Hydroxyethyl Cellulose; Hydroxyethylpiperazine Ethane Sulfonic Acid; Hydroxymethyl Cellulose; Hydroxyoctacosanyl Hydroxystearate; Hydroxypropyl Cellulose; Hydroxypropyl Methylcellulose 2906; Hydroxypropyl-Beta-cyclodextrin; Hypromellose 2208 (15000 Mpa.S); Hypromellose 2910 (15000 Mpa.S); Hypromelloses; Imidurea; Iodine; Iodoxamic Acid; Iofetamine Hydrochloride; Irish Moss Extract; Isobutane; Isoceteth-20; Isoleucine; Isooctyl Acrylate; Isopropyl Alcohol; Isopropyl Isostearate; Isopropyl Myristate; Isopropyl Myristate - Myristyl Alcohol; Isopropyl Palmitate; Isopropyl Stearate; Isostearic Acid; Isostearyl Alcohol; Isotonic Sodium Chloride Solution; Jelene; Kaolin; Kathon Cg; Kathon Cg II; Lactate; Lactic Acid; Lactic Acid, Dl-; Lactic Acid, L-; Lactobionic Acid; Lactose; Lactose Monohydrate; Lactose, Hydrous; Laneth; Lanolin; Lanolin Alcohol - Mineral Oil; Lanolin Alcohols; Lanolin Anhydrous; Lanolin Cholesterols; Lanolin Nonionic Derivatives; Lanolin, Ethoxylated; Lanolin, Hydrogenated; Lauralkonium Chloride; Lauramine Oxide; Laurdimonium Hydrolyzed Animal Collagen; Laureth Sulfate; Laureth-2; Laureth-23; Laureth-4; Lauric Diethanolamide; Lauric Myristic Diethanolamide; Lauroyl Sarcosine; Lauryl Lactate; Lauryl Sulfate; Lavandula Angustifolia Flowering Top; Lecithin; Lecithin Unbleached; Lecithin, Egg; Lecithin, Hydrogenated; Lecithin, Hydrogenated Soy; Lecithin, Soybean; Lemon Oil; Leucine; Levulinic Acid; Lidofenin; Light Mineral Oil; Light Mineral Oil (85 Ssu); Limonene, (+/-)-; Lipocol Sc-15; Lysine; Lysine Acetate; Lysine Monohydrate; Magnesium Aluminum Silicate; Magnesium Aluminum Silicate Hydrate; Magnesium Chloride; Magnesium Nitrate; Magnesium Stearate; Maleic Acid; Mannitol; Maprofix; Mebrofenin; Medical Adhesive Modified S-15; Medical Antiform A-F Emulsion; Medronate Disodium; Medronic Acid; Meglumine; Menthol; Metacresol; Metaphosphoric Acid; Methanesulfonic Acid; Methionine; Methyl Alcohol;

Methyl Gluceth-10; Methyl Gluceth-20; Methyl Gluceth-20 Sesquistearate; Methyl Glucose Sesquistearate; Methyl Laurate; Methyl Pyrrolidone; Methyl Salicylate; Methyl Stearate; Methylboronic Acid; Methylcellulose (4000 Mpa.S); Methylcelluloses; Methylchloroisothiazolinone; Methylene Blue; Methylisothiazolinone; Methylparaben; Microcrystalline Wax; Mineral Oil; Mono And Diglyceride; Monostearyl Citrate; Monothioglycerol; Multisterol Extract; Myristyl Alcohol; Myristyl Lactate; Myristyl-.Gamma.-Picolinium Chloride; N-(Carbamoyl-Methoxy Peg-40)-1,2-Distearoyl-Cephalin Sodium; N,N-Dimethylacetamide; Niacinamide; Nioxime; Nitric Acid; Nitrogen; Nonoxynol Iodine; Nonoxynol-15; Nonoxynol-9; Norflurane; Oatmeal; Octadecene-1/Maleic Acid Copolymer; Octanoic Acid; Octisalate; Octoxynol-1; Octoxynol-40; Octoxynol-9; Octyldodecanol; Octylphenol Polymethylene; Oleic Acid; Oleth-10/Oleth-5; Oleth-2; Oleth-20; Oleyl Alcohol; Oleyl Oleate; Olive Oil; Oxidronate Disodium; Oxyquinoline; Palm Kernel Oil; Palmitamine Oxide; Parabens; Paraffin; Paraffin, White Soft; Parfum Creme 45/3; Peanut Oil; Peanut Oil, Refined; Pectin; Peg 6-32 Stearate/Glycol Stearate; Peg Vegetable Oil; Peg-100 Stearate; Peg-12 Glyceryl Laurate; Peg-120 Glyceryl Stearate; Peg-120 Methyl Glucose Dioleate; Peg-15 Cocamine; Peg-150 Distearate; Peg-2 Stearate; Peg-20 Sorbitan Isostearate; Peg-22 Methyl Ether/Dodecyl Glycol Copolymer; Peg-25 Propylene Glycol Stearate; Peg-4 Dilaurate; Peg-4 Laurate; Peg-40 Castor Oil; Peg-40 Sorbitan Diisostearate; Peg-45/Dodecyl Glycol Copolymer; Peg-5 Oleate; Peg-50 Stearate; Peg-54 Hydrogenated Castor Oil; Peg-6 Isostearate; Peg-60 Castor Oil; Peg-60 Hydrogenated Castor Oil; Peg-7 Methyl Ether; Peg-75 Lanolin; Peg-8 Laurate; Peg-8 Stearate; Pegoxol 7 Stearate; Pentadecalactone; Pentaerythritol Cocoate; Pentasodium Pentetate; Pentetate Calcium Trisodium; Pentetic Acid; Peppermint Oil; Perflutren; Perfume 25677; Perfume Bouquet; Perfume E-1991; Perfume Gd 5604; Perfume Tana 90/42 Scba; Perfume W-1952-1; Petrolatum; Petrolatum, White; Petroleum Distillates; Phenol; Phenol, Liquefied; Phenonip; Phenoxyethanol; Phenylalanine; Phenylethyl Alcohol; Phenylmercuric Acetate; Phenylmercuric Nitrate; Phosphatidyl Glycerol, Egg; Phospholipid; Phospholipid, Egg; Phospholipon 90g; Phosphoric Acid; Pine Needle Oil (Pinus Sylvestris); Piperazine Hexahydrate; Plastibase-50w; Polacrilin; Polidronium Chloride; Poloxamer 124; Poloxamer 181; Poloxamer 182; Poloxamer 188; Poloxamer 237; Poloxamer 407; Poly(Bis(P-Carboxyphenoxy)Propane Anhydride):Sebacic Acid; Poly(Dimethylsiloxane/Methylvinylsiloxane/Methylhydrogensiloxane) Dimethylvinyl Or Dimethylhydroxy Or Trimethyl Endblocked; Poly(Dl-Lactic-Co-Glycolic Acid), (50:50;

Poly(Dl-Lactic-Co-Glycolic Acid), Ethyl Ester Terminated, (50:50; Polyacrylic Acid (250000 Mw); Polybutene (1400 Mw); Polycarbophil; Polyester; Polyester Polyamine Copolymer; Polyester Rayon; Polyethylene Glycol 1000; Polyethylene Glycol 1450; Polyethylene Glycol 1500; Polyethylene Glycol 1540; Polyethylene Glycol 200; Polyethylene Glycol 300; Polyethylene Glycol 300-1600; Polyethylene Glycol 3350; Polyethylene Glycol 400; Polyethylene Glycol 4000; Polyethylene Glycol 540; Polyethylene Glycol 600; Polyethylene Glycol 6000; Polyethylene Glycol 8000; Polyethylene Glycol 900; Polyethylene High Density Containing Ferric Oxide Black (<1%); Polyethylene Low Density Containing Barium Sulfate (20-24%); Polyethylene T; Polyethylene Terephthalates; Polyglactin; Polyglyceryl-3 Oleate; Polyglyceryl-4 Oleate; Polyhydroxyethyl Methacrylate; Polyisobutylene; Polyisobutylene (1100000 Mw); Polyisobutylene (35000 Mw); Polyisobutylene 178-236; Polyisobutylene 241-294; Polyisobutylene 35-39; Polyisobutylene Low Molecular Weight; Polyisobutylene Medium Molecular Weight; Polyisobutylene/Polybutene Adhesive; Polylactide; Polyols; Polyoxyethylene - Polyoxypropylene 1800; Polyoxyethylene Alcohols; Polyoxyethylene Fatty Acid Esters; Polyoxyethylene Propylene; Polyoxyl 20 Cetostearyl Ether; Polyoxyl 35 Castor Oil; Polyoxyl 40 Hydrogenated Castor Oil; Polyoxyl 40 Stearate; Polyoxyl 400 Stearate; Polyoxyl 6 And Polyoxyl 32 Palmitostearate; Polyoxyl Distearate; Polyoxyl Glyceryl Stearate; Polyoxyl Lanolin; Polyoxyl Palmitate; Polyoxyl Stearate; Polypropylene; Polypropylene Glycol; Polyquaternium-10; Polyquaternium-7 (70/30 Acrylamide/Dadmac; Polysiloxane; Polysorbate 20; Polysorbate 40; Polysorbate 60; Polysorbate 65; Polysorbate 80; Polyurethane; Polyvinyl Acetate; Polyvinyl Alcohol; Polyvinyl Chloride; Polyvinyl Chloride-Polyvinyl Acetate Copolymer; Polyvinylpyridine; Poppy Seed Oil; Potash; Potassium Acetate; Potassium Alum; Potassium Bicarbonate; Potassium Bisulfite; Potassium Chloride; Potassium Citrate; Potassium Hydroxide; Potassium Metabisulfite; Potassium Phosphate, Dibasic; Potassium Phosphate, Monobasic; Potassium Soap; Potassium Sorbate; Povidone Acrylate Copolymer; Povidone Hydrogel; Povidone K17; Povidone K25; Povidone K29/32; Povidone K30; Povidone K90; Povidone K90f; Povidone/Eicosene Copolymer; Povidones; Ppg-12/Smdi Copolymer; Ppg-15 Stearyl Ether; Ppg-20 Methyl Glucose Ether Distearate; Ppg-26 Oleate; Product Wat; Proline; Promulgen D; Promulgen G; Propane; Propellant A-46; Propyl Gallate; Propylene Carbonate; Propylene Glycol; Propylene Glycol Diacetate; Propylene Glycol Dicaprylate; Propylene Glycol Monolaurate; Propylene Glycol Monopalmitostearate; Propylene Glycol Palmitostearate; Propylene Glycol Ricinoleate;

Propylene Glycol/Diazolidinyl Urea/Methylparaben/Propylparben; Propylparaben; Protamine Sulfate; Protein Hydrolysate; Pvm/Ma Copolymer; Quaternium-15; Quaternium-15 Cis-Form; Quaternium-52; Ra-2397; Ra-3011; Saccharin; Saccharin Sodium; Saccharin Sodium Anhydrous; Safflower Oil; Sd Alcohol 3a; Sd Alcohol 40; Sd Alcohol 40-2; Sd Alcohol 40b; Sepineo P 600; Serine; Sesame Oil; Shea Butter; Silastic Brand Medical Grade Tubing; Silastic Medical Adhesive,Silicone Type A; Silica, Dental; Silicon; Silicon Dioxide; Silicon Dioxide, Colloidal; Silicone; Silicone Adhesive 4102; Silicone Adhesive 4502; Silicone Adhesive Bio-Psa Q7-4201; Silicone Adhesive Bio-Psa Q7-4301; Silicone Emulsion; Silicone/Polyester Film Strip; Simethicone; Simethicone Emulsion; Sipon Ls 20np; Soda Ash; Sodium Acetate; Sodium Acetate Anhydrous; Sodium Alkyl Sulfate; Sodium Ascorbate; Sodium Benzoate; Sodium Bicarbonate; Sodium Bisulfate; Sodium Bisulfite; Sodium Borate; Sodium Borate Decahydrate; Sodium Carbonate; Sodium Carbonate Decahydrate; Sodium Carbonate Monohydrate; Sodium Cetostearyl Sulfate; Sodium Chlorate; Sodium Chloride; Sodium Chloride Injection; Sodium Chloride Injection, Bacteriostatic; Sodium Cholesteryl Sulfate; Sodium Citrate; Sodium Cocoyl Sarcosinate; Sodium Desoxycholate; Sodium Dithionite; Sodium Dodecylbenzenesulfonate; Sodium Formaldehyde Sulfoxylate; Sodium Gluconate; Sodium Hydroxide; Sodium Hypochlorite; Sodium Iodide; Sodium Lactate; Sodium Lactate, L-; Sodium Laureth-2 Sulfate; Sodium Laureth-3 Sulfate; Sodium Laureth-5 Sulfate; Sodium Lauroyl Sarcosinate; Sodium Lauryl Sulfate; Sodium Lauryl Sulfoacetate; Sodium Metabisulfite; Sodium Nitrate; Sodium Phosphate; Sodium Phosphate Dihydrate; Sodium Phosphate, Dibasic; Sodium Phosphate, Dibasic, Anhydrous; Sodium Phosphate, Dibasic, Dihydrate; Sodium Phosphate, Dibasic, Dodecahydrate; Sodium Phosphate, Dibasic, Heptahydrate; Sodium Phosphate, Monobasic; Sodium Phosphate, Monobasic, Anhydrous; Sodium Phosphate, Monobasic, Dihydrate; Sodium Phosphate, Monobasic, Monohydrate; Sodium Polyacrylate (2500000 Mw); Sodium Pyrophosphate; Sodium Pyrrolidone Carboxylate; Sodium Starch Glycolate; Sodium Succinate Hexahydrate; Sodium Sulfate; Sodium Sulfate Anhydrous; Sodium Sulfate Decahydrate; Sodium Sulfite; Sodium Sulfosuccinated Undecyclenic Monoalkylolamide; Sodium Tartrate; Sodium Thioglycolate; Sodium Thiomalate; Sodium Thiosulfate; Sodium Thiosulfate Anhydrous; Sodium Trimetaphosphate; Sodium Xylenesulfonate; Somay 44; Sorbic Acid; Sorbitan; Sorbitan Isostearate; Sorbitan Monolaurate; Sorbitan Monooleate; Sorbitan Monopalmitate; Sorbitan Monostearate; Sorbitan Sesquioleate; Sorbitan Trioleate; Sorbitan Tristearate; Sorbitol; Sorbitol Solution; Soybean Flour; Soybean Oil; Spearmint Oil;

Spermaceti; Squalane; Stabilized Oxychloro Complex; Stannous 2-Ethylhexanoate; Stannous Chloride; Stannous Chloride Anhydrous; Stannous Fluoride; Stannous Tartrate; Starch; Starch 1500, Pregelatinized; Starch, Corn; Stearalkonium Chloride; Stearalkonium Hectorite/Propylene Carbonate; Stearamidoethyl Diethylamine; Steareth-10; Steareth-100; Steareth-2; Steareth-20; Steareth-21; Steareth-40; Stearic Acid; Stearic Diethanolamide; Stearoxytrimethylsilane; Steartrimonium Hydrolyzed Animal Collagen; Stearyl Alcohol; Sterile Water For Inhalation; Styrene/Isoprene/Styrene Block Copolymer; Succimer; Succinic Acid; Sucralose; Sucrose; Sucrose Distearate; Sucrose Polyesters; Sulfacetamide Sodium; Sulfobutylether .Beta.-Cyclodextrin; Sulfur Dioxide; Sulfuric Acid; Sulfurous Acid; Surfactol Qs; Tagatose, D-; Talc; Tall Oil; Tallow Glycerides; Tartaric Acid; Tartaric Acid, Dl-; Tenox; Tenox-2; Tert-Butyl Alcohol; Tert-Butyl Hydroperoxide; Tert-Butylhydroquinone; Tetrakis(2-Methoxyisobutylisocyanide)Copper(I) Tetrafluoroborate; Tetrapropyl Orthosilicate; Tetrofosmin; Theophylline; Thimerosal; Threonine; Thymol; Tin; Titanium Dioxide; Tocopherol; Tocophersolan; Total parenteral nutrition, lipid emulsion; Triacetin; Tricaprylin; Trichloromonofluoromethane; Trideceth-10; Triethanolamine Lauryl Sulfate; Trifluoroacetic Acid; Triglycerides, Medium Chain; Trihydroxystearin; Trilaneth-4 Phosphate; Trilaureth-4 Phosphate; Trisodium Citrate Dihydrate; Trisodium Hedta; Triton 720; Triton X-200; Trolamine; Tromantadine; Tromethamine (TRIS); Tryptophan; Tyloxapol; Tyrosine; Undecylenic Acid; Union 76 Amsco-Res 6038; Urea; Valine; Vegetable Oil; Vegetable Oil Glyceride, Hydrogenated; Vegetable Oil, Hydrogenated; Versetamide; Viscarin; Viscose/Cotton; Vitamin E; Wax, Emulsifying; Wecobee Fs; White Ceresin Wax; White Wax; Xanthan Gum; Zinc; Zinc Acetate; Zinc Carbonate; Zinc Chloride; and Zinc Oxide.

[0437] Pharmaceutical composition formulations of AAV particles disclosed herein may include cations or anions. In one embodiment, the formulations include metal cations such as, but not limited to, Zn2+, Ca2+, Cu2+, Mn2+, Mg+ and combinations thereof. As a non-limiting example, formulations may include polymers and complexes with a metal cation (*See e.g.*, U.S. Pat. Nos. 6,265,389 and 6,555,525, the contents of each of which are herein incorporated by reference in their entirety).

[0438] Formulations of the invention may also include one or more pharmaceutically acceptable salts. As used herein, "pharmaceutically acceptable salts" refers to derivatives of the disclosed compounds wherein the parent compound is modified by converting an existing acid or base moiety to its salt form (e.g., by reacting the free base group with a suitable

organic acid). Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic acids; and the like. Representative acid addition salts include acetate, acetic acid, adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzene sulfonic acid, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptonate, glycerophosphate, hemisulfate, heptonate, hexanoate, hydrobromide, hydrochloride, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like, as well as nontoxic ammonium, quaternary ammonium, and amine cations, including, but not limited to ammonium, tetramethylammonium, tetraethylammonium, methylamine, dimethylamine, trimethylamine, triethylamine, ethylamine, and the like. The pharmaceutically acceptable salts of the present disclosure include the conventional non-toxic salts of the parent compound formed, for example, from non-toxic inorganic or organic acids.

[0439] The pharmaceutically acceptable salts of the present disclosure can be synthesized from the parent compound which contains a basic or acidic moiety by conventional chemical methods. Generally, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in water or in an organic solvent, or in a mixture of the two; generally, nonaqueous media like ether, ethyl acetate, ethanol, isopropanol, or acetonitrile are preferred. Lists of suitable salts are found in Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Company, Easton, Pa., 1985, p. 1418, Pharmaceutical Salts: Properties, Selection, and Use, P.H. Stahl and C.G. Wermuth (eds.), Wiley-VCH, 2008, and Berge et al., Journal of Pharmaceutical Science, 66, 1-19 (1977); the contents of each of which are incorporated herein by reference in their entirety.

[0440] The term "pharmaceutically acceptable solvate," as used herein, means a compound of the invention wherein molecules of a suitable solvent are incorporated in the crystal lattice. A suitable solvent is physiologically tolerable at the dosage administered. Solvates may be prepared by crystallization, recrystallization, or precipitation from a solution

that includes organic solvents, water, or a mixture thereof. Examples of suitable solvents are ethanol, water (for example, mono-, di-, and tri-hydrates), *N*-methylpyrrolidinone (NMP), dimethyl sulfoxide (DMSO), *N,N'*-dimethylformamide (DMF), *N,N'*-dimethylacetamide (DMAC), 1,3-dimethyl-2-imidazolidinone (DMEU), 1,3-dimethyl-3,4,5,6-tetrahydro-2-(1H)-pyrimidinone (DMPU), acetonitrile (ACN), propylene glycol, ethyl acetate, benzyl alcohol, 2-pyrrolidone, benzyl benzoate, and the like. When water is the solvent, the solvate is referred to as a "hydrate."

III. ADMINISTRATION AND DOSING

Administration

[0441] In one embodiment, the AAV particle may be administered to a subject (e.g., to the CNS of a subject) in a therapeutically effective amount to reduce the symptoms of neurological disease of a subject (e.g., determined using a known evaluation method).

[0442] The AAV particles of the present invention may be administered by any delivery route which results in a therapeutically effective outcome. These include, but are not limited to, enteral (into the intestine), gastroenteral, epidural (into the dura mater), oral (by way of the mouth), transdermal, intracerebral (into the cerebrum), intracerebroventricular (into the cerebral ventricles), sub-pial (between pia and CNS parenchyma), intracarotid arterial (into the intracarotid artery), epicutaneous (application onto the skin), intradermal, (into the skin itself), subcutaneous (under the skin), nasal administration (through the nose), intravenous (into a vein), intravenous bolus, intravenous drip, intra-arterial (into an artery), systemic, intramuscular (into a muscle), intracardiac (into the heart), intraosseous infusion (into the bone marrow), intrathecal (into the spinal canal), intraparenchymal (into brain tissue), intraperitoneal, (infusion or injection into the peritoneum), intravesical infusion, intravitreal, (through the eye), intracavernous injection (into a pathologic cavity) intracavitary (into the base of the penis), intravaginal administration, intrauterine, extra-amniotic administration, transdermal (diffusion through the intact skin for systemic distribution), transmucosal (diffusion through a mucous membrane), transvaginal, insufflation (snorting), sublingual, sublabial, enema, eye drops (onto the conjunctiva), or in ear drops, auricular (in or by way of the ear), buccal (directed toward the cheek), conjunctival, cutaneous, dental (to a tooth or teeth), electro-osmosis, endocervical, endosinusial, endotracheal, extracorporeal, hemodialysis, infiltration, interstitial, intra-abdominal, intra-amniotic, intra-articular, intrabiliary, intrabronchial, intrabursal, intracartilaginous (within a cartilage), intracaudal (within the cauda equine), intracisternal (within the cisterna magna cerebellomedularis),

intracorneal (within the cornea), dental intracoronal, intracoronary (within the coronary arteries), intracorporus cavernosum (within the dilatable spaces of the corporus cavernosa of the penis), intradiscal (within a disc), intraductal (within a duct of a gland), intraduodenal (within the duodenum), intradural (within or beneath the dura), intraepidermal (to the epidermis), intraesophageal (to the esophagus), intragastric (within the stomach), intragingival (within the gingivae), intraileal (within the distal portion of the small intestine), intralesional (within or introduced directly to a localized lesion), intraluminal (within a lumen of a tube), intralymphatic (within the lymph), intramedullary (within the marrow cavity of a bone), intrameningeal (within the meninges), intramyocardial (within the myocardium), intraocular (within the eye), intraovarian (within the ovary), intrapericardial (within the pericardium), intrapleural (within the pleura), intraprostatic (within the prostate gland), intrapulmonary (within the lungs or its bronchi), intrasinal (within the nasal or periorbital sinuses), intraspinal (within the vertebral column), intrasynovial (within the synovial cavity of a joint), intratendinous (within a tendon), intratesticular (within the testicle), intrathecal (within the cerebrospinal fluid at any level of the cerebrospinal axis), intrathoracic (within the thorax), intratubular (within the tubules of an organ), intratumor (within a tumor), intratympanic (within the aurus media), intravascular (within a vessel or vessels), intraventricular (within a ventricle), iontophoresis (by means of electric current where ions of soluble salts migrate into the tissues of the body), irrigation (to bathe or flush open wounds or body cavities), laryngeal (directly upon the larynx), nasogastric (through the nose and into the stomach), occlusive dressing technique (topical route administration which is then covered by a dressing which occludes the area), ophthalmic (to the external eye), oropharyngeal (directly to the mouth and pharynx), parenteral, percutaneous, periarticular, peridural, perineural, periodontal, rectal, respiratory (within the respiratory tract by inhaling orally or nasally for local or systemic effect), retrobulbar (behind the pons or behind the eyeball), soft tissue, subarachnoid, subconjunctival, submucosal, topical, transplacental (through or across the placenta), transtracheal (through the wall of the trachea), transtympanic (across or through the tympanic cavity), ureteral (to the ureter), urethral (to the urethra), vaginal, caudal block, diagnostic, nerve block, biliary perfusion, cardiac perfusion, photopheresis and spinal.

[0443] In some embodiments, the AAV particles and compositions comprising the AAV particles may be administered in a way which allows them to cross the blood-brain barrier, vascular barrier, or other epithelial barrier. The AAV particles of the present invention may be administered in any suitable form, either as a liquid solution or suspension, as a solid form

suitable for liquid solution or suspension in a liquid solution. The AAV particles may be formulated with any appropriate and pharmaceutically acceptable excipient.

[0444] In one embodiment, the AAV particles of the present invention may be delivered to a subject via a single route administration.

[0445] In one embodiment, the AAV particles of the present invention may be delivered to a subject via a multi-site route of administration. AAV particles may be administered at 2, 3, 4, 5 or more than 5 sites.

[0446] In one embodiment, a subject may be administered the AAV particles of the present invention using a bolus infusion.

[0447] In one embodiment, a subject may be administered the AAV particles of the present invention using sustained delivery over a period of minutes, hours or days. The infusion rate may be changed depending on the subject, distribution, formulation or another delivery parameter.

[0448] In one embodiment, the AAV particles of the present invention may be delivered by intramuscular delivery route. (See, e.g., U. S. Pat. No. 6506379; the contents of which are incorporated herein by reference in their entirety). Non-limiting examples of intramuscular administration include an intravenous injection or a subcutaneous injection.

[0449] In one embodiment, the AAV particles of the present invention may be delivered by intraocular delivery route. A non-limiting example of intraocular administration include an intravitreal injection.

[0450] In some embodiments, the AAV particles that may be administered to a subject by peripheral injections. Non-limiting examples of peripheral injections include intraperitoneal, intramuscular, intravenous, conjunctival or joint injection. It was disclosed in the art that the peripheral administration of AAV particles can be transported to the central nervous system, for example, to the motor neurons (e.g., U. S. Patent Application Publication Nos. 20100240739; and 20100130594; the contents of each of which are incorporated herein by reference in their entirety).

[0451] In one embodiment, the AAV particles may be delivered by injection into the CSF pathway. Non-limiting examples of delivery to the CSF pathway include intrathecal and intracerebroventricular administration.

[0452] In one embodiment, the AAV particles may be delivered by systemic delivery. As a non-limiting example, the systemic delivery may be by intravascular administration.

[0453] In one embodiment, the AAV particles of the present invention may be administered to a subject by intracranial delivery (See, e.g., U. S. Pat. No. 8,119,611; the content of which are incorporated herein by reference in their entirety).

[0454] In some embodiments, the AAV particles of the present invention may be administered by injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by injection.

[0455] In some embodiments, the AAV particles of the present invention may be administered by muscular injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by muscular administration.

[0456] In some embodiments, the AAV particles of the present invention may be administered by intramuscular administration. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intramuscular administration.

[0457] In one embodiment, the AAV particles of the present invention are administered to a subject and transduce muscle of a subject. As a non-limiting example, the AAV particles are administered by intramuscular administration.

[0458] In some embodiments, the AAV particles of the present invention may be administered via intraparenchymal injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intraparenchymal administration.

[0459] In some embodiments, the AAV particles of the present invention may be administered by intravenous administration. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intravenous administration.

[0460] In one embodiment, the AAV particles of the present invention may be administered via intravenous delivery.

[0461] In one embodiment, the AAV particles of the present invention may be administrated via intracarotid artery delivery.

[0462] In one embodiment, the AAV particles of the present invention may be administered via a single dose intravenous delivery. As a non-limiting example, the single dose intravenous delivery may be a one-time treatment. In the context of neurological disease, the single dose intravenous delivery can produce durable relief for subjects with a neurological disease and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50,

51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[0463] In one embodiment, the AAV particles of the present invention may be administered via intravenous delivery to the DRG nociceptive neurons.

[0464] In one embodiment, the AAV particles of the present invention may be administered via a single dose intravenous delivery to the DRG nociceptive neurons. As a non-limiting example, the single dose intravenous delivery may be a one-time treatment. In the context of neurological disease, the single dose intravenous delivery can produce durable relief for subjects with a neurological disease and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[0465] In some embodiments, the AAV particles of the present invention may be administered by intrathecal injection. As a non-limiting example, the AAV particles of the present invention may be administered by intrathecal injection.

[0466] In one embodiment, the AAV particle may be administered to the cisterna magna in a therapeutically effective amount to transduce spinal cord motor neurons and/or astrocytes. As a non-limiting example, the AAV particle may be administered intrathecally.

[0467] In one embodiment, the AAV particle may be administered using intrathecal infusion in a therapeutically effective amount to transduce spinal cord motor neurons and/or astrocytes.

[0468] In some embodiments, the AAV particles of the present invention may be administered via a single dose intrathecal injection. As a non-limiting example, the single dose intrathecal injection may be a one-time treatment. In the context of neurological disease, the single dose intrathecal injection can produce durable relief for subjects with a neurological disease and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[0469] In some embodiments, the AAV particles of the present invention may be administered via intrathecal injection to the DRG nociceptive neurons.

[0470] In some embodiments, the AAV particles of the present invention may be administered via a single dose intrathecal injection to the DRG nociceptive neurons. As a non-limiting example, the single dose intrathecal injection may be a one-time treatment. In the context of neurological disease, the single dose intrathecal injection can produce durable relief for subjects with a neurological disease and/or related symptoms. The relief may last for minutes such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 minutes or more than 59 minutes; hours such as, but not limited to, 1, 2, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15,

16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, or more than 48 hours; days such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, or more than 31 days; weeks such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more than 16 weeks; months such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or more than 24 months; years such as, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more than 15 years.

[0471] In one embodiment, the AAV particle described herein is administered via intrathecal (IT) infusion at C1. The infusion may be for 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more than 15 hours.

[0472] In some embodiments, the AAV particles of the present invention may be administered by intraparenchymal injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by intraparenchymal injection.

[0473] In some embodiments, the AAV particles of the present invention may be administered by intraparenchymal injection and intrathecal injection. As a non-limiting example, the AAV particles of the present invention may be administered via intraparenchymal injection and intrathecal injection.

[0474] In some embodiments, the AAV particles of the present invention may be administered by subcutaneous injection. As a non-limiting example, the AAV particles of the present invention may be administered to a subject by subcutaneous injection.

[0475] In some embodiments, the AAV particles of the present invention may be administered topically. As a non-limiting example, the AAV particles of the present invention may be administered to a subject topically.

[0476] In one embodiment, the AAV particles may be delivered by direct injection into the brain. As a non-limiting example, the brain delivery may be by intrastriatal administration.

[0477] In one embodiment, the AAV particles of the present invention may be administered via intrastriatal injection.

[0478] In one embodiment, the AAV particles of the present invention may be administered via intrastriatal injection and another route of administration described herein.

[0479] In one embodiment, the AAV particles may be delivered by more than one route of administration. As non-limiting examples of combination administrations, AAV particles

may be delivered by intrathecal and intracerebroventricular, or by intravenous and intraparenchymal administration.

[0480] In one embodiment, the AAV particle may be administered to the CNS in a therapeutically effective amount to improve function and/or survival for a subject with a neurological disease. As a non-limiting example, the vector may be administered intravenously.

[0481] The AAV particle may be administered in a "therapeutically effective" amount, i.e., an amount that is sufficient to alleviate and/or prevent at least one symptom associated with the disease, or provide improvement in the condition of the subject.

[0482] In one embodiment, the catheter may be located at more than one site in the spine for multi-site delivery. The AAV particle may be delivered in a continuous and/or bolus infusion. Each site of delivery may be a different dosing regimen or the same dosing regimen may be used for each site of delivery. As a non-limiting example, the sites of delivery may be in the cervical and the lumbar region. As another non-limiting example, the sites of delivery may be in the cervical region. As another non-limiting example, the sites of delivery may be in the lumbar region.

[0483] In one embodiment, a subject may be analyzed for spinal anatomy and pathology prior to delivery of the AAV particle described herein. As a non-limiting example, a subject with scoliosis may have a different dosing regimen and/or catheter location compared to a subject without scoliosis.

[0484] In one embodiment, the orientation of the spine of the subject during delivery of the AAV particle may be vertical to the ground.

[0485] In another embodiment, the orientation of the spine of the subject during delivery of the AAV particle may be horizontal to the ground.

[0486] In one embodiment, the spine of the subject may be at an angle as compared to the ground during the delivery of the AAV particle. The angle of the spine of the subject as compared to the ground may be at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150 or 180 degrees.

[0487] In one embodiment, the delivery method and duration is chosen to provide broad transduction in the spinal cord. As a non-limiting example, intrathecal delivery is used to provide broad transduction along the rostral-caudal length of the spinal cord. As another non-limiting example, multi-site infusions provide a more uniform transduction along the rostral-

caudal length of the spinal cord. As yet another non-limiting example, prolonged infusions provide a more uniform transduction along the rostral-caudal length of the spinal cord.

Parenteral and injectable administration

[0488] In some embodiments, pharmaceutical compositions, AAV particles of the present invention may be administered parenterally. Liquid dosage forms for oral and parenteral administration include, but are not limited to, pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups, and/or elixirs. In addition to active ingredients, liquid dosage forms may comprise inert diluents commonly used in the art such as, for example, water or other solvents, solubilizing agents and emulsifiers such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, dimethylformamide, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor, and sesame oils), glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof. Besides inert diluents, oral compositions can include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, and/or perfuming agents. In certain embodiments for parenteral administration, compositions are mixed with solubilizing agents such as CREMOPHOR®, alcohols, oils, modified oils, glycols, polysorbates, cyclodextrins, polymers, and/or combinations thereof. In other embodiments, surfactants are included such as hydroxypropylcellulose.

[0489] Injectable preparations, for example, sterile injectable aqueous or oleaginous suspensions may be formulated according to the known art using suitable dispersing agents, wetting agents, and/or suspending agents. Sterile injectable preparations may be sterile injectable solutions, suspensions, and/or emulsions in nontoxic parenterally acceptable diluents and/or solvents, for example, as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, U.S.P., and isotonic sodium chloride solution. Sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono- or diglycerides. Fatty acids such as oleic acid can be used in the preparation of injectables.

[0490] Injectable formulations may be sterilized, for example, by filtration through a bacterial-retaining filter, and/or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable medium prior to use.

[0491] In order to prolong the effect of active ingredients, it is often desirable to slow the absorption of active ingredients from subcutaneous or intramuscular injections. This may be accomplished by the use of liquid suspensions of crystalline or amorphous material with poor water solubility. The rate of absorption of active ingredients depends upon the rate of dissolution which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle. Injectable depot forms are made by forming microencapsule matrices of the drug in biodegradable polymers such as polylactide-polyglycolide. Depending upon the ratio of drug to polymer and the nature of the particular polymer employed, the rate of drug release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are prepared by entrapping the drug in liposomes or microemulsions which are compatible with body tissues.

Depot administration

[0492] As described herein, in some embodiments, pharmaceutical compositions, AAV particles of the present invention are formulated in depots for extended release. Generally, specific organs or tissues ("target tissues") are targeted for administration.

[0493] In some aspects of the invention, pharmaceutical compositions, AAV particles of the present invention are spatially retained within or proximal to target tissues. Provided are methods of providing pharmaceutical compositions, AAV particles, to target tissues of mammalian subjects by contacting target tissues (which comprise one or more target cells) with pharmaceutical compositions, AAV particles, under conditions such that they are substantially retained in target tissues, meaning that at least 10, 20, 30, 40, 50, 60, 70, 80, 85, 90, 95, 96, 97, 98, 99, 99.9, 99.99 or greater than 99.99% of the composition is retained in the target tissues. Advantageously, retention is determined by measuring the amount of pharmaceutical compositions, and AAV particles that enter one or more target cells. For example, at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99% or greater than 99.99% of pharmaceutical compositions, AAV particles, administered to subjects are present intracellularly at a period of time following administration. For example, intramuscular injection to mammalian subjects may be performed using aqueous compositions comprising pharmaceutical compositions, AAV particles of the present invention and one or more transfection reagents,

and retention is determined by measuring the amount of pharmaceutical compositions, AAV particles, present in target cells.

[0494] Certain aspects of the invention are directed to methods of providing pharmaceutical compositions, AAV particles of the present invention to target tissues of mammalian subjects, by contacting target tissues (comprising one or more target cells) with pharmaceutical compositions, AAV particles under conditions such that they are substantially retained in such target tissues. Pharmaceutical compositions, AAV particles comprise enough active ingredient such that the effect of interest is produced in at least one target cell. In some embodiments, pharmaceutical compositions, AAV particles generally comprise one or more cell penetration agents, although "naked" formulations (such as without cell penetration agents or other agents) are also contemplated, with or without pharmaceutically acceptable carriers.

Pulmonary administration

[0495] In some embodiments, pharmaceutical compositions, AAV particles of the present invention may be prepared, packaged, and/or sold in formulations suitable for pulmonary administration. In some embodiments, such administration is via the buccal cavity. In some embodiments, formulations may comprise dry particles comprising active ingredients. In such embodiments, dry particles may have a diameter in the range from about 0.5 nm to about 7 nm or from about 1 nm to about 6 nm. In some embodiments, formulations may be in the form of dry powders for administration using devices comprising dry powder reservoirs to which streams of propellant may be directed to disperse such powder. In some embodiments, self-propelling solvent/powder dispensing containers may be used. In such embodiments, active ingredients may be dissolved and/or suspended in low-boiling propellant in sealed containers. Such powders may comprise particles wherein at least 98% of the particles by weight have diameters greater than 0.5 nm and at least 95% of the particles by number have diameters less than 7 nm. Alternatively, at least 95% of the particles by weight have a diameter greater than 1 nm and at least 90% of the particles by number have a diameter less than 6 nm. Dry powder compositions may include a solid fine powder diluent such as sugar and are conveniently provided in a unit dose form.

[0496] Low boiling propellants generally include liquid propellants having a boiling point of below 65 °F at atmospheric pressure. Generally, propellants may constitute 50% to 99.9% (w/w) of the composition, and active ingredient may constitute 0.1% to 20% (w/w) of the composition. Propellants may further comprise additional ingredients such as liquid non-ionic

and/or solid anionic surfactant and/or solid diluent (which may have particle sizes of the same order as particles comprising active ingredients).

[0497] Pharmaceutical compositions formulated for pulmonary delivery may provide active ingredients in the form of droplets of solution and/or suspension. Such formulations may be prepared, packaged, and/or sold as aqueous and/or dilute alcoholic solutions and/or suspensions, optionally sterile, comprising active ingredients, and may conveniently be administered using any nebulization and/or atomization device. Such formulations may further comprise one or more additional ingredients including, but not limited to, a flavoring agent such as saccharin sodium, a volatile oil, a buffering agent, a surface active agent, and/or a preservative such as methylhydroxybenzoate. Droplets provided by this route of administration may have an average diameter in the range from about 0.1 nm to about 200 nm.

Intranasal, nasal and buccal administration

[0498] In some embodiments, pharmaceutical compositions, AAV particles of the present invention may be administered nasally and/or intranasal. In some embodiments, formulations described herein useful for pulmonary delivery may also be useful for intranasal delivery. In some embodiments, formulations for intranasal administration comprise a coarse powder comprising the active ingredient and having an average particle size from about 0.2 μm to 500 μm. Such formulations are administered in the manner in which snuff is taken, *i.e.* by rapid inhalation through the nasal passage from a container of the powder held close to the nose.

[0499] Formulations suitable for nasal administration may, for example, comprise from about as little as 0.1% (w/w) and as much as 100% (w/w) of active ingredient, and may comprise one or more of the additional ingredients described herein. A pharmaceutical composition may be prepared, packaged, and/or sold in a formulation suitable for buccal administration. Such formulations may, for example, be in the form of tablets and/or lozenges made using conventional methods, and may, for example, comprise 0.1% to 20% (w/w) active ingredient, the balance comprising an orally dissolvable and/or degradable composition and, optionally, one or more of the additional ingredients described herein. Alternately, formulations suitable for buccal administration may comprise powders and/or an aerosolized and/or atomized solutions and/or suspensions comprising active ingredients. Such powdered, aerosolized, and/or aerosolized formulations, when dispersed, may comprise

average particle and/or droplet sizes in the range of from about 0.1 nm to about 200 nm, and may further comprise one or more of any additional ingredients described herein.

Ophthalmic or otic administration

[0500] In some embodiments, pharmaceutical compositions, AAV particles of the present invention may be prepared, packaged, and/or sold in formulations suitable for ophthalmic and/or otic administration. Such formulations may, for example, be in the form of eye and/or ear drops including, for example, a 0.1/1.0% (w/w) solution and/or suspension of the active ingredient in aqueous and/or oily liquid excipients. Such drops may further comprise buffering agents, salts, and/or one or more other of any additional ingredients described herein. Other ophthalmically-administrable formulations which are useful include those which comprise active ingredients in microcrystalline form and/or in liposomal preparations. Subretinal inserts may also be used as forms of administration.

Delivery, Dose and Regimen

[0501] The present invention provides methods of administering AAV particles in accordance with the invention to a subject in need thereof. The pharmaceutical, diagnostic, or prophylactic AAV particles and compositions of the present invention may be administered to a subject using any amount and any route of administration effective for preventing, treating, managing, or diagnosing diseases, disorders and/or conditions. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of the disease, the particular composition, its mode of administration, its mode of activity, and the like. The subject may be a human, a mammal, or an animal. Compositions in accordance with the invention are typically formulated in unit dosage form for ease of administration and uniformity of dosage. It will be understood, however, that the total daily usage of the compositions of the present invention may be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective, prophylactically effective, or appropriate diagnostic dose level for any particular individual will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific payload employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific AAV particle employed; the duration of the treatment; drugs used in combination or coincidental with the specific AAV particle employed; and like factors well known in the medical arts.

[0502] In one embodiment, delivery of the AAV particles of the present invention results in minimal serious adverse events (SAEs) as a result of the delivery of the AAV particles.

[0503] In one embodiment, the AAV particle may be delivered in a multi-dose regimen. The multi-dose regimen may be 2, 3, 4, 5, 6, 7, 8, 9, 10 or more than 10 doses.

[0504] In one embodiment, the AAV particle may be delivered to a subject via a multi-site route of administration. A subject may be administered the AAV particle at 2, 3, 4, 5 or more than 5 sites.

[0505] In certain embodiments, AAV particle pharmaceutical compositions in accordance with the present invention may be administered at dosage levels sufficient to deliver from about 0.0001 mg/kg to about 100 mg/kg, from about 0.001 mg/kg to about 0.05 mg/kg, from about 0.005 mg/kg to about 0.05 mg/kg, from about 0.001 mg/kg to about 0.005 mg/kg, from about 0.05 mg/kg to about 0.5 mg/kg, from about 0.01 mg/kg to about 50 mg/kg, from about 0.1 mg/kg to about 40 mg/kg, from about 0.5 mg/kg to about 30 mg/kg, from about 0.01 mg/kg to about 10 mg/kg, from about 0.1 mg/kg to about 10 mg/kg, or from about 1 mg/kg to about 25 mg/kg, of subject body weight per day, one or more times a day, to obtain the desired therapeutic, diagnostic, or prophylactic, effect. It will be understood that the above dosing concentrations may be converted to vg or viral genomes per kg or into total viral genomes administered by one of skill in the art.

[0506] In certain embodiments, AAV particle pharmaceutical compositions in accordance with the present disclosure may be administered at about 10 to about 600 µl/site, 50 to about 500 µl/site, 100 to about 400 µl/site, 120 to about 300 µl/site, 140 to about 200 µl/site, about 160 µl/site. As non-limiting examples, AAV particles may be administered at 50 µl/site and/or 150 µl/site.

[0507] In one embodiment, delivery of the compositions in accordance with the present invention to cells comprises a rate of delivery defined by [VG/hour = mL/hour * VG/mL] wherein VG is viral genomes, VG/mL is composition concentration, and mL/hour is rate of prolonged delivery.

[0508] In one embodiment, delivery of compositions comprising the AAV particles in accordance with the present invention to cells may comprise a total concentration per subject between about $1x10^6$ VG (Viral Genome) and about $1x10^{16}$ VG. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$,

$4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $2.1x10^{11}$, $2.2x10^{11}$, $2.3x10^{11}$, $2.4x10^{11}$, $2.5x10^{11}$, $2.6x10^{11}$, $2.7x10^{11}$, $2.8x10^{11}$, $2.9x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $7.1x10^{11}$, $7.2x10^{11}$, $7.3x10^{11}$, $7.4x10^{11}$, $7.5x10^{11}$, $7.6x10^{11}$, $7.7x10^{11}$, $7.8x10^{11}$, $7.9x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1\ x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$,$4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $8.1x10^{12}$, $8.2x10^{12}$, $8.3x10^{12}$, $8.4x10^{12}$, $8.5x10^{12}$, $8.6x10^{12}$, $8.7x10^{12}$, $8.8\ x10^{12}$, $8.9x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/subject.

[0509] In one embodiment, delivery of compositions comprising the AAV particles in accordance with the present invention to cells may comprise a total concentration per subject between about $1x10^6$ VG/kg and about $1x10^{16}$ VG/kg. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $2.1x10^{11}$, $2.2x10^{11}$, $2.3x10^{11}$, $2.4x10^{11}$, $2.5x10^{11}$, $2.6x10^{11}$, $2.7x10^{11}$, $2.8x10^{11}$, $2.9x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $7.1x10^{11}$, $7.2x10^{11}$, $7.3x10^{11}$, $7.4x10^{11}$, $7.5x10^{11}$, $7.6x10^{11}$, $7.7x10^{11}$, $7.8x10^{11}$, $7.9x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1\ x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$,$4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $8.1x10^{12}$, $8.2x10^{12}$, $8.3x10^{12}$, $8.4x10^{12}$, $8.5x10^{12}$, $8.6x10^{12}$, $8.7x10^{12}$, $8.8\ x10^{12}$, $8.9x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $1x10^{13}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $2.1x10^{12}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $1x10^{13}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of

$6.7x10^{12}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $7x10^{12}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $2x10^{13}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $3x10^{11}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $3x10^{12}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $3x10^{13}$ VG/kg. In one embodiment, the delivery comprises a composition concentration of $6.3x10^{12}$ VG/kg.

[0510] In one embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) may comprise a total dose between about $1x10^6$ VG and about $1x10^{16}$ VG. In some embodiments, delivery may comprise a total dose of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $1.9x10^{10}$, $2x10^{10}$, $3x10^{10}$, $3.73x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $2.5x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG. As a non-limiting example, the total dose is $1x10^{13}$ VG. As another non-limiting example, the total dose is $2.1x10^{12}$ VG. As another non-limiting example, the total dose is $6.3x10^{12}$ VG.

[0511] In one embodiment, about 10^5 to 10^6 viral genome (unit) may be administered per dose.

[0512] In one embodiment, delivery of the compositions comprising the AAV particles in accordance with the present invention to cells may comprise a total concentration between about $1x10^6$ VG/mL and about $1x10^{16}$ VG/mL. In some embodiments, delivery may comprise a composition concentration of about $1x10^6$, $2x10^6$, $3x10^6$, $4x10^6$, $5x10^6$, $6x10^6$, $7x10^6$, $8x10^6$, $9x10^6$, $1x10^7$, $2x10^7$, $3x10^7$, $4x10^7$, $5x10^7$, $6x10^7$, $7x10^7$, $8x10^7$, $9x10^7$, $1x10^8$, $2x10^8$, $3x10^8$, $4x10^8$, $5x10^8$, $6x10^8$, $7x10^8$, $8x10^8$, $9x10^8$, $1x10^9$, $2x10^9$, $3x10^9$, $4x10^9$, $5x10^9$, $6x10^9$, $7x10^9$, $8x10^9$, $9x10^9$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $1.1x10^{12}$, $1.2x10^{12}$, $1.3x10^{12}$, $1.4x10^{12}$, $1.5x10^{12}$, $1.6x10^{12}$, $1.7x10^{12}$, $1.8x10^{12}$, $1.9x10^{12}$, $2x10^{12}$, $2.1x10^{12}$, $2.2x10^{12}$, $2.3x10^{12}$, $2.4x10^{12}$, $2.5x10^{12}$, $2.6x10^{12}$, $2.7x10^{12}$, $2.8x10^{12}$, $2.9x10^{12}$, $3x10^{12}$,

$3.1x10^{12}$, $3.2x10^{12}$, $3.3x10^{12}$, $3.4x10^{12}$, $3.5x10^{12}$, $3.6x10^{12}$, $3.7x10^{12}$, $3.8x10^{12}$, $3.9x10^{12}$, $4x10^{12}$, $4.1x10^{12}$, $4.2x10^{12}$, $4.3x10^{12}$, $4.4x10^{12}$, $4.5x10^{12}$, $4.6x10^{12}$, $4.7x10^{12}$, $4.8x10^{12}$, $4.9x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $6.7x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/mL.

[0513] In one embodiment, delivery of AAV particles to cells of the central nervous system (e.g., parenchyma) may comprise a composition concentration between about $1x10^{6}$ VG/mL and about $1x10^{16}$ VG/mL. In some embodiments, delivery may comprise a composition concentration of about $1x10^{6}$, $2x10^{6}$, $3x10^{6}$, $4x10^{6}$, $5x10^{6}$, $6x10^{6}$, $7x10^{6}$, $8x10^{6}$, $9x10^{6}$, $1x10^{7}$, $2x10^{7}$, $3x10^{7}$, $4x10^{7}$, $5x10^{7}$, $6x10^{7}$, $7x10^{7}$, $8x10^{7}$, $9x10^{7}$, $1x10^{8}$, $2x10^{8}$, $3x10^{8}$, $4x10^{8}$, $5x10^{8}$, $6x10^{8}$, $7x10^{8}$, $8x10^{8}$, $9x10^{8}$, $1x10^{9}$, $2x10^{9}$, $3x10^{9}$, $4x10^{9}$, $5x10^{9}$, $6x10^{9}$, $7x10^{9}$, $8x10^{9}$, $9x10^{9}$, $1x10^{10}$, $2x10^{10}$, $3x10^{10}$, $4x10^{10}$, $5x10^{10}$, $6x10^{10}$, $7x10^{10}$, $8x10^{10}$, $9x10^{10}$, $1x10^{11}$, $2x10^{11}$, $3x10^{11}$, $4x10^{11}$, $5x10^{11}$, $6x10^{11}$, $7x10^{11}$, $8x10^{11}$, $9x10^{11}$, $1x10^{12}$, $2x10^{12}$, $3x10^{12}$, $4x10^{12}$, $5x10^{12}$, $6x10^{12}$, $6.1x10^{12}$, $6.2x10^{12}$, $6.3x10^{12}$, $6.4x10^{12}$, $6.5x10^{12}$, $6.6x10^{12}$, $6.7x10^{12}$, $6.8x10^{12}$, $6.9x10^{12}$, $7x10^{12}$, $8x10^{12}$, $9x10^{12}$, $1x10^{13}$, $2x10^{13}$, $3x10^{13}$, $4x10^{13}$, $5x10^{13}$, $6x10^{13}$, $7x10^{13}$, $8x10^{13}$, $9x10^{13}$, $1x10^{14}$, $2x10^{14}$, $3x10^{14}$, $4x10^{14}$, $5x10^{14}$, $6x10^{14}$, $7x10^{14}$, $8x10^{14}$, $9x10^{14}$, $1x10^{15}$, $2x10^{15}$, $3x10^{15}$, $4x10^{15}$, $5x10^{15}$, $6x10^{15}$, $7x10^{15}$, $8x10^{15}$, $9x10^{15}$, or $1x10^{16}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $1x10^{13}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $2.1x10^{12}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $1x10^{13}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $2x10^{13}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $3x10^{11}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $3x10^{12}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $6.3x10^{12}$ VG/mL. In one embodiment, the delivery comprises a composition concentration of $3x10^{13}$ VG/mL.

[0514] In certain embodiments, the desired dosage may be delivered using multiple administrations (*e.g.*, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, or more administrations). When multiple administrations are employed, split dosing regimens such as those described herein may be used. As used herein, a "split dose" is the division of "single unit dose" or total daily dose into two or more doses, *e.g.*, two

or more administrations of the "single unit dose". As used herein, a "single unit dose" is a dose of any therapeutic administered in one dose/at one time/single route/single point of contact, i.e., single administration event.

[0515] The desired dosage of the AAV particles of the present invention may be administered as a "pulse dose" or as a "continuous flow". As used herein, a "pulse dose" is a series of single unit doses of any therapeutic administered with a set frequency over a period of time. As used herein, a "continuous flow" is a dose of therapeutic administered continuously for a period of time in a single route/single point of contact, i.e., continuous administration event. A total daily dose, an amount given or prescribed in 24 hour period, may be administered by any of these methods, or as a combination of these methods, or by any other methods suitable for a pharmaceutical administration.

[0516] In one embodiment, delivery of the AAV particles of the present invention to a subject provides regulating activity of a target gene in a subject. The regulating activity may be an increase in the production of the target protein in a subject or the decrease of the production of target protein in a subject. The regulating activity can be for at least 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years or more than 10 years.

[0517] In some embodiments, the AAV particle of the present invention may be administered to a subject using a single dose, one-time treatment. The dose of the one-time treatment may be administered by any methods known in the art and/or described herein. As used herein, a "one-time treatment" refers to a composition which is only administered one time. If needed, a booster dose may be administered to the subject to ensure the appropriate efficacy is reached. A booster may be administered 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, or more than 10 years after the one-time treatment.

Delivery Methods

[0518] In one embodiment, the AAV particles or pharmaceutical compositions of the present invention may be administered or delivered using the methods for treatment of disease described in US Patent No. 8,999,948, or International Publication No.

WO2014178863, the contents of each of which are herein incorporated by reference in their entirety.

[0519] In one embodiment, the AAV particles or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering gene therapy in Alzheimer's Disease or other neurodegenerative conditions as described in U.S. Patent Application Publication No. 20150126590, the contents of which are herein incorporated by reference in their entirety.

[0520] In one embodiment, the AAV particles or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivery of a CNS gene therapy as described in US Patent Nos. 6,436,708, and 8,946,152, and International Publication No. WO2015168666, the contents of each of which are herein incorporated by reference in their entirety.

[0521] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering proteins using AAV particles described in European Patent Application No. EP2678433, the contents of which are herein incorporated by reference in their entirety.

[0522] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering DNA to the bloodstream described in US Patent No. US 6,211,163, the contents of which are herein incorporated by reference in their entirety.

[0523] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload to the central nervous system described in US Patent No. US 7,588,757, the contents of which are herein incorporated by reference in their entirety.

[0524] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload described in US Patent No. US 8,283,151, the contents of which are herein incorporated by reference in their entirety.

[0525] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload using a glutamic acid decarboxylase (GAD) delivery vector described in International Patent Publication No. WO2001089583, the contents of which are herein incorporated by reference in their entirety.

[0526] In one embodiment, the AAV particle or pharmaceutical compositions of the present invention may be administered or delivered using the methods for delivering a payload to neural cells described in International Patent Publication No. WO2012057363, the contents of which are herein incorporated by reference in their entirety.

Delivery to Cells

[0527] The present disclosure provides a method of delivering to a cell or tissue or an organ any of the above-described AAV particles, comprising contacting the cell or tissue or organ with said AAV particle or contacting the cell or tissue or organ with a formulation comprising said AAV particle, or contacting the cell or tissue or organ with any of the described compositions, including pharmaceutical compositions comprising the AAV particles. The method of delivering the AAV particle to a cell or tissue or organ can be accomplished in *vitro, ex vivo*, or *in vivo*.

Delivery to Subjects

[0528] The present disclosure additionally provides a method of delivering to a subject, including a mammalian subject, any of the above-described AAV particles comprising administering to the subject said AAV particle, or administering to the subject a formulation comprising said AAV particle, or administering to the subject any of the described compositions, including pharmaceutical compositions.

[0529] In one embodiment, the mammalian subject is human. In some aspects, the human subject is a patient with a disease, for example, a neuological disease, or a cardiovascular disease.

Combinations

[0530] The AAV particles may be used in combination with one or more other therapeutic, prophylactic, research or diagnostic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present invention. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent. In some embodiments, the present disclosure encompasses the delivery of pharmaceutical, prophylactic, research, or diagnostic compositions in combination with agents that may improve their bioavailability, reduce and/or modify their metabolism, inhibit their excretion, and/or modify their distribution within the body.

Measurement of Expression

[0531] Expression of payloads from viral genomes may be determined using various methods known in the art such as, but not limited to immunochemistry (e.g., IHC), *in situ* hybridization (ISH), enzyme-linked immunosorbent assay (ELISA), affinity ELISA, ELISPOT, flow cytometry, immunocytology, surface plasmon resonance analysis, kinetic exclusion assay, liquid chromatography-mass spectrometry (LCMS), high-performance liquid chromatography (HPLC), BCA assay, immunoelectrophoresis, Western blot, SDS-PAGE, protein immunoprecipitation, and/or PCR.

Bioavailability

[0532] The AAV particles, when formulated into a composition with a delivery agent as described herein, can exhibit an increase in bioavailability as compared to a composition lacking a delivery agent as described herein. As used herein, the term "bioavailability" refers to the systemic availability of a given amount of AAV particle or expressed payload administered to a mammal. Bioavailability can be assessed by measuring the area under the curve (AUC) or the maximum serum or plasma concentration (C_{max}) of the composition following. AUC is a determination of the area under the curve plotting the serum or plasma concentration of a compound (e.g., AAV particles or expressed payloads) along the ordinate (Y-axis) against time along the abscissa (X-axis). Generally, the AUC for a particular compound can be calculated using methods known to those of ordinary skill in the art and as described in G. S. Banker, Modern Pharmaceutics, Drugs and the Pharmaceutical Sciences, v. 72, Marcel Dekker, New York, Inc., 1996, the contents of which are herein incorporated by reference in its entirety.

[0533] The C_{max} value is the maximum concentration of the AAV particle or expressed payload achieved in the serum or plasma of a mammal following administration of the AAV particle to the mammal. The C_{max} value can be measured using methods known to those of ordinary skill in the art. The phrases "increasing bioavailability" or "improving the pharmacokinetics," as used herein mean that the systemic availability of a first AAV particle or expressed payload, measured as AUC, C_{max}, or C_{min} in a mammal is greater, when co-administered with a delivery agent as described herein, than when such co-administration does not take place. In some embodiments, the bioavailability can increase by at least about 2%, at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about

70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100%.

Therapeutic Window

[0534] As used herein "therapeutic window" refers to the range of plasma concentrations, or the range of levels of therapeutically active substance at the site of action, with a high probability of eliciting a therapeutic effect. In some embodiments, the therapeutic window of the AAV particle as described herein can increase by at least about 2%, at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 100%.

Volume of Distribution

[0535] As used herein, the term "volume of distribution" refers to the fluid volume that would be required to contain the total amount of the drug in the body at the same concentration as in the blood or plasma: V_{dist} equals the amount of drug in the body/concentration of drug in blood or plasma. For example, for a 10 mg dose and a plasma concentration of 10 mg/L, the volume of distribution would be 1 liter. The volume of distribution reflects the extent to which the drug is present in the extravascular tissue. A large volume of distribution reflects the tendency of a compound to bind to the tissue components compared with plasma protein binding. In a clinical setting, V_{dist} can be used to determine a loading dose to achieve a steady state concentration. In some embodiments, the volume of distribution of the AAV particles as described herein can decrease at least about 2%, at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%.

Biological Effect

[0536] In one embodiment, the biological effect of the AAV particles delivered to the animals may be categorized by analyzing the payload expression in the animals. The payload expression may be determined from analyzing a biological sample collected from a mammal administered the AAV particles of the present invention. For example, a protein expression of 50-200 pg/ml for the protein encoded by the AAV particles delivered to the mammal may be seen as a therapeutically effective amount of protein in the mammal.

IV. METHODS AND USES OF THE COMPOSITIONS OF THE INVENTION

Gene expression

[0537] The AAV particles, compositions comprising the AAV particles of the present invention may be used for regulating expression of a gene of interest in a cell, tissue, organ or subject.

[0538] In accordance with the present invention, methods for increasing expression of a target protein in a cell, tissue, organ or subject are provided; the method comprising administering the cell, tissue, organ or subject an effective amount of the AAV particles comprising a functional payload that comprises a nucleic acid sequence encoding the target protein.

[0539] Accordingly, the target protein may be increased by at least about 10%, preferably by at least about 10%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[0540] In one embodiment, the AAV particles, compositions and formulations of the present invention may be used to increase the expression of a target protein in a cell of the CNS, such as a neuron, astrocyte and/or oligodendrocyte. In some embodiments, the gene may encode a protein including but not limited to an antibody, AADC, APOE2, and Frataxin.

[0541] In some embodiments, AAV particles, compositions and formulations of the present invention may be used to decrease, inhibit and suppress the expression of a gene of interest in a cell, tissue, organ or subject. Accordingly, the AAV particles comprise at least one functional payload that comprises siRNA duplexes or dsRNA specific to the target gene of interest.

[0542] In some embodiments, the present invention provides methods for inhibiting/silencing target gene expression in a cell. Accordingly, the siRNA duplexes or encoded dsRNA can be used to substantially inhibit target gene expression in a cell, such as but not limited to, astrocytes or microglia, cortical, hippocampal, entorhinal, thalamic, motor or primary sensory neurons. In some aspects, the inhibition of target gene expression refers to an inhibition by at least about 20%, such as by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-

80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. Accordingly, the protein product of the targeted gene may be inhibited by at least about 20%, preferably by at least about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[0543] In some embodiments, the gene to be inhibited may include but are not limited to SOD1, HTT, APOE, and/or MAPT.

Neurological Disease

[0544] Various neurological diseases may be treated with pharmaceutical compositions, AAV particles, especially blood brain barrier crossing AAV particles of the present invention. As a non-limiting example, the neurological disease may be Absence of the Septum Pellucidum, Acid Lipase Disease, Acid Maltase Deficiency, Acquired Epileptiform Aphasia, Acute Disseminated Encephalomyelitis, Attention Deficit-Hyperactivity Disorder (ADHD), Adie's Pupil, Adie's Syndrome, Adrenoleukodystrophy, Agenesis of the Corpus Callosum, Agnosia, Aicardi Syndrome, Aicardi-Goutieres Syndrome Disorder, AIDS - Neurological Complications, Alexander Disease, Alpers' Disease, Alternating Hemiplegia, Alzheimer's Disease, Amyotrophic Lateral Sclerosis (ALS), Anencephaly, Aneurysm, Angelman Syndrome, Angiomatosis, Anoxia, Antiphospholipid Syndrome, Aphasia, Apraxia, Arachnoid Cysts, Arachnoiditis, Arnold-Chiari Malformation, Arteriovenous Malformation, Asperger Syndrome, Ataxia, Ataxia Telangiectasia, Ataxias and Cerebellar or Spinocerebellar Degeneration, Atrial Fibrillation and Stroke, Attention Deficit-Hyperactivity Disorder, Autism Spectrum Disorder, Autonomic Dysfunction, Back Pain, Barth Syndrome, Batten Disease, Becker's Myotonia, Behcet's Disease, Bell's Palsy, Benign Essential Blepharospasm, Benign Focal Amyotrophy, Benign Intracranial Hypertension, Bernhardt-Roth Syndrome, Binswanger's Disease, Blepharospasm, Bloch-Sulzberger Syndrome, Brachial Plexus Birth Injuries, Brachial Plexus Injuries, Bradbury-Eggleston Syndrome, Brain and Spinal Tumors, Brain Aneurysm, Brain Injury, Brown-Sequard Syndrome,

Bulbospinal Muscular Atrophy, Cerebral Autosomal Dominant Arteriopathy with Sub-cortical Infarcts and Leukoencephalopathy (CADASIL), Canavan Disease, Carpal Tunnel Syndrome, Causalgia, Cavernomas, Cavernous Angioma, Cavernous Malformation, Central Cervical Cord Syndrome, Central Cord Syndrome, Central Pain Syndrome, Central Pontine Myelinolysis, Cephalic Disorders, Ceramidase Deficiency, Cerebellar Degeneration, Cerebellar Hypoplasia, Cerebral Aneurysms, Cerebral Arteriosclerosis, Cerebral Atrophy, Cerebral Beriberi, Cerebral Cavernous Malformation, Cerebral Gigantism, Cerebral Hypoxia, Cerebral Palsy, Cerebro-Oculo-Facio-Skeletal Syndrome (COFS), Charcot-Marie-Tooth Disease, Chiari Malformation, Cholesterol Ester Storage Disease, Chorea, Choreoacanthocytosis, Chronic Inflammatory Demyelinating Polyneuropathy (CIDP), Chronic Orthostatic Intolerance, Chronic Pain, Cockayne Syndrome Type II, Coffin Lowry Syndrome, Colpocephaly, Coma, Complex Regional Pain Syndrome, Congenital Facial Diplegia, Congenital Myasthenia, Congenital Myopathy, Congenital Vascular Cavernous Malformations, Corticobasal Degeneration, Cranial Arteritis, Craniosynostosis, Cree encephalitis, Creutzfeldt-Jakob Disease, Cumulative Trauma Disorders, Cushing's Syndrome, Cytomegalic Inclusion Body Disease, Cytomegalovirus Infection, Dancing Eyes-Dancing Feet Syndrome, Dandy-Walker Syndrome, Dawson Disease, De Morsier's Syndrome, Dejerine-Klumpke Palsy, Dementia, Dementia -Multi-Infarct, Dementia - Semantic, Dementia -Subcortical, Dementia With Lewy Bodies, Dentate Cerebellar Ataxia, Dentatorubral Atrophy, Dermatomyositis, Developmental Dyspraxia, Devic's Syndrome, Diabetic Neuropathy, Diffuse Sclerosis, Dravet Syndrome, Dysautonomia, Dysgraphia, Dyslexia, Dysphagia, Dyspraxia, Dyssynergia Cerebellaris Myoclonica, Dyssynergia Cerebellaris Progressiva, Dystonias, Early Infantile Epileptic Encephalopathy, Empty Sella Syndrome, Encephalitis, Encephalitis Lethargica, Encephaloceles, Encephalopathy, Encephalopathy (familial infantile), Encephalotrigeminal Angiomatosis, Epilepsy, Epileptic Hemiplegia, Erb's Palsy, Erb-Duchenne and Dejerine-Klumpke Palsies, Essential Tremor, Extrapontine Myelinolysis, Fabry Disease, Fahr's Syndrome, Fainting, Familial Dysautonomia, Familial Hemangioma, Familial Idiopathic Basal Ganglia Calcification, Familial Periodic Paralyses, Familial Spastic Paralysis, Farber's Disease, Febrile Seizures, Fibromuscular Dysplasia, Fisher Syndrome, Floppy Infant Syndrome, Foot Drop, Friedreich's Ataxia, Frontotemporal Dementia, Gaucher Disease, Generalized Gangliosidoses, Gerstmann's Syndrome, Gerstmann-Straussler-Scheinker Disease, Giant Axonal Neuropathy, Giant Cell Arteritis, Giant Cell Inclusion Disease, Globoid Cell Leukodystrophy,

Glossopharyngeal Neuralgia, Glycogen Storage Disease, Guillain-Barré Syndrome, Hallervorden-Spatz Disease, Head Injury, Headache, Hemicrania Continua, Hemifacial Spasm, Hemiplegia Alterans, Hereditary Neuropathies, Hereditary Spastic Paraplegia, Heredopathia Atactica Polyneuritiformis, Herpes Zoster, Herpes Zoster Oticus, Hirayama Syndrome, Holmes-Adie syndrome, Holoprosencephaly, HTLV-1 Associated Myelopathy, Hughes Syndrome, Huntington's Disease, Hydranencephaly, Hydrocephalus, Hydrocephalus - Normal Pressure, Hydromyelia, Hypercortisolism, Hypersomnia, Hypertonia, Hypotonia, Hypoxia, Immune-Mediated Encephalomyelitis, Inclusion Body Myositis, Incontinentia Pigmenti, Infantile Hypotonia, Infantile Neuroaxonal Dystrophy, Infantile Phytanic Acid Storage Disease, Infantile Refsum Disease, Infantile Spasms, Inflammatory Myopathies, Iniencephaly, Intestinal Lipodystrophy, Intracranial Cysts, Intracranial Hypertension, Isaacs' Syndrome, Joubert Syndrome, Kearns-Sayre Syndrome, Kennedy's Disease, Kinsbourne syndrome, Kleine-Levin Syndrome, Klippel-Feil Syndrome, Klippel-Trenaunay Syndrome (KTS), Klüver-Bucy Syndrome, Korsakoff's Amnesic Syndrome, Krabbe Disease, Kugelberg-Welander Disease, Kuru, Lambert-Eaton Myasthenic Syndrome, Landau-Kleffner Syndrome, Lateral Femoral Cutaneous Nerve Entrapment, Lateral Medullary Syndrome, Learning Disabilities, Leigh's Disease, Lennox-Gastaut Syndrome, Lesch-Nyhan Syndrome, Leukodystrophy, Levine-Critchley Syndrome, Lewy Body Dementia, Lipid Storage Diseases, Lipoid Proteinosis, Lissencephaly, Locked-In Syndrome, Lou Gehrig's Disease, Lupus - Neurological Sequelae, Lyme Disease - Neurological Complications, Machado-Joseph Disease, Macrencephaly, Megalencephaly, Melkersson-Rosenthal Syndrome, Meningitis, Meningitis and Encephalitis, Menkes Disease, Meralgia Paresthetica, Metachromatic Leukodystrophy, Microcephaly, Migraine, Miller Fisher Syndrome, Mini Stroke, Mitochondrial Myopathy, Moebius Syndrome, Monomelic Amyotrophy, Motor Neuron Diseases, Moyamoya Disease, Mucolipidoses, Mucopolysaccharidoses, Multi-Infarct Dementia, Multifocal Motor Neuropathy, Multiple Sclerosis, Multiple System Atrophy, Multiple System Atrophy with Orthostatic Hypotension, Muscular Dystrophy, Myasthenia - Congenital, Myasthenia Gravis, Myelinoclastic Diffuse Sclerosis, Myoclonic Encephalopathy of Infants, Myoclonus, Myopathy, Myopathy- Congenital, Myopathy -Thyrotoxic, Myotonia, Myotonia Congenita, Narcolepsy, Neuroacanthocytosis, Neurodegeneration with Brain Iron Accumulation, Neurofibromatosis, Neuroleptic Malignant Syndrome, Neurological Complications of AIDS, Neurological Complications of Lyme Disease, Neurological Consequences of Cytomegalovirus Infection, Neurological Manifestations of Pompe Disease,

Neurological Sequelae Of Lupus, Neuromyelitis Optica, Neuromyotonia, Neuronal Ceroid Lipofuscinosis, Neuronal Migration Disorders, Neuropathy- Hereditary, Neurosarcoidosis, Neurosyphilis, Neurotoxicity, Nevus Cavernosus, Niemann-Pick Disease, O'Sullivan-McLeod Syndrome, Occipital Neuralgia, Ohtahara Syndrome, Olivopontocerebellar Atrophy, Opsoclonus Myoclonus, Orthostatic Hypotension, Overuse Syndrome, Pain -Chronic, Pantothenate Kinase-Associated Neurodegeneration, Paraneoplastic Syndromes, Paresthesia, Parkinson's Disease, Paroxysmal Choreoathetosis, Paroxysmal Hemicrania, Parry-Romberg, Pelizaeus-Merzbacher Disease, Pena Shokeir II Syndrome, Perineural Cysts, Periodic Paralyses, Peripheral Neuropathy, Periventricular Leukomalacia, Persistent Vegetative State, Pervasive Developmental Disorders, Phytanic Acid Storage Disease, Pick's Disease, Pinched Nerve, Piriformis Syndrome, Pituitary Tumors, Polymyositis, Pompe Disease, Porencephaly, Post-Polio Syndrome, Postherpetic Neuralgia, Postinfectious Encephalomyelitis, Postural Hypotension, Postural Orthostatic Tachycardia Syndrome, Postural Tachycardia Syndrome, Primary Dentatum Atrophy, Primary Lateral Sclerosis, Primary Progressive Aphasia, Prion Diseases, Progressive Hemifacial Atrophy, Progressive Locomotor Ataxia, Progressive Multifocal Leukoencephalopathy, Progressive Sclerosing Poliodystrophy, Progressive Supranuclear Palsy, Prosopagnosia, Pseudo-Torch syndrome, Pseudotoxoplasmosis syndrome, Pseudotumor Cerebri, Psychogenic Movement, Ramsay Hunt Syndrome I, Ramsay Hunt Syndrome II, Rasmussen's Encephalitis, Reflex Sympathetic Dystrophy Syndrome, Refsum Disease, Refsum Disease - Infantile, Repetitive Motion Disorders, Repetitive Stress Injuries, Restless Legs Syndrome, Retrovirus-Associated Myelopathy, Rett Syndrome, Reye's Syndrome, Rheumatic Encephalitis, Riley-Day Syndrome, Sacral Nerve Root Cysts, Saint Vitus Dance, Salivary Gland Disease, Sandhoff Disease, Schilder's Disease, Schizencephaly, Seitelberger Disease, Seizure Disorder, Semantic Dementia, Septo-Optic Dysplasia, Severe Myoclonic Epilepsy of Infancy (SMEI), Shaken Baby Syndrome, Shingles, Shy-Drager Syndrome, Sjögren's Syndrome, Sleep Apnea, Sleeping Sickness, Sotos Syndrome, Spasticity, Spina Bifida, Spinal Cord Infarction, Spinal Cord Injury, Spinal Cord Tumors, Spinal Muscular Atrophy, Spinocerebellar Atrophy, Spinocerebellar Degeneration, Steele-Richardson-Olszewski Syndrome, Stiff-Person Syndrome, Striatonigral Degeneration, Stroke, Sturge-Weber Syndrome, Subacute Sclerosing Panencephalitis, Subcortical Arteriosclerotic Encephalopathy, Short-lasting, Unilateral, Neuralgiform (SUNCT) Headache, Swallowing Disorders, Sydenham Chorea, Syncope, Syphilitic Spinal Sclerosis, Syringohydromyelia, Syringomyelia, Systemic Lupus Erythematosus, Tabes Dorsalis,

Tardive Dyskinesia, Tarlov Cysts, Tay-Sachs Disease, Temporal Arteritis, Tethered Spinal Cord Syndrome, Thomsen's Myotonia, Thoracic Outlet Syndrome, Thyrotoxic Myopathy, Tic Douloureux, Todd's Paralysis, Tourette Syndrome, Transient Ischemic Attack, Transmissible Spongiform Encephalopathies, Transverse Myelitis, Traumatic Brain Injury, Tremor, Trigeminal Neuralgia, Tropical Spastic Paraparesis, Troyer Syndrome, Tuberous Sclerosis, Vascular Erectile Tumor, Vasculitis Syndromes of the Central and Peripheral Nervous Systems, Von Economo's Disease, Von Hippel-Lindau Disease (VHL), Von Recklinghausen's Disease, Wallenberg's Syndrome, Werdnig-Hoffman Disease, Wernicke-Korsakoff Syndrome, West Syndrome, Whiplash, Whipple's Disease, Williams Syndrome, Wilson Disease, Wolman's Disease, X-Linked Spinal and Bulbar Muscular Atrophy.

[0545] The present disclosure additionally provides a method for treating or ameliorating neurological disorders in a mammalian subject, including a human subject, comprising administering to the subject a pharmaceutically effective amount of any of the AAV particles or pharmaceutical compositions of the invention. In one embodiment, the AAV particle is a blood brain barrier crossing particle. In some embodiments, neurological disorders treated according to the methods described herein include, but are not limited to, tauopathies, Alzheimer's disease (AD), Amyotrophic lateral sclerosis (ALS), Huntington's Disease (HD), Parkinson's Disease (PD), and/or Friedreich's Ataxia (FA). In some embodiments, at least one sympotom of neurological disorders in the subject is ameliorated and/or treated.

[0546] The present disclosure provides a method for administering to a subject in need thereof, including a human subject, a therapeutically effective amount of the AAV particles of the invention to slow, stop or reverse disease progression. As a non-limiting example, disease progression may be measured by tests or diagnostic tool(s) known to those skilled in the art. As another non-limiting example, disease progression may be measured by change in the pathological features of the brain, CSF or other tissues of the subject.

Tauopathies

[0547] Tauopathies are a group of neurodegenerative diseases characterized by the dysfunction and/or aggregation of the microtubule associated protein tau. Tau is normally a very soluble protein known to associate with microtubules based on the extent of its phosphorylation. Tau is considered a critical component of intracellular trafficking processes, particularly in neuronal cells, given their unique structure. Hyperphosphorylation of tau depresses its binding to microtubules and microtubule assembly activity. Further, hyperphosphorylation of tau renders it prone to misfolding and aggregation. In tauopathies,

the tau becomes hyperphosphorylated, misfolds and aggregates as NFT of paired helical filaments (PHF), twisted ribbons or straight filaments. These NFT are largely considered indicative of impending neuronal cell death and thought to contribute to widespread neuronal cell loss, leading to a variety of behavioral and cognitive deficits.

[0548] The first genetically defined tauopathy was described when mutations in the tau gene were shown to lead to an autosomal dominantly inherited tauopathy known as frontemporal dementia and parkinsonism linked to chromosome 17 (FTDP-17). This was the first causal evidence that changes in tau could lead to neurodegenerative changes in the brain. These molecules are considered to be more amyloidogenic, meaning they are more likely to become hyperphosphorylated and more likely to aggregate into NFT (Hutton, M. et al., 1998, Nature 393(6686):702-5).

[0549] Other known tauopathies include, but are not limited to, Alzheimer's disease (AD), frontotemporal dementia (FTD), Frontotemporal lobar degeneration (FTLD), chronic traumatic encephalopathy (CTE), Progressive Supranuclear Palsy (PSP), Down's syndrome, Pick's disease, Corticobasal degeneration (CBD), Amyotrophic lateral sclerosis (ALS), Prion diseases, Creutzfeldt-Jakob disease (CJD), Multiple system atrophy, Tangle-only dementia, and Progressive subcortical gliosis.

[0550] Though tauopathies are predominantly associated with tau protein malfunction and aggregation, much like in AD, ApoE is also considered to play a role in the pathogenesis of this group of diseases. ApoE, a cholesterol trafficking molecule, was first suspected to have a role in tauopathy when it was discovered that NFT are also immunoreactive for ApoE. Investigation of the correlations between tau and ApoE in tauopathies have shown contradictory results but suggest a link between ApoE4 and increased NFT load. However, the correlation to cognitive decline has not been shown. Work in this area is still actively being pursued.

[0551] Treatments for tauopathies have yet to be identified, though some symptomatic relief may be provided. Delivery of AAV particles of the invention may be used to treat subjects suffering from tauopathy. In some cases, methods of the present invention may be used to treat subjects suspected of developing a tauopathy. Delivery of AAV particles of the invention may result in decreased accumulation of NFT. Further, these decreases in NFT load may or may not be associated with improvements in cognitive, language or behavioral arenas.

[0552] In one embodiment, delivery of AAV particles of the invention, comprising ApoE2, ApoE3 or ApoE4 polynucleotides, may be used to treat subjects suffering from tauopathy.

[0553] In one embodiment, delivery of AAV particles of the invention comprising modulatory polynucleotides for the silencing of ApoE2, ApoE3 or ApoE4 gene and/or protein expression may be used to treat subjects suffering from tauopathy.

[0554] In one embodiment, delivery of AAV particles of the invention comprising modulatory polynucleotides for the silencing of tau gene and/or protein expression may be used to treat subjects suffering from tauopathy.

[0555] In one embodiment, the modulatory polynucleotides are siRNA duplexes or nucleic acids encoding siRNA duplexes or encoded dsRNA.

[0556] In one embodiment, delivery of AAV particles of the invention comprising a nucleic acid encoding an anti-tau antibody may be used to treat subjects suffering from tauopathy.

[0557] In one embodiment, the compositions described herein are used in combination with one or more known or exploratory treatments for tauopathy. Non-limiting examples of such treatments include inhibitors of tau aggregation, such as Methylene blue, phenothiazines, anthraquinones, n-phenylamines or rhodamines, microtubule stabilizers such as NAP, taxol or paclitaxel, kinase or phosphatase inhibitors such as those targeting GSK3β (lithium) or PP2A, and/or immunization with tau phospho-epitopes or treatment with anti-tau antibodies.

Alzheimer's Disease

[0558] Alzheimer Disease (AD) is a debilitating neurodegenerative disease and the leading cause of dementia in the elderly today, currently afflicting an estimated 5 million people in the United States and more than 35 million people worldwide. AD is largely a disease of extreme forgetfulness, wherein the ability to lead a normal life is incredibly impaired. Clinical manifestations of the disease include progressive declines in memory, executive function (decision making) and language. Individuals with AD often die from secondary illnesses such as cachexia, pneumonia or sepsis.

[0559] AD is likely the most well-known tauopathy, though it is often characterized as an amyloid based disorder. The AD brain is characterized by the presence of two forms of pathological aggregates, the extracellular plaques composed of β-amyloid (Aβ) and the intracellular neurofibrillary tangles (NFT) comprised of hyperphosphorylated microtubule

associated protein tau. Based on early genetic findings, β-amyloid alterations were thought to initiate disease, with changes in tau considered downstream. For this reason, most clinical trials have been Aβ-centric.

[0560] In addition to the traditional hallmarks of the disease (Aβ and tau), apolipoprotein E has proven to be an important risk factor in the pathogenesis of late onset AD (the form of AD that is not genetically linked to alterations in Aβ processing or production and accounts for 99% of the AD population). ApoE, like other apolipoproteins, contributes to the structure of specific lipoprotein particles and directs lipoprotein trafficking to specific cell surface receptors, and is an important cholesterol transporter. ApoE is expressed in a variety of cell types with highest expression levels evident in the liver and brain. In the brain, ApoE is predominantly expressed in astrocytes and microglia, and is thought to contribute to maintenance of synaptic connections and synaptogenesis. ApoE is thought to contribute to AD pathogenesis through its roles in the blood brain barrier, the innate immune system, synaptic function and accumulation of Aβ.

[0561] The three most common variants of ApoE are ApoE2, ApoE3 and ApoE4, with ApoE2 and ApoE4 carrying differential risks associated with development of AD. ApoE2 is considered to be a protective allele, decreasing risk of AD and delaying the age of onset, whereas ApoE4 has the opposite effect, significantly increasing risk of developing AD and reducing the age of onset of disease. Further, ApoE2 is associated with a decreased burden of accumulated Aβ, whereas ApoE4 is associated with increased Aβ load.

[0562] Early onset forms of AD (before 65 years, which accounts for <5% of AD cases), may be caused by familial mutations in amyloid beta precursor protein (APP), presenilin 1 (PS1 or PSEN1) or presenilin 2 (PS2 or PSEN2). Common symptoms include progressive delcine in memory, executive function, language, and other areas of cognition. These symptoms are often caused by amyloid plaques and/or neurofibrillary tangles in the brain, neuronal loss, synaptic loss, brain atrophy, and/or inflammation.

[0563] Symptomatic treatments for AD have been available for many years, but none are able to alter the course of the disease. Delivery of AAV particles of the invention may be used to treat subjects suffering from AD and other tauopathies. In some cases, methods of the present invention may be used to treat subjects suspected of developing AD or other tauopathies. Delivery of AAV particles of the invention may result in decreased Aβ burden both in the brain and in the cardiovascular system of the subject or in decreased accumulation

of NFT. Further, these decreases in Aβ or NFT load, may or may not be associated with improvements in cognitive, language or behavioral arenas.

[0564] In one embodiment, delivery of AAV particles of the invention, comprising ApoE2, ApoE3 or ApoE4 polynucleotides, may be used to treat subjects suffering from AD and other tauopathies.

[0565] In one embodiment, delivery of AAV particles of the invention comprising modulatory polynucleotides for the silencing of the ApoE2, ApoE3 or ApoE4 gene and/or protein may be used to treat subjects suffering from AD and other tauopathies.

[0566] In one embodiment, delivery of AAV particles of the invention comprising modulatory polynucleotides for the silencing of the tau gene and/or protein may be used to treat subjects suffering from AD and other tauopathies.

[0567] In one embodiment, the modulatory polynucleotides are siRNA duplexes or nucleic acids encoding siRNA duplexes or encoded dsRNA.

[0568] In one embodiment, delivery of AAV particles of the invention comprising a nucleic acid encoding an anti-tau antibody may be used to treat subjects suffering from AD and other tauopathies.

[0569] In one embodiment, the compositions described herein are used in combination with one or more known or exploratory treatments for AD or tauopathy. Non-limiting examples of such treatments include cholinesterase inhibitors (donepezil, rivastigmine, galantamine), NMDA receptor antagonists such as memantine, anti-psychotics, anti-depressants, anti-convulsants, secretase inhibitors, amyloid aggregation inhibitors, copper or zinc modulators, BACE inhibitors, inhibitors of tau aggregation, such as Methylene blue, phenothiazines, anthraquinones, n-phenylamines or rhodamines, microtubule stabilizers such as NAP, taxol or paclitaxel, kinase or phosphatase inhibitors such as those targeting GSK3β (lithium) or PP2A, and/or immunization with Aβ peptides or tau phospho-epitopes or treatment with anti-tau or anti-amyloid antibodies.

[0570] In one embodiment, the compositions described herein are evaluated using mammalian models, such as, but not limited to, mouse models of tauopathy and/or Alzheimer's Disease. A great number of mouse models are available that mimic the phenotypes of tauopathies and/or Alzheimer's Disease. However, no existing mouse model exhibits all features of human tauopathies and/or Alzheimer's Disease. Therefore, in some cases, more than one mouse model, or a mouse model cross of one or more of these models, may be used to evaluate the activities of the compositions of the present invention.

Exemplary mouse models of tauopathies and/or Alzheimer's Disease include, but are not limited to, 3XTg-AD, 5XFAD, J20, Tg-SwDI, Tg-SwDI/Nos2, Tg2576, R1.40, APPPS1, APP23, PDAPP, APP NL-G-F, TgCRND8, TASD-41, BRI-Aβ42A, PSAPP (Tg2576xPS1), APPswe/PSEN1dE9, 2xKI, TAPP (Tg2576xJNPL3), hTau, PS1M146V, rTg4510, rTg4510xCamk2a-tTA, PS19, rTg4510xNop-tTA, GFAP-apoE4, Apoe$^{tm3(APOE*4)}$, APP.PS1/TRE4 and ApoE knock-out or knock-in mouse lines. (See Onos et al., Brain Res Bull. 2016;122:1-11; Hall and Roberson., Brain Res Bull. 2012; 88(1): 3–12; Elder et al., Mt Sinai J Med. 2010; 77(1): 69–81, the contents of which are herein incorporated by reference in their entirety).

[0571] Tau transgenic mouse models overexpress wild-type or mutant human tau protein. More than 20 lines have been generated that contain different tau mutations (See Table 2 of Denk and Wade-Martins, Neurobiol Aging. 2009; 30(1): 1–13, the contents of which are herein incorporated by reference in their entirety). These are mutations present in patients with tauopathies and/or Alzheimer's Disease, including G272V, P301L, P301S, N297K, V337M, and R406W. The P301S transgenic mice express the human tau protein containing the P301S mutation. One P301S model (4R/0N tau under the control of the Thy1.2 promoter), created by Allen et al., exhibits similar characteristics to human tauopathies including filament accumulation of hyperphosphorylated tau, neuronal degeneration, and neuroinflammation. In addition, these mice develop a pronounced motor phenotype by 5-6 months of age (Allen et al., J Neurosci. 2002;22(21):9340-51; Bellucci et al., Am J Pathol. 2004;165(5):1643-52, the contents of which are herein incorporated by reference in their entirety). Another P301S mouse line (4R/1N tau under the control of the mouse prion promoter), created by Yoshiyama et al., displays hippocampal synapse loss, impaired synaptic function and concomitant microglial activation by 3–6 months of age. The animals also showed pathological hyperphosphorylated tau accumulations, neuronal loss, as well as hippocampal and entorhinal cortical atrophy by 9-12 months of age (Yoshiyama et al., Neuron. 2007;53(3):337-51, the contents of which are herein incorporated by reference in their entirety).

[0572] APOE knock-in mice express human isoforms of APOE. In some cases, the human APOE genes were engineered in to replace the endogenous mouse APOE alleles (targeted replacement). These targeted placement (TR) models of ApoE2, ApoE3 or ApoE4 were developed in the laboratory of Nobuya Maeda (Sullivan et al., J Clin Invest. 1998;102(1):130-5; Sullivan et al., J Biol Chem. 1997;272(29):17972-80; Knouff et al., J

Clin Invest. 1999;103(11):1579-86, the contents of which are herein incorporated by reference in their entirety) and characterized in many studies. The ApoE TR mice differ on spatial memory performance and avoidance behavior. ApoE4-TR mice show cognitive and synaptic plasticity impairment compared to ApoE3-TR mice. In addition, ApoE4-TR mice exhibit anatomical and functional abnormalities in the hippocampus and the amygdala (Grootendorst, Behav Brain Res. 2005;159(1):1-14; Bour et al., Behav Brain Res. 2008;193(2):174-82, the contents of which are herein incorporated by reference in their entirety).

[0573] In one embodiment, an AAV-ApoE2 particle may be administered to PDAPP or APP.PS1/TRE4 mice as described in Zhao et al 2016 Neurobiol Aging 159-172, the contents of which are herein incorporated by reference in their entirety. Intracerebral or intrathalamic administration of AAV-ApoE2 (AAV9-CAG-APOE2 or AAVrh.10-CAG-APOE2) showed significant decreases in brain Aβ (oligomeric, soluble and insoluble), amyloid deposition and amyloid pathology, as determined by immunohistochemistry, ELISA or Western blot. More specifically, AAV preparations (2μL, 1.0×10^{10} vg) were bilaterally injected by stereotactic surgery into either the hippocampus or the thalamus of adult mice at a rate of 0.2 μL/min and allowed to express for 8 weeks prior to tissue collection for post-mortem analysis. Lower doses of AAV-ApoE2, or delivery at a late stage of pathology, proved to be less effective.

Frontotemporal Dementia (FTD)

[0574] Frontotemporal Demenia (FTD), also known as frontotemporal degenerations or Pick's disease, refers to a group of disorders which are caused by progressive nerve cell loss in the brain. This nerve cell loss can cause a loss of unction in the frontal and/or temporal lobes of the brain. There are about 45,000 people in the United States who have FTD and the majority are between 45 and 65.

[0575] There are three subtypes of FTD, behavrior variant frontotemporal dementia (bvFTD), primary progressive aphasia (PPA) and distrubances of motor function. Subjects with bvFTD tend to have major changes in personality, interpersonal relationships and conduct and the nerve loss is most prominent in areas that control conduct, empathy, foresight, and judgment. PPA affects language skills, speaking, writing, and comprehension. Both bvFTD and PPA are less common than AD in those over the age of 65, however bvFTD and PPA are nearly as common as AD in those between 45 and 65.

[0576] A mutation of tau is genetically associated with those subjects who have FTD.

Amyotrophic Lateral Sclerosis (ALS)

[0577] Amyotrophic Lateral Sclerosis (ALS), also known as Lou Gehrig's disease or classical motor neuron disease, is a rapidly progressive and fatal neurological disease. ALS is associated with cell degeneration and death of upper and lower motor neurons, leading to disablement of muscle movement, weakening, wasting and loss of control over voluntary muscle movement. Early symptoms include muscle weakness of hands, legs and swallowing muscles, eventually progressing to inability to breathe due to diaphragm failure. According to Centers for Disease Control and Prevention (CDC), ALS affects an estimated 12, 000-15, 000 individuals in the US. About 5-10% of cases are familial.

[0578] ALS, as other non-infectious neurodegenerative diseases, has been characterized by presence of misfolded proteins, including, but not limited to, tau, amyloid- beta (A beta), alpha- synuclein, HTT (huntingtin) or SOD1 (superoxide dismutase 1 protein), and myelin associated inhibitors and their receptors, (see, e.g., Krishnamurthy and Sigurdsson, 2011, *N Biotechnol.* 28(5):511-7, and Musaro, 2013, FEBS J.;280(17):4315-22, and references therein). Familial ALS has been associated with mutations of TAR DNA-binding protein 43 (TDP-43) and RNA-binding protein FUS/TLS. Some proteins have been identified to slow down progression of ALS, such as, but not limited, to growth factors, e.g. insulin-like growth factor 1 (IGF-1), glial cell line-derived growth factor, brain-derived growth factor, vascular endothelial growth factor and ciliary neurotrophic factor, or growth factors promoting muscle growth, e.g. myostatin.

[0579] As of today, there is no prevention or cure for ALS. FDA approved drug niluzole has been approved to prolong life expectancy, but does not have an effect on symptoms. Additionally, drugs and medical devices are available to tolerate pain and attacks associated with ALS. There remains a need for therapy affecting the underlying pathophysiology.

[0580] In some embodiment, methods of the present invention may be used to treat subjects suffering from ALS. In some cases, methods of the present invention may be used to treat subjects suspected of developing ALS.

[0581] AAV Particles and methods of using the AAV particles described in the present invention may be used to prevent, manage and/or treat ALS. As non-limiting examples, the AAV particles of the present invention that may be used for the treatment, prevention or management of ALS may comprise modulatory polynucleotides targeting SOD1, HTT and/or Tau.

Huntington's disease

[0582] Huntington's disease (HD) is a rare, inherited disorder causing degeneration of neurons in the motor control region of the brain, as well as other areas. Typical symptoms of the disease include uncontrolled movements (chorea), abnormal postures, impaired coordination, slurred speech and difficulty of feeding and swallowing accompanied by changes in behavior, judgment and cognition. HD is caused by mutations in the gene associated with the huntingtin (HTT) protein. The mutation causes the (CAG) blocks of DNA to repeat abnormally. HD affects approximately 30, 000 individuals in the US.

[0583] HD is characterized by mutations of the huntingtin (HTT) protein with abnormal expansions of polyglutamine tracts, e.g. expansion of the length of glutamine residues encoded by CAG repeats. The expansion threshold for occurrence of the disease is considered to be approximately 35-40 residues. HD is also associated with beta sheet rich aggregates in striatal neurons formed by N-terminal regions of HTT. The expansions and aggregates lead to gradual loss of neurons as HD progresses. Additionally, the cell death in HD is associated with death receptor 6 (DR6) which is known to induce apoptosis.

[0584] As of today, there is no therapy or cure, to prevent the progression of the disease. Drug therapies available are aimed at management of the symptoms. For example, the FDA has approved tetrabenezine to be prescribed for prevention of chorea. Additionally, e.g. antipsychotic drugs may help to control delusions, hallucinations and violent outbursts. There remains a need for therapy affecting the underlying pathophysiology.

[0585] In some embodiment, methods of the present invention may be used to treat subjects suffering from HD. In some cases, methods of the present invention may be used to treat subjects suspected of developing HD.

[0586] AAV particles and methods of using the AAV particles described in the present invention may be used to prevent, manage and/or treat HD. As a non-limiting example, the AAV particles of the present invention used to treat, prevent and/or manage HD may comprise modulatory polynucleotides targeting HTT, wherein the modulatory polynucleotides are siRNA duplexes or nucleic acids encoding siRNA duplexes or encoded dsRNA.

Parkinson's Disease

[0587] Parkinson's Disease (PD) is a progressive disorder of the nervous system affecting especially the substantia nigra of the brain. PD develops as a result of the loss of dopamine producing brain cells. Typical early symptoms of PD include shaking or trembling of a limb, e.g. hands, arms, legs, feet and face. Additional characteristic symptoms are stiffness of the

limbs and torso, slow movement or an inability to move, impaired balance and coordination, cognitive changes, and psychiatric conditions e.g. depression and visual hallucinations. PD has both familial and idiopathic forms and it is suggested to be linked to genetic and environmental causes. PD affects more than 4 million people worldwide. In the US, approximately 60, 000 cases are identified annually. Generally, PD begins at the age of 50 or older. An early-onset form of the condition begins at age younger than 50, and juvenile-onset PD begins before the age of 20.

[0588] Death of dopamine producing brain cells related to PD has been associated with aggregation, deposition and dysfunction of alpha-synuclein protein (see, e.g. Marques and Outeiro, 2012, *Cell Death Dis.* 3:e350, Jenner, 1989, *J Neurol Neurosurg Psychiatry.* Special Supplement, 22-28, and references therein). Studies have suggested that alpha-synuclein has a role in presynaptic signaling, membrane trafficking and regulation of dopamine release and transport. Alpha-synuclein aggregates, e.g. in forms of oligomers, have been suggested to be species responsible for neuronal dysfunction and death. Mutations of the alpha-synuclein gene (SNCA) have been identified in the familial forms of PD, but also environmental factors, e.g. neurotoxin affect alpha-synuclein aggregation. Other suggested causes of brain cell death in PD are dysfunction of proteosomal and lysosomal systems, reduced mitochondrial activity.

[0589] PD is related to other diseases related to alpha-synuclein aggregation, referred to as "synucleinopathies." Such diseases include, but are not limited to, Parkinson's Disease Dementia (PDD), multiple system atrophy (MSA), dementia with Lewy bodies, juvenile-onset generalized neuroaxonal dystrophy (Hallervorden-Spatz disease), pure autonomic failure (PAF), neurodegeneration with brain iron accumulation type-1 (NBIA-1) and combined Alzheimer's and Parkinson's disease.

[0590] As of today, no cure or preventative therapy for PD has been identified. A variety of drug therapies available provide symptomatic relief. Non-limiting examples of symptomatic medical treatments include carbidopa and levodopa combination reducing stiffness and slow movement, and anticholinergics to reduce trembling and stiffness. Other optional therapies include e.g. deep brain stimulation and surgery. There remains a need for therapy affecting the underlying pathophysiology.

[0591] In some embodiment, methods of the present invention may be used to treat subjects suffering from PD and other synucleinopathies. In some cases, methods of the

present invention may be used to treat subjects suspected of developing PD and other synucleinopathies.

Friedreich's Ataxia

[0592] Friedreich's Ataxia (FA) is an autosomal recessive inherited disease that causes progressive damage to the nervous system. See, Parkinson et al., *Journal of Neurochemistry*, 2013, 126 (Suppl. 1), 103-117, the contents of which are herein incorporated by reference in their entirety. Onset usually occurs at puberty, and always by age 25. See, Campuzano, et al., Science, 271.5254 (Mar 8, 1996): 1423, the contents of which are herein incorporated by reference in their entirety. FA results from the degeneration of nervous tissue in the spinal cord due to reduced expression of the mitochondrial protein frataxin (FXN) in sensory neurons that are essential (through connections with the cerebellum) for directing muscle movement of the arms and legs. See, Koeppen, Arnulf; *J Neurol Sci.*, 2011, April 15; 303(1-2): 1–12, the contents of which are herein incorporated by reference in their entirety. Initial symptoms include poor coordination such as gait disturbance, poor balance, leg weakness, decreased walking, impaired coordination, dysarthria, nystagmus, impaired sensation, kyphoscoliosis, and foot deformities. See, Parkinson et al., *Journal of Neurochemistry*, 2013, 126 (Suppl. 1), 103-117. The disease generally progresses until a wheelchair is required for mobility. Incidence of FA among the Caucasian populations is between about 1 in 20,000 and about 1 in 50,000, with a deduced carrier frequency of about 1 in 120 in European populations. See, Nageshwaran and Festenstein, *Frontiers in Neurology*, Vol. 6, Art. 262 (2015); Campuzano, et al., Science, 271.5254 (Mar 8, 1996): 1423, the contents of each of which are herein incorporated by reference in their entirety.

[0593] The expansion of an intronic GAA triplet repeat in the FXN gene is the genetic cause of reduced expression of frataxin resulting in FA. See, Parkinson et al., *Journal of Neurochemistry*, 2013, 126 (Suppl. 1), 103-117. Over time the deficiency causes the aforementioned symptoms, as well as frequent fatigue due to effects on cellular metabolism.

[0594] Currently, no effective treatments exist for FA and patients are most often simply monitored for symptom management. Consequently, there remains a long felt need in the art to develop pharmaceutical compositions and methods for the treatment of FXN related disorders and to ameliorate deficiencies of the protein in patients afflicted with FA.

[0595] Delivery of AAV particles of the invention may be used to treat subjects suffering from Friedreich's Ataxia. In some cases, methods of the present invention may be used to treat subjects suspected of developing Friedreich's Ataxia. Delivery of AAV particles of the

invention may result in increased frataxin protein. Further, this increase in frataxin protein may or may not be associated with improvements in mobility.

[0596] In one embodiment, delivery of AAV particles of the invention, comprising frataxin polynucleotides, may be used to treat subjects suffering from Friedreich's Ataxia.

[0597] In one embodiment, the AAV particles of the invention, comprising frataxin polynucleotides, may be delivered to the dentate nucleus of the cerebellum, brainstem nuclei and/or Clarke's column of the spinal cord. Delivery to one or more of these regions may treat and/or reduce the effects of Friedreich's Ataxia in a subject.

[0598] In one embodiment, the AAV particles of the invention, comprising frataxin polynucleotides, may be delivered by intravenous administration to the central nervous system, peripheral nervous system, and/or peripheral organs for the treatment of Friedreich's Ataxia in a subject.

Cardiovascular Disease

[0599] Cardiovascular disease, also called heart disease or heart and blood vessel disease, is a general term describing many diseases or disorders of the heart and/or blood vessels. Many of the diseases or disorders in cardiovascular disease are related to atherosclerosis where plaque builds up in the walls of the arteries. This buildup narrows the arteries making it harder for blood to flow through. Non-limiting examples of cardiovascular disease include, heart failure (when the heart is not pumping blood as well as it should be), arrhythmia (abnormal rhythm of the heart, e.g., bradycardia (heart rate of less than 60 beats per minute) or tachycardia (heart rate of more than 100 beats per minute)), heart valve problems (e.g., stenosis (valves don't open enough to allow blood to flow through as it should), regurgitation (valves do not close properly), and prolapse (valve leaflets bulge or prolapse back into the upper chamber)), stroke (e.g., an ischemic stroke when there is a blockage of the blood vessel that feeds to the brain), and heart attack (when the blood flow is blocked to the heart).

[0600] The AAV particles of the invention may be used to treat subjects suffering from cardiovascular disease.

Heart Failure

[0601] Heart failure is the leading cause of mortality in the United States with approximately 5.8 million patients and 300,000 deaths per year. Heart failure is the common endpoint of cardiac disease caused by various factors including, but not limited to, diet, smoking, hypertension or genetics. Heart failure may be cause by the dysregulation of calcium handling which leads to impaired heart muscle contractility. Current treatments for

heart failure include, but are not limited to, symptomatic therapy (e.g., diuretics, β-adrenergic blockers, and/or angiotensin-converting enzyme (ACE) inhibitors), and device or surgery therapy (e.g., left ventricular assist device (LVAD), valve replacement, and/or angioplasty). These currently therapies do not directly correct heart contractility but provide only a short term solution to the disease. A long term therapeutic option to treat heart failure is gene therapy using AAV delivery.

[0602] A majority of cardiac AAV gene therapeutic approaches have focused on the β-adrenergic system (βARKct, Adenylyl Cyclase 6) or calcium handling proteins (SERCA2a, PP1, S100A1) to rescue cardiac contractility. See e.g., Hulot et al., 2016 and Zouein & Booz 2013, the contents of each of which are incorporated by reference in their entireties. However, increased transduction of cardiomyocytes by systemic or targeted delivery of the AAV capsids described herein, provides the best opportunity for the treatment of heart failure.

[0603] The New York Heart Association (NYHA) created a functional classification system to categorize subjects with heart failure. NYHA provides 4 classes of patient symptom assessment and 4 classes of objective assessments based on how much a subject is limited during physical activity. Class I patient symptom assessment means a subject has no limit of physical activity as ordinary physical activity does not cause a subject undue fatigue, palpitation, or shortness of breath. Class II patient symptom assessment means a subject has a slight limitation of physical activity as they are comfortable at rest but ordinary physical activity results in fatigue, palpitation, and shortness of breath. Class III patient symptom assessment means a subject has a limitation of physical activity as the subject is comfortable at rest but activity other than normal activity causes fatigue, palpitation, or shortness of breath. Class IV patient symptom assessment means a subject is unable to carry on any physical activity without discomfort. An objective assessment means that a subject has no objective evidence of cardiovascular disease and there are no symptoms nor limitation to ordinary physical activity. A Class B objective assessment means that there is objective evidence of minimal cardiovascular disease with mild symptoms and a slight limitation during ordinary activity but the subject is comfortable at rest. A Class C objective assessment means that there is objective evidence of moderately severe cardiovascular disease, the subject is only comfortable at rest and has marked limitation activity due to symptoms even during activity which is less than ordinary. A Class D objective assessment

means that there is objective evidence of severe cardiovascular disease, the subject has symptoms even at rest, and has severe activity limitations.

[0604] In one embodiment, delivery of the AAV particles of the invention may be used to treat subjects who has heart failure.

[0605] In one embodiment, delivery of the AAV particles of the present invention occurs after a myocardial injury. In one embodiment, delivery of the AAV particles of the present invention occurs after a subject has depressed ventricular performance. In one embodiment, delivery of the AAV particles of the present invention occurs after administration of digoxin to a subject. In one embodiment, delivery of the AAV particles of the present invention occurs at the same time as administration of digoxin to a subject. In one embodiment, delivery of the AAV particles of the present invention occurs after a subject has depressed ventricular performance but prior to a subject having reduced cardiac output. In one embodiment, delivery of the AAV particles of the present invention occurs prior to administration of beta-blockers to a subject.

[0606] In one embodiment, the AAV particles of the present invention are administered in combination with digoxin, beta-blockers, ACE1, aRB, spironolactone, diuretics, and/or vasodilators.

[0607] In one embodiment, the AAV particles of the present invention, comprising ATP2A2 (also called SERCA2a) polynucleotides, are administered to treat a subject who has heart failure. While not wishing to be bound by theory, ATPase Sarcoplasmic/Endoplasmic Reticulum Ca2+ Transporting 2 (also called Sarcoplasmic Reticulum Ca2+ ATPase (SERCA2a) is a component of calcium cycling in cardiomyocytes. Decreased function of proteins responsible for calcium transport (Ca2+) in the sarcoplasmic reticulum (SR) may cause the contraction/relaxation defect seen after heart failure. Decreased expression and activity of ATP2A2 has been observed in human tissue after heart failure (see Arai et al. Circulation Research 72(2) February 2013; the contents of which are herein incorporated by reference in their entirety). The calcium cycle and contractility may be restored by ATP2A2 overexpression in a subject.

[0608] In one embodiment, delivery of the AAV particles of the present invention comprising ATP2A2 polynucleotides increases the expression of ATP2A2 in a subject. The expression may be increased in a cell, tissue and/or organ of interest. As a non-limiting example, the expression of ATP2A2 is increased in the heart. As a non-limiting example, the expression of ATP2A2 is increased in cardiomyocytes.

[0609] In one embodiment, the AAV particles of the present invention, comprising S100A1 polynucleotides, are administered to treat a subject who has heart failure. While not wishing to be bound by theory, S100 Calcium Binding Protein A1 enhances the activity of ATP2A2, RyR, mitochondrial ATP production and/or titin-mediated contraction. Increased activity of ATP2A2, protein responsible for calcium transport (Ca2+) in the sarcoplasmic reticulum (SR), may correct the contraction/relaxation defect seen after heart failure.

[0610] In one embodiment, delivery of the AAV particles of the present invention comprising S100A1 polynucleotides increases the expression of S100A1 in a subject. The expression may be increased in a cell, tissue and/or organ of interest. As a non-limiting example, the expression of S100A1 is increased in the heart. As a non-limiting example, the expression of S100A1 is increased in cardiomyocytes.

[0611] In one embodiment, delivery of the AAV particles of the present invention comprising S100A1 polynucleotides increases the expression of ATP2A2in a subject. The expression may be increased in a cell, tissue and/or organ of interest. As a non-limiting example, the expression of ATP2A2is increased in the heart. As a non-limiting example, the expression of ATP2A2is increased in cardiomyocytes.

Methods of Treatment of Neurological Disease

AAV Particles Encoding protein payloads

[0612] Provided in the present invention are methods for introducing the AAV particles of the present invention into cells, the method comprising introducing into said cells any of the vectors in an amount sufficient for an increase in the production of target mRNA and protein to occur. In some aspects, the cells may be muscle cells, stem cells, neurons such as but not limited to, motor, hippocampal, entorhinal, thalamic or cortical neurons, and glial cells such as astrocytes or microglia.

[0613] Disclosed in the present invention are methods for treating neurological disease associated with insufficient function/presence of a target protein (e.g., ApoE, FXN) in a subject in need of treatment. The method optionally comprises administering to the subject a therapeutically effective amount of a composition comprising AAV particles of the present invention. As a non-limiting example, the AAV particles can increase target gene expression, increase target protein production, and thus reduce one or more symptoms of neurological disease in the subject such that the subject is therapeutically treated.

[0614] In some embodiments, the AAV particle of the present invention comprising a nucleic acid encoding a protein payload comprise an AAV capsid that allows for transmission

across the blood brain barrier after intravenous administration. In one example, the AAV capsid is VOY101 and in another example, the AAV capsid is VOY201.

[0615] In one embodiment, the composition comprising the AAV particles of the present invention is administered to the central nervous system of the subject via systemic administration. In one embodiment, the systemic administration is intravenous injection.

[0616] In some embodiments, the composition comprising the AAV particles of the present invention is administered to the central nervous system of the subject. In other embodiments, the composition comprising the AAV particles of the present invention is administered to a tissue of a subject (e.g., brain of the subject).

[0617] In one embodiment, the composition comprising the AAV particles of the present invention is administered to the central nervous system of the subject via intraparenchymal injection. Non-limiting examples of intraparenchymal injections include intrathalamic, intrastriatal, intrahippocampal or targeting the entorhinal cortex.

[0618] In one embodiment, the composition comprising the AAV particles of the present invention is administered to the central nervous system of the subject via intraparenchymal injection and intrathecal injection.

[0619] In one embodiment, the AAV particles of the present invention may be delivered into specific types of targeted cells, including, but not limited to, hippocampal, cortical, motor or entorhinal neurons; glial cells including oligodendrocytes, astrocytes and microglia; and/or other cells surrounding neurons such as T cells.

[0620] In one embodiment, the AAV particles of the present invention may be delivered to neurons in the striatum and/or cortex.

[0621] In some embodiments, the AAV particles of the present invention may be used as a therapy for neurological disease.

[0622] In some embodiments, the AAV particles of the present invention may be used as a therapy for tauopathies.

[0623] In some embodiments, the AAV particles of the present invention may be used as a therapy for Alzheimer's Disease.

[0624] In some embodiments, the AAV particles of the present invention may be used as a therapy for Amyotrophic Lateral Sclerosis.

[0625] In some embodiments, the AAV particles of the present invention may be used as a therapy for Huntington's Disease.

[0626] In some embodiments, the AAV particles of the present invention may be used as a therapy for Parkinson's Disease.

[0627] In some embodiments, the AAV particles of the present invention may be used as a therapy for Friedreich's Ataxia.

[0628] In some embodiments, the AAV particles of the present invention may be used to increase target protein expression in astrocytes in order to treat a neurological disease. Target protein in astrocytes may be increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0629] In some embodiments, the AAV particles may be used to increase target protein in microglia. The increase of target protein in microglia may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-

65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0630] In some embodiments, the AAV particles may be used to increase target protein in cortical neurons. The increase of target protein in the cortical neurons may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0631] In some embodiments, the AAV particles may be used to increase target protein in hippocampal neurons. The increase of target protein in the hippocampal neurons may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%,

5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0632] In some embodiments, the AAV particles may be used to increase target protein in DRG and/or sympathetic neurons. The increase of target protein in the DRG and/or sympathetic neurons may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%,

65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0633] In some embodiments, the AAV particles of the present invention may be used to increase target protein in sensory neurons in order to treat neurological disease. Target protein in sensory neurons may be increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0634] In some embodiments, the AAV particles of the present invention may be used to increase target protein and reduce symptoms of neurological disease in a subject. The increase of target protein and/or the reduction of symptoms of neurological disease may be, independently, altered (increased for the production of target protein and reduced for the symptoms of neurological disease) by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%,

25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0635] In one embodiment, the AAV particles of the present invention may be used to reduce the decline of functional capacity and activities of daily living as measured by a standard evaluation system such as, but not limited to, the total functional capacity (TFC) scale.

[0636] In one embodiment, the AAV particles of the present invention may be used to improve performance on any assessment used to measure symptoms of neurological disease. Such assessments include, but are not limited to ADAS-cog (Alzheimer Disease Assessment Scale – cognitive), MMSE (Mini-Mental State Examination), GDS (Geriatric Depression Scale), FAQ (Functional Activities Questionnaire), ADL (Activities of Daily Living), GPCOG (General Practitioner Assessment of Cognition), Mini-Cog, AMTS (Abbreviated Mental Test Score), Clock-drawing test, 6-CIT (6-item Cognitive Impairment Test), TYM (Test Your Memory), MoCa (Montreal Cognitive Assessment), ACE-R (Addenbrookes Cognitive Assessment), MIS (Memory Impairment Screen), BADLS (Bristol Activities of Daily Living Scale), Barthel Index, Functional Independence Measure, Instrumental Activities of Daily Living, IQCODE (Informant Questionnaire on Cognitive Decline in the Elderly), Neuropsychiatric Inventory, The Cohen-Mansfield Agitation Inventory, BEHAVE-AD, EuroQol, Short Form-36 and/or MBR Caregiver Strain Instrument, or any of the other tests as described in Sheehan B (Ther Adv Neurol Disord. 5(6):349-358 (2012)), the contents of which are herein incorporated by reference in their entirety.

[0637] In some embodiments, the present composition is administered as a solo therapeutic or as combination therapeutic for the treatment of neurological disease.

[0638] The AAV particles encoding the target protein may be used in combination with one or more other therapeutic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together,

although these methods of delivery are within the scope of the present disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent.

[0639] Therapeutic agents that may be used in combination with the AAV particles of the present invention can be small molecule compounds which are antioxidants, anti-inflammatory agents, anti-apoptosis agents, calcium regulators, antiglutamatergic agents, structural protein inhibitors, compounds involved in muscle function, and compounds involved in metal ion regulation. As a non-limiting example, the combination therapy may be in combination with one or more neuroprotective agents such as small molecule compounds, growth factors and hormones which have been tested for their neuroprotective effect on motor neuron degeneration.

[0640] Compounds tested for treating neurological disease which may be used in combination with the AAV particles described herein include, but are not limited to, cholinesterase inhibitors (donepezil, rivastigmine, galantamine), NMDA receptor antagonists such as memantine, anti-psychotics, anti-depressants, anti-convulsants (e.g., sodium valproate and levetiracetam for myoclonus), secretase inhibitors, amyloid aggregation inhibitors, copper or zinc modulators, BACE inhibitors, inhibitors of tau aggregation, such as Methylene blue, phenothiazines, anthraquinones, n-phenylamines or rhodamines, microtubule stabilizers such as NAP, taxol or paclitaxel, kinase or phosphatase inhibitors such as those targeting GSK3β (lithium) or PP2A, immunization with Aβ peptides or tau phospho-epitopes, anti-tau or anti-amyloid antibodies, dopamine-depleting agents (e.g., tetrabenazine for chorea), benzodiazepines (e.g., clonazepam for myoclonus, chorea, dystonia, rigidity, and/or spasticity), , amino acid precursors of dopamine (e.g., levodopa for rigidity), skeletal muscle relaxants (e.g., baclofen, tizanidine for rigidity and/or spasticity), inhibitors for acetycholine release at the neuromuscular junction to cause muscle paralysis (e.g., botulinum toxin for bruxism and/or dystonia), atypical neuroleptics (e.g., olanzapine and quetiapine for psychosis and/or irritability, risperidone, sulpiride and haloperidol for psychosis, chorea and/or irritability, clozapine for treatment-resistant psychosis, aripiprazole for psychosis with prominent negative symptoms), selective serotonin reuptake inhibitors (SSRIs) (e.g., citalopram, fluoxetine, paroxetine, sertraline, mirtazapine, venlafaxine for depression, anxiety, obsessive compulsive behavior and/or irritability), hypnotics (e.g., xopiclone and/or zolpidem for altered sleep-wake cycle), anticonvulsants (e.g., sodium valproate and

carbamazepine for mania or hypomania) and mood stabilizers (e.g., lithium for mania or hypomania).

[0641] Neurotrophic factors may be used in combination therapy with the AAV particles of the present invention for treating neurological disease. Generally, a neurotrophic factor is defined as a substance that promotes survival, growth, differentiation, proliferation and/or maturation of a neuron, or stimulates increased activity of a neuron. In some embodiments, the present methods further comprise delivery of one or more trophic factors into the subject in need of treatment. Trophic factors may include, but are not limited to, IGF-I, GDNF, BDNF, CTNF, VEGF, Colivelin, Xaliproden, Thyrotrophin-releasing hormone and ADNF, and variants thereof.

[0642] In one aspect, the AAV particle described herein may be co-administered with AAV particles expressing neurotrophic factors such as AAV-IGF-I (See e.g., Vincent et al., *Neuromolecular medicine*, 2004, 6, 79-85; the contents of which are incorporated herein by reference in their entirety) and AAV-GDNF (See e.g., Wang et al., *J Neurosci.*, 2002, 22, 6920-6928; the contents of which are incorporated herein by reference in their entirety).

[0643] In some embodiments, the composition of the present invention for treating neurological disease is administered to the subject in need intravenously, intramuscularly, subcutaneously, intraperitoneally, intraparenchymally, intrathecally and/or intraventricularly, allowing the AAV particles to pass through one or both the blood-brain barrier and the blood spinal cord barrier. In some aspects, the method includes administering (e.g., intraparenchymal administration, intraventricular administration and/or intrathecally administration) directly to the central nervous system (CNS) of a subject (using, e.g., an infusion pump and/or a delivery scaffold) a therapeutically effective amount of a composition comprising AAV particles of the present invention. The vectors may be used to increase target gene expression, and/or reducing one or more symptoms of neurological disease in the subject such that the subject is therapeutically treated.

[0644] In one embodiment, administration of the AAV particles described herein to a subject may increase target protein levels in a subject. The target protein levels may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%,

80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the proteins levels of a target protein by at least 40%. As a non-limiting example, a subject may have an increase of 10% of target protein. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by fold increases over baseline. In one embodiment, AAV particles lead to 5-6 times higher levels of a target protein.

[0645] In one embodiment, administration of the AAV particles described herein to a subject may increase the expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may increase the expression of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein by at least 40%.

[0646] In one embodiment, intravenous administration of the AAV particles described herein to a subject may increase the CNS expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may increase the expression of a target protein in the CNS by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein in the CNS by at least 40%.

[0647] In one embodiment, administration of the AAV particles to a subject will increase the expression of a target protein in a subject and the increase of the expression of the target protein will reduce the effects and/or symptoms of neurological disease in a subject.

AAV Particles Comprising Modulatory Polynucleotides

[0648] Provided in the present invention are methods for introducing the AAV particles, comprising a nucleic acid sequence encoding the siRNA molecules of the present invention into cells, the method comprising introducing into said cells any of the vectors in an amount sufficient for degradation of a target mRNA to occur, thereby activating target-specific RNAi in the cells. In some aspects, the cells may be muscle cells, stem cells, neurons such as but not limited to, motor, hippocampal, entorhinal, thalamic or cortical neurons, and glial cells such as astrocytes or microglia.

[0649] Disclosed in the present invention are methods for treating neurological diseases associated with dysfunction of a target protein in a subject in need of treatment. The method optionally comprises administering to the subject a therapeutically effective amount of a composition comprising AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention. As a non-limiting example, the siRNA molecules can silence target gene expression, inhibit target protein production, and reduce one or more symptoms of neurological disease in the subject such that the subject is therapeutically treated.

[0650] In some embodiments, the composition comprising the AAV particles of the present invention comprising a nucleic acid sequence encoding siRNA molecules comprise an AAV capsid that allows for transmission across the blood brain barrier after intravenous administration.

[0651] In some embodiments, the composition comprising the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention is administered to the central nervous system of the subject. In other embodiments, the composition comprising the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention is administered to a tissue of a subject (e.g., brain of the subject).

[0652] In one embodiment, the composition comprising the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention is administered to the central nervous system of the subject via systemic administration. In one embodiment, the systemic administration is intravenous injection.

[0653] In one embodiment, the composition comprising the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention is administered to the central nervous system of the subject via intraparenchymal injection. Non-limiting examples of intraparenchymal injections include intrathalamic, intrastriatal, intrahippocampal or targeting the entorhinal cortex.

[0654] In one embodiment, the composition comprising the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention is administered to the central nervous system of the subject via intraparenchymal injection and intrathecal injection.

[0655] In one embodiment, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be delivered into specific types of targeted cells, including, but not limited to, hippocampal, cortical, motor or entorhinal neurons; glial cells including oligodendrocytes, astrocytes and microglia; and/or other cells surrounding neurons such as T cells.

[0656] In one embodiment, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be delivered to neurons in the striatum and/or cortex.

[0657] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used as a therapy for neurological disease.

[0658] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used as a therapy for tauopathies.

[0659] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used as a therapy for Alzheimer's Disease.

[0660] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used as a therapy for Amyotrophic Lateral Sclerosis.

[0661] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used as a therapy for Huntington's Disease.

[0662] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used as a therapy for Parkinson's Disease.

[0663] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used as a therapy for Friedreich's Ataxia.

[0664] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to suppress a target protein in astrocytes in order to treat neurological disease. Target protein in astrocytes may be suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. Target protein in astrocytes may be reduced may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-

70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0665] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to suppress a target protein in microglia. The suppression of the target protein in microglia may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%,

10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0666] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to suppress target protein in cortical neurons. The suppression of a target protein in cortical neurons may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-

90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0667] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to suppress a target protein in hippocampal neurons. The suppression of a target protein in the hippocampal neurons may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-

75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0668] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to suppress a target protein in DRG and/or sympathetic neurons. The suppression of a target protein in the DRG and/or sympathetic neurons may be, independently, suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-

90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. The reduction may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0669] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to suppress a target protein in sensory neurons in order to treat neurological disease. Target protein in sensory neurons may be suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-

60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. Target protein in the sensory neurons may be reduced may be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0670] In some embodiments, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to suppress a target protein and reduce symptoms of neurological disease in a subject. The suppression of target

protein and/or the reduction of symptoms of neurological disease may be, independently, reduced or suppressed by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0671] In one embodiment, the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention may be used to reduce the decline of functional capacity and activities of daily living as measured by a standard evaluation system such as, but not limited to, the total functional capacity (TFC) scale.

[0672] In some embodiments, the present composition is administered as a solo therapeutic or as combination therapeutic for the treatment of neurological disease.

[0673] The AAV particles encoding siRNA duplexes targeting the gene of interest may be used in combination with one or more other therapeutic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent.

[0674] Therapeutic agents that may be used in combination with the AAV particles encoding the nucleic acid sequence for the siRNA molecules of the present invention can be

small molecule compounds which are antioxidants, anti-inflammatory agents, anti-apoptosis agents, calcium regulators, antiglutamatergic agents, structural protein inhibitors, compounds involved in muscle function, and compounds involved in metal ion regulation.

[0675] Compounds tested for treating neurological disease which may be used in combination with the AAV particles comprising a nucleic acid sequence encoding the siRNA molecules of the present invention include, but are not limited to, cholinesterase inhibitors (donepezil, rivastigmine, galantamine), NMDA receptor antagonists such as memantine, anti-psychotics, anti-depressants, anti-convulsants (e.g., sodium valproate and levetiracetam for myoclonus), secretase inhibitors, amyloid aggregation inhibitors, copper or zinc modulators, BACE inhibitors, inhibitors of tau aggregation, such as Methylene blue, phenothiazines, anthraquinones, n-phenylamines or rhodamines, microtubule stabilizers such as NAP, taxol or paclitaxel, kinase or phosphatase inhibitors such as those targeting GSK3β (lithium) or PP2A, immunization with Aβ peptides or tau phospho-epitopes, anti-tau or anti-amyloid antibodies, dopamine-depleting agents (e.g., tetrabenazine for chorea), benzodiazepines (e.g., clonazepam for myoclonus, chorea, dystonia, rigidity, and/or spasticity), , amino acid precursors of dopamine (e.g., levodopa for rigidity), skeletal muscle relaxants (e.g., baclofen, tizanidine for rigidity and/or spasticity), inhibitors for acetycholine release at the neuromuscular junction to cause muscle paralysis (e.g., botulinum toxin for bruxism and/or dystonia), atypical neuroleptics (e.g., olanzapine and quetiapine for psychosis and/or irritability, risperidone, sulpiride and haloperidol for psychosis, chorea and/or irritability, clozapine for treatment-resistant psychosis, aripiprazole for psychosis with prominent negative symptoms), selective serotonin reuptake inhibitors (SSRIs) (e.g., citalopram, fluoxetine, paroxetine, sertraline, mirtazapine, venlafaxine for depression, anxiety, obsessive compulsive behavior and/or irritability), hypnotics (e.g., xopiclone and/or zolpidem for altered sleep-wake cycle), anticonvulsants (e.g., sodium valproate and carbamazepine for mania or hypomania) and mood stabilizers (e.g., lithium for mania or hypomania).

[0676] Neurotrophic factors may be used in combination therapy with the AAV particles encoding the nucleic acid sequence for the siRNA molecules of the present invention for treating neurological disease. Generally, a neurotrophic factor is defined as a substance that promotes survival, growth, differentiation, proliferation and/or maturation of a neuron, or stimulates increased activity of a neuron. In some embodiments, the present methods further comprise delivery of one or more trophic factors into the subject in need of treatment.

Trophic factors may include, but are not limited to, IGF-I, GDNF, BDNF, CTNF, VEGF, Colivelin, Xaliproden, Thyrotrophin-releasing hormone and ADNF, and variants thereof.

[0677] In one aspect, the AAV particle encoding the nucleic acid sequence for the at least one siRNA duplex targeting the gene of interest may be co-administered with AAV particles expressing neurotrophic factors such as AAV-IGF-I (See e.g., Vincent et al., *Neuromolecular medicine*, 2004, 6, 79-85; the content of which is incorporated herein by reference in its entirety) and AAV-GDNF (See e.g., Wang et al., *J Neurosci.*, 2002, 22, 6920-6928; the contents of which are incorporated herein by reference in their entirety).

[0678] In some embodiments, the composition of the present invention for treating neurological disease is administered to the subject in need intravenously, intramuscularly, subcutaneously, intraperitoneally, intraparenchymally, intrathecally and/or intraventricularly, allowing the siRNA molecules or vectors comprising the siRNA molecules to pass through one or both the blood-brain barrier and the blood spinal cord barrier. In some aspects, the method includes administering (e.g., intraparenchymal administration, intraventricular administration and/or intrathecally administration) directly to the central nervous system (CNS) of a subject (using, e.g., an infusion pump and/or a delivery scaffold) a therapeutically effective amount of a composition comprising AAV particles encoding the nucleic acid sequence for the siRNA molecules of the present invention. The vectors may be used to silence or suppress target gene expression, and/or reducing one or more symptoms of neurological disease in the subject such that the subject is therapeutically treated.

[0679] In one embodiment, administration of the AAV particles encoding a siRNA of the invention, to a subject may lower target protein levels in a subject. The target protein levels may be lowered by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may lower the protein levels of a target protein by at least 50%. As a non-limiting example, the AAV particles may lower the proteins levels of a target protein by at least 40%.

[0680] In one embodiment, administration of the AAV particles encoding a siRNA of the invention, to a subject may lower the expression of a target protein in a subject. The expression of a target protein may be lowered by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may lower the expression of a target protein by at least 50%. As a non-limiting example, the AAV particles may lower the expression of a target protein by at least 40%.

[0681] In one embodiment, intravenous administration of the AAV particles encoding a siRNA of the invention, to a subject may lower the expression of a target protein in the CNS of a subject. The expression of a target protein may be lowered by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the CNS, a region of the CNS, or a specific cell of the CNS of a subject. As a non-limiting example, the AAV particles may lower the expression of a target protein by at least 50%. As a non-limiting example, the AAV particles may lower the expression of a target protein by at least 40%.

[0682] In one embodiment, administration of the AAV particles to a subject will reduce the expression of a target protein in a subject and the reduction of expression of the target protein will reduce the effects and/or symptoms of neurological disease in a subject.

[0683] In one embodiment, the AAV particles may be used to decrease target protein in a subject. The decrease may independently be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-

25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%. As a non-limiting example, a subject may have a decrease of 70% of target protein. As a non-limiting example, a subject may have a 50% decrease of target protein. As a non-limiting example, a subject may have a 40% decrease of target protein. As a non-limiting example, a subject may have a decrease of 10% of target protein.

Methods of Treatment of Cardiovascular Disease

[0684] Provided in the present invention are methods for introducing the AAV particles of the present invention into cells, the method comprising introducing into said cells any of the vectors in an amount sufficient for an increase in the production of target mRNA and protein to occur. In some aspects, the cells may be muscle cells such as but not limited to, cardiomyocytes.

[0685] Disclosed in the present invention are methods for treating cardiovascular disease associated with insufficient function/presence of a target protein (e.g., ATP2A2) in a subject in need of treatment. The method optionally comprises administering to the subject a therapeutically effective amount of a composition comprising AAV particles of the present invention. As a non-limiting example, the AAV particles can increase target gene expression, increase target protein production, and thus reduce one or more symptoms of cardiovascular disease in the subject such that the subject is therapeutically treated.

[0686] In some embodiments, the AAV particle of the present invention comprising a nucleic acid encoding a protein payload comprise an AAV capsid that allows for distribution to cardiomyocytes after intravenous administration.

[0687] In one embodiment, the composition comprising the AAV particles of the present invention is administered to a subject via systemic administration. In one embodiment, the systemic administration is intravenous injection.

[0688] In some embodiments, the composition comprising the AAV particles of the present invention is administered directly to the cardiovascular system of the subject. In other embodiments, the composition comprising the AAV particles of the present invention is administered to a tissue of a subject (e.g., heart of the subject).

[0689] In one embodiment, the composition comprising the AAV particles of the present invention is administered to the cardiovascular system of the subject via intrathecal injection.

[0690] In one embodiment, the AAV particles of the present invention may be delivered into specific types of targeted cells, including, but not limited to, cardiomyocytes.

[0691] In one embodiment, the AAV particles of the present invention may be delivered to cardiomyocytes.

[0692] In some embodiments, the AAV particles of the present invention may be used as a therapy for cardiovascular disease.

[0693] In some embodiments, the AAV particles of the present invention may be used as a therapy for dilated cardiomyopathy (DCM). DCM affects the heart's ventricles and atria, where the heart muscle begins to dilate causing the heart muscle to contract abnormally resulting in the heart not pumping blood efficiently.

[0694] In some embodiments, the AAV particles of the present invention may be used as a therapy for hypertrophic cardiomyopathy. Hypertrophic cardiomyopathy is where a portion of the heart muscle is enlarged making it difficult for the heart to pump blood.

[0695] In some embodiments, the AAV particles may be used to increase target protein in cardiac tissue. The increase of target protein in cardiac tissue may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%,

30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0696] In some embodiments, the AAV particles of the present invention may be used to increase target protein expression in cardiomyocytes in order to treat a cardiovascular disease. Target protein in cardiomyocytes may be increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0697] In some embodiments, the AAV particles of the present invention may be used to increase target protein and reduce symptoms of cardiovascular disease in a subject. The increase of target protein and/or the reduction of symptoms of cardiovascular disease may be, independently, altered (increased for the production of target protein and reduced for the symptoms of cardiovascular disease) by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%,

50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0698] In some embodiments, the present composition is administered as a solo therapeutic or as combination therapeutic for the treatment of cardiovascular disease.

[0699] The AAV particles encoding the target protein may be used in combination with one or more other therapeutic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent.

[0700] Therapeutic agents that may be used in combination with the AAV particles of the present invention can be small molecule compounds which are antioxidants, anti-inflammatory agents, anti-apoptosis agents, calcium regulators, antiglutamatergic agents, structural protein inhibitors, compounds involved in muscle function, diuretics, ACE inhibitors, β-adrenergic blockers, and compounds involved in metal ion regulation.

[0701] In some embodiments, the composition of the present invention for treating cardiovascular disease is administered to the subject in need intravenously, intramuscularly, subcutaneously, intrathecally, anterograde coronary injection, and/or intraventricularly,

allowing the AAV particles to be delivered to the desired cell, tissue, and/or organ. In some aspects, the method includes administering (e.g., intraparenchymal administration, intraventricular administration and/or intrathecally administration) directly to the cardiovascular system of a subject (using, e.g., an infusion pump and/or a delivery scaffold) a therapeutically effective amount of a composition comprising AAV particles of the present invention. The vectors may be used to increase target gene expression, and/or reducing one or more symptoms of cardiovascular disease in the subject such that the subject is therapeutically treated.

[0702] In one embodiment, administration of the AAV particles described herein to a subject may increase target protein levels in a subject. The target protein levels may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the cardiovascular system, a region of the cardiovascular system, or a specific cell of the cardiovascular of a subject. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the proteins levels of a target protein by at least 40%. As a non-limiting example, a subject may have an increase of 10% of target protein. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by fold increases over baseline. In one embodiment, AAV particles lead to 5-6 times higher levels of a target protein.

[0703] In one embodiment, administration of the AAV particles described herein to a subject may increase the expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the cardiovascular system, a region of the cardiovascular system,

or a specific cell of the cardiovascular system of a subject. As a non-limiting example, the AAV particles may increase the expression of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein by at least 40%.

[0704] In one embodiment, intravenous administration of the AAV particles described herein to a subject may increase the cardiovascular system expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the cardiovascular system, a region of the cardiovascular system, or a specific cell of the cardiovascular system of a subject. As a non-limiting example, the AAV particles may increase the expression of a target protein in the cardiovascular system by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein in the cardiovascular system by at least 40%.

[0705] In one embodiment, administration of the AAV particles to a subject will increase the expression of a target protein in a subject and the increase of the expression of the target protein will reduce the effects and/or symptoms of cardiovascular disease in a subject.

Methods of Treatment of Heart Failure

[0706] Provided in the present invention are methods for introducing the AAV particles of the present invention into cells, the method comprising introducing into said cells any of the vectors in an amount sufficient for an increase in the production of target mRNA and protein to occur. In some aspects, the cells may be muscle cells such as but not limited to, cardiomyocytes.

[0707] Disclosed in the present invention are methods for treating heart failure associated with insufficient function/presence of a target protein (e.g., ATP2A2) in a subject in need of treatment. The method optionally comprises administering to the subject a therapeutically effective amount of a composition comprising AAV particles of the present invention. As a non-limiting example, the AAV particles can increase target gene expression, increase target protein production, and thus reduce one or more symptoms of heart failure in the subject such that the subject is therapeutically treated.

[0708] In some embodiments, the AAV particle of the present invention comprising a nucleic acid encoding a protein payload comprise an AAV capsid that allows for distribution to cardiomyocytes after intravenous administration.

[0709] In one embodiment, the composition comprising the AAV particles of the present invention is administered to a subject via systemic administration. In one embodiment, the systemic administration is intravenous injection.

[0710] In some embodiments, the composition comprising the AAV particles of the present invention is administered directly to the cardiovascular system of the subject. In other embodiments, the composition comprising the AAV particles of the present invention is administered to a tissue of a subject (e.g., heart of the subject).

[0711] In one embodiment, the composition comprising the AAV particles of the present invention is administered to the cardiovascular system of the subject via intrathecal injection.

[0712] In one embodiment, the AAV particles of the present invention may be delivered into specific types of targeted cells, including, but not limited to, cardiomyocytes.

[0713] In one embodiment, the AAV particles of the present invention may be delivered to cardiomyocytes.

[0714] In one embodiment, the AAV particles of the present invention may be used as a therapy for heart failure.

[0715] In one embodiment, the AAV particles of the present invention may be used to reduce the number of hospitalization of a subject.

[0716] In one embodiment, the AAV particles of the present invention may be used to prolong survival of a subject

[0717] In some embodiments, the AAV particles may be used to increase target protein in cardiac tissue. The increase of target protein in cardiac tissue may be, independently, increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%,

30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0718] In some embodiments, the AAV particles of the present invention may be used to increase target protein expression in cardiomyocytes in order to treat heart failure. Target protein in cardiomyocytes may be increased by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0719] In some embodiments, the AAV particles of the present invention may be used to increase target protein and reduce symptoms of heart failure in a subject. The increase of target protein and/or the reduction of symptoms of heart failure may be, independently, altered (increased for the production of target protein and reduced for the symptoms of heart failure) by 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more than 95%, 5-15%, 5-20%, 5-25%, 5-30%, 5-35%, 5-

40%, 5-45%, 5-50%, 5-55%, 5-60%, 5-65%, 5-70%, 5-75%, 5-80%, 5-85%, 5-90%, 5-95%, 10-20%, 10-25%, 10-30%, 10-35%, 10-40%, 10-45%, 10-50%, 10-55%, 10-60%, 10-65%, 10-70%, 10-75%, 10-80%, 10-85%, 10-90%, 10-95%, 15-25%, 15-30%, 15-35%, 15-40%, 15-45%, 15-50%, 15-55%, 15-60%, 15-65%, 15-70%, 15-75%, 15-80%, 15-85%, 15-90%, 15-95%, 20-30%, 20-35%, 20-40%, 20-45%, 20-50%, 20-55%, 20-60%, 20-65%, 20-70%, 20-75%, 20-80%, 20-85%, 20-90%, 20-95%, 25-35%, 25-40%, 25-45%, 25-50%, 25-55%, 25-60%, 25-65%, 25-70%, 25-75%, 25-80%, 25-85%, 25-90%, 25-95%, 30-40%, 30-45%, 30-50%, 30-55%, 30-60%, 30-65%, 30-70%, 30-75%, 30-80%, 30-85%, 30-90%, 30-95%, 35-45%, 35-50%, 35-55%, 35-60%, 35-65%, 35-70%, 35-75%, 35-80%, 35-85%, 35-90%, 35-95%, 40-50%, 40-55%, 40-60%, 40-65%, 40-70%, 40-75%, 40-80%, 40-85%, 40-90%, 40-95%, 45-55%, 45-60%, 45-65%, 45-70%, 45-75%, 45-80%, 45-85%, 45-90%, 45-95%, 50-60%, 50-65%, 50-70%, 50-75%, 50-80%, 50-85%, 50-90%, 50-95%, 55-65%, 55-70%, 55-75%, 55-80%, 55-85%, 55-90%, 55-95%, 60-70%, 60-75%, 60-80%, 60-85%, 60-90%, 60-95%, 65-75%, 65-80%, 65-85%, 65-90%, 65-95%, 70-80%, 70-85%, 70-90%, 70-95%, 75-85%, 75-90%, 75-95%, 80-90%, 80-95%, or 90-95%.

[0720] In some embodiments, the present composition is administered as a solo therapeutic or as combination therapeutic for the treatment of heart failure.

[0721] The AAV particles encoding the target protein may be used in combination with one or more other therapeutic agents. By "in combination with," it is not intended to imply that the agents must be administered at the same time and/or formulated for delivery together, although these methods of delivery are within the scope of the present disclosure. Compositions can be administered concurrently with, prior to, or subsequent to, one or more other desired therapeutics or medical procedures. In general, each agent will be administered at a dose and/or on a time schedule determined for that agent.

[0722] Therapeutic agents that may be used in combination with the AAV particles of the present invention can be small molecule compounds which are antioxidants, anti-inflammatory agents, anti-apoptosis agents, calcium regulators, antiglutamatergic agents, structural protein inhibitors, compounds involved in muscle function, diuretics, ACE inhibitors, β-adrenergic blockers, and compounds involved in metal ion regulation.

[0723] In some embodiments, the composition of the present invention for treating cardiovascular disease is administered to the subject in need intravenously, intramuscularly, subcutaneously, intrathecally, anterograde coronary injection, and/or intraventricularly, allowing the AAV particles to be delivered to the desired cell, tissue, and/or organ. In some

aspects, the method includes administering (e.g., intraparenchymal administration, intraventricular administration and/or intrathecally administration) directly to the cardiovascular system of a subject (using, e.g., an infusion pump and/or a delivery scaffold) a therapeutically effective amount of a composition comprising AAV particles of the present invention. The vectors may be used to increase target gene expression, and/or reducing one or more symptoms of heart failure in the subject such that the subject is therapeutically treated.

[0724] In one embodiment, administration of the AAV particles described herein to a subject may increase target protein levels in a subject. The target protein levels may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the cardiovascular system, a region of the cardiovascular system, or a specific cell of the cardiovascular of a subject. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the proteins levels of a target protein by at least 40%. As a non-limiting example, a subject may have an increase of 10% of target protein. As a non-limiting example, the AAV particles may increase the protein levels of a target protein by fold increases over baseline. In one embodiment, AAV particles lead to 5-6 times higher levels of a target protein.

[0725] In one embodiment, administration of the AAV particles described herein to a subject may increase the expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the cardiovascular system, a region of the cardiovascular system, or a specific cell of the cardiovascular system of a subject. As a non-limiting example, the

AAV particles may increase the expression of a target protein by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein by at least 40%.

[0726] In one embodiment, intravenous administration of the AAV particles described herein to a subject may increase the cardiovascular system expression of a target protein in a subject. The expression of the target protein may be increased by about 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100% in a subject such as, but not limited to, the cardiovascular system, a region of the cardiovascular system, or a specific cell of the cardiovascular system of a subject. As a non-limiting example, the AAV particles may increase the expression of a target protein in the cardiovascular system by at least 50%. As a non-limiting example, the AAV particles may increase the expression of a target protein in the cardiovascular system by at least 40%.

[0727] In one embodiment, administration of the AAV particles described herein to a subject may increase the expression of a target protein in cardiomyocytes of a subject. The expression of the target protein may be increased by about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%.

[0728] In one embodiment, administration of the AAV particles described herein to a subject may express ATP2A2 in cardiomyocytes of a subject. The expression of ATP2A2 in cardiomyocytes may be 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. In one embodiment, the

expression of ATP2A2 may be seen in 30% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 30-40% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 30-50% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 30% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 30-60% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 30-70% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 30-80% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 30-90% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20-40% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20-50% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20-60% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20-70% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20-80% of cardiomyocytes. In one embodiment, the expression of ATP2A2 may be seen in 20-90% of cardiomyocytes.

[0729] In one embodiment, administration of the AAV particles described herein to a subject may express S100A1 in cardiomyocytes of a subject. The expression of S100A1 in cardiomyocytes may be 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%, or at least 20-30%, 20-40%, 20-50%, 20-60%, 20-70%, 20-80%, 20-90%, 20-95%, 20-100%, 30-40%, 30-50%, 30-60%, 30-70%, 30-80%, 30-90%, 30-95%, 30-100%, 40-50%, 40-60%, 40-70%, 40-80%, 40-90%, 40-95%, 40-100%, 50-60%, 50-70%, 50-80%, 50-90%, 50-95%, 50-100%, 60-70%, 60-80%, 60-90%, 60-95%, 60-100%, 70-80%, 70-90%, 70-95%, 70-100%, 80-90%, 80-95%, 80-100%, 90-95%, 90-100% or 95-100%. In one embodiment, the expression of S100A1 may be seen in 30% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 30-40% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 30-50% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 30% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 30-60% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 30-70% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 30-80% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 30-90% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 20% of cardiomyocytes. In one embodiment, the

expression of S100A1 may be seen in 20-40% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 20-50% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 20% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 20-60% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 20-70% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 20-80% of cardiomyocytes. In one embodiment, the expression of S100A1 may be seen in 20-90% of cardiomyocytes.

[0730] In one embodiment, administration of the AAV particles to a subject will increase the expression of a target protein in a subject and the increase of the expression of the target protein will reduce the effects and/or symptoms of heart failure in a subject.

[0731] In one embodiment, a subject is administered a dose of $1x10^{13}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by percutaneous intracoronary administration.

[0732] In one embodiment, a subject is administered a dose of $1x10^{13}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by intravenous administration.

[0733] In one embodiment, a subject is administered a dose of $2x10^{13}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by percutaneous intracoronary administration.

[0734] In one embodiment, a subject is administered a dose of $2x10^{13}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by intravenous administration.

[0735] In one embodiment, a subject is administered a dose of $3x10^{13}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by percutaneous intracoronary administration.

[0736] In one embodiment, a subject is administered a dose of $3x10^{13}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by intravenous administration.

[0737] In one embodiment, a subject is administered a dose of $3x10^{11}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by percutaneous intracoronary administration.

[0738] In one embodiment, a subject is administered a dose of $3x10^{11}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by intravenous administration.

[0739] In one embodiment, a subject is administered a dose of $3x10^{12}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by percutaneous intracoronary administration.

[0740] In one embodiment, a subject is administered a dose of $3x10^{12}$ VG of the AAV particles of the present invention to treat heart failure. As a non-limiting example, the subject is administered the dose of AAV particles by intravenous administration.

V. KITS AND DEVICES

Kits

[0741] In one embodiment, the invention provides a variety of kits for conveniently and/or effectively carrying out methods of the present invention. Typically kits will comprise sufficient amounts and/or numbers of components to allow a user to perform multiple treatments of a subject(s) and/or to perform multiple experiments.

[0742] Any of the AAV particles of the present invention may be comprised in a kit. In some embodiments, kits may further include reagents and/or instructions for creating and/or synthesizing compounds and/or compositions of the present invention. In some embodiments, kits may also include one or more buffers. In some embodiments, kits of the invention may include components for making protein or nucleic acid arrays or libraries and thus, may include, for example, solid supports.

[0743] In some embodiments, kit components may be packaged either in aqueous media or in lyophilized form. The container means of the kits will generally include at least one vial, test tube, flask, bottle, syringe or other container means, into which a component may be placed, and preferably, suitably aliquoted. Where there is more than one kit component, (labeling reagent and label may be packaged together), kits may also generally contain second, third or other additional containers into which additional components may be separately placed. In some embodiments, kits may also comprise second container means for containing sterile, pharmaceutically acceptable buffers and/or other diluents. In some embodiments, various combinations of components may be comprised in one or more vial. Kits of the present invention may also typically include means for containing compounds and/or compositions of the present invention, e.g., proteins, nucleic acids, and any other

reagent containers in close confinement for commercial sale. Such containers may include injection or blow-molded plastic containers into which desired vials are retained.

[0744] In some embodiments, kit components are provided in one and/or more liquid solutions. In some embodiments, liquid solutions are aqueous solutions, with sterile aqueous solutions being particularly preferred. In some embodiments, kit components may be provided as dried powder(s). When reagents and/or components are provided as dry powders, such powders may be reconstituted by the addition of suitable volumes of solvent. In some embodiments, it is envisioned that solvents may also be provided in another container means. In some embodiments, labeling dyes are provided as dried powders. In some embodiments, it is contemplated that 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 120, 130, 140, 150, 160, 170, 180, 190, 200, 300, 400, 500, 600, 700, 800, 900, 1000 micrograms or at least or at most those amounts of dried dye are provided in kits of the invention. In such embodiments, dye may then be resuspended in any suitable solvent, such as DMSO.

[0745] In some embodiments, kits may include instructions for employing kit components as well the use of any other reagent not included in the kit. Instructions may include variations that may be implemented.

Devices

[0746] In one embodiment, the AAV particles may delivered to a subject using a device to deliver the AAV particles and a head fixation assembly. The head fixation assembly may be, but is not limited to, any of the head fixation assemblies sold by MRI interventions. As a non-limiting example, the head fixation assembly may be any of the assemblies described in US Patent Nos. 8,099,150, 8,548,569 and 9,031,636 and International Patent Publication Nos. WO201108495 and WO2014014585, the contents of each of which are incorporated by reference in their entireties. A head fixation assembly may be used in combination with an MRI compatible drill such as, but not limited to, the MRI compatible drills described in International Patent Publication No. WO2013181008 and US Patent Publication No. US20130325012, the contents of which are herein incorporated by reference in its entirety.

[0747] In one embodiment, the AAV particles may be delivered using a method, system and/or computer program for positioning apparatus to a target point on a subject to deliver the AAV particles. As a non-limiting example, the method, system and/or computer program may be the methods, systems and/or computer programs described in US Patent No. 8, 340,743, the contents of which are herein incorporated by reference in their entirety. The method may include: determining a target point in the body and a reference point, wherein

the target point and the reference point define a planned trajectory line (PTL) extending through each; determining a visualization plane, wherein the PTL intersects the visualization plane at a sighting point; mounting the guide device relative to the body to move with respect to the PTL, wherein the guide device does not intersect the visualization plane; determining a point of intersection (GPP) between the guide axis and the visualization plane; and aligning the GPP with the sighting point in the visualization plane.

[0748] In one embodiment, the AAV particles may be delivered to a subject using a convention-enhanced delivery device. Non-limiting examples of targeted delivery of drugs using convection are described in US Patent Application Publication Nos. US20100217228, US20130035574 and US20130035660 and International Patent Publication No. WO2013019830 and WO2008144585, the contents of each of which are herein incorporated by reference in their entirety.

[0749] In one embodiment, a subject may be imaged prior to, during and/or after delivery of the AAV particles. The imaging method may be a method known in the art and/or described herein, such as but not limited to, magnetic resonance imaging (MRI). As a non-limiting example, imaging may be used to assess therapeutic effect. As another non-limiting example, imaging may be used for assisted delivery of AAV particles.

[0750] In one embodiment, the AAV particles may be delivered using an MRI-guided device. Non-limiting examples of MRI-guided devices are described in US Patent Nos. 9,055,884, 9,042,958, 8,886,288, 8,768,433, 8,396,532, 8,369,930, 8,374,677 and 8,175,677 and US Patent Application Publication No. US20140024927 the contents of each of which are herein incorporated by reference in their entirety. As a non-limiting example, the MRI-guided device may be able to provide data in real time such as those described in US Patent Nos. 8,886,288 and 8,768,433, the contents of each of which are herein incorporated by reference in their entirety. As another non-limiting example, the MRI-guided device or system may be used with a targeting cannula such as the systems described in US Patent Nos. 8,175,677 and 8,374,677, the contents of each of which are herein incorporated by reference in their entireties. As yet another non-limiting example, the MRI-guided device includes a trajectory guide frame for guiding an interventional device as described, for example, in US Patent No. 9,055,884 and US Patent Application No. US20140024927, the contents of each of which are herein incorporated by reference in their entirety.

[0751] In one embodiment, the AAV particles may be delivered using an MRI-compatible tip assembly. Non-limiting examples of MRI-compatible tip assemblies are described in US

Patent Publication No. US20140275980, the contents of which are herein incorporated by reference in their entirety.

[0752] In one embodiment, the AAV particles may be delivered using a cannula which is MRI-compatible. Non-limiting examples of MRI-compatible cannulas include those taught in International Patent Publication No. WO2011130107, the contents of which are herein incorporated by reference in their entirety.

[0753] In one embodiment, the AAV particles may be delivered using a catheter which is MRI-compatible. Non-limiting examples of MRI-compatible catheters include those taught in International Patent Publication No. WO2012116265, US Patent Publication No. 8,825,133 and US Patent Publication No. US20140024909, the contents of each of which are herein incorporated by reference in their entireties.

[0754] In one embodiment, the AAV particles may be delivered using a device with an elongated tubular body and a diaphragm as described in US Patent Publication Nos. US20140276582 and US20140276614, the contents of each of which are herein incorporated by reference in their entireties.

[0755] In one embodiment, the AAV particles may be delivered using an MRI compatible localization and/or guidance system such as, but not limited to, those described in US Patent Application Publication Nos. US20150223905 and US20150230871, the contents of each of which are herein incorporated by reference in their entirety. As a non-limiting example, the MRI compatible localization and/or guidance systems may comprise a mount adapted for fixation to a patient, a targeting cannula with a lumen configured to attach to the mount so as to be able to controllably translate in at least three dimensions, and an elongate probe configured to snugly advance via slide and retract in the targeting cannula lumen, the elongate probe comprising at least one of a stimulation or recording electrode.

[0756] In one embodiment, the AAV particles may be delivered to a subject using a trajectory frame as described in US Patent Application Publication Nos. US20150031982 and US20140066750 and International Patent Publication Nos. WO2015057807 and WO2014039481, the contents of each of which are herein incorporated by reference in their entirety.

[0757] In one embodiment, the AAV particles may be delivered to a subject using a gene gun.

VI. DEFINITIONS

[0758] At various places in the present specification, substituents of compounds of the present disclosure are disclosed in groups or in ranges. It is specifically intended that the present disclosure include each and every individual subcombination of the members of such groups and ranges.

[0759] Unless stated otherwise, the following terms and phrases have the meanings described below. The definitions are not meant to be limiting in nature and serve to provide a clearer understanding of certain aspects of the present invention.

[0760] *About:* As used herein, the term "about" means +/- 10% of the recited value.

[0761] *Adeno-associated virus*: The term "adeno-associated virus" or "AAV" as used herein refers to members of the dependovirus genus comprising any particle, sequence, gene, protein, or component derived therefrom.

[0762] *AAV Particle*: As used herein, an "AAV particle" is a virus which comprises a capsid and a viral genome with at least one payload region and at least one ITR region. AAV particles of the present disclosure may be produced recombinantly and may be based on adeno-associated virus (AAV) parent or reference sequences. AAV particle may be derived from any serotype, described herein or known in the art, including combinations of serotypes (i.e., "pseudotyped" AAV) or from various genomes (e.g., single stranded or self-complementary). In addition, the AAV particle may be replication defective and/or targeted.

[0763] *Activity:* As used herein, the term "activity" refers to the condition in which things are happening or being done. Compositions of the invention may have activity and this activity may involve one or more biological events.

[0764] *Administering:* As used herein, the term "administering" refers to providing a pharmaceutical agent or composition to a subject.

[0765] *Administered in combination:* As used herein, the term "administered in combination" or "combined administration" means that two or more agents are administered to a subject at the same time or within an interval such that there may be an overlap of an effect of each agent on the patient. In some embodiments, they are administered within about 60, 30, 15, 10, 5, or 1 minute of one another. In some embodiments, the administrations of the agents are spaced sufficiently closely together such that a combinatorial (*e.g.*, a synergistic) effect is achieved.

[0766] *Amelioration*: As used herein, the term "amelioration" or "ameliorating" refers to a lessening of severity of at least one indicator of a condition or disease. For example, in the context of neurodegeneration disorder, amelioration includes the reduction of neuron loss.

[0767] *Animal:* As used herein, the term "animal" refers to any member of the animal kingdom. In some embodiments, "animal" refers to humans at any stage of development. In some embodiments, "animal" refers to non-human animals at any stage of development. In certain embodiments, the non-human animal is a mammal (*e.g.*, a rodent, a mouse, a rat, a rabbit, a monkey, a dog, a cat, a sheep, cattle, a primate, or a pig). In some embodiments, animals include, but are not limited to, mammals, birds, reptiles, amphibians, fish, and worms. In some embodiments, the animal is a transgenic animal, genetically-engineered animal, or a clone.

[0768] *Antisense strand:* As used herein, the term "the antisense strand" or "the first strand" or "the guide strand" of a siRNA molecule refers to a strand that is substantially complementary to a section of about 10-50 nucleotides, e.g., about 15-30, 16-25, 18-23 or 19-22 nucleotides of the mRNA of the gene targeted for silencing. The antisense strand or first strand has sequence sufficiently complementary to the desired target mRNA sequence to direct target-specific silencing, e.g., complementarity sufficient to trigger the destruction of the desired target mRNA by the RNAi machinery or process.

[0769] *Approximately:* As used herein, the term "approximately" or "about," as applied to one or more values of interest, refers to a value that is similar to a stated reference value. In certain embodiments, the term "approximately" or "about" refers to a range of values that fall within 25%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context (except where such number would exceed 100% of a possible value).

[0770] *Associated with:* As used herein, the terms "associated with," "conjugated," "linked," "attached," and "tethered," when used with respect to two or more moieties, means that the moieties are physically associated or connected with one another, either directly or via one or more additional moieties that serves as a linking agent, to form a structure that is sufficiently stable so that the moieties remain physically associated under the conditions in which the structure is used, *e.g.*, physiological conditions. An "association" need not be strictly through direct covalent chemical bonding. It may also suggest ionic or hydrogen bonding or a hybridization based connectivity sufficiently stable such that the "associated" entities remain physically associated.

[0771] *Bifunctional:* As used herein, the term "bifunctional" refers to any substance, molecule or moiety which is capable of or maintains at least two functions. The functions

may affect the same outcome or a different outcome. The structure that produces the function may be the same or different.

[0772] *Biocompatible*: As used herein, the term "biocompatible" means compatible with living cells, tissues, organs or systems posing little to no risk of injury, toxicity or rejection by the immune system.

[0773] *Biodegradable*: As used herein, the term "biodegradable" means capable of being broken down into innocuous products by the action of living things.

[0774] *Biologically active*: As used herein, the phrase "biologically active" refers to a characteristic of any substance that has activity in a biological system and/or organism. For instance, a substance that, when administered to an organism, has a biological effect on that organism, is considered to be biologically active. In particular embodiments, an AAV particle of the present invention may be considered biologically active if even a portion of the encoded payload is biologically active or mimics an activity considered biologically relevant.

[0775] *Capsid*: As used herein, the term "capsid" refers to the protein shell of a virus particle.

[0776] *Complementary and substantially complementary:* As used herein, the term "complementary" refers to the ability of polynucleotides to form base pairs with one another. Base pairs are typically formed by hydrogen bonds between nucleotide units in antiparallel polynucleotide strands. Complementary polynucleotide strands can form base pair in the Watson-Crick manner (e.g., A to T, A to U, C to G), or in any other manner that allows for the formation of duplexes. As persons skilled in the art are aware, when using RNA as opposed to DNA, uracil rather than thymine is the base that is considered to be complementary to adenosine. However, when a U is denoted in the context of the present invention, the ability to substitute a T is implied, unless otherwise stated. Perfect complementarity or 100% complementarity refers to the situation in which each nucleotide unit of one polynucleotide strand can form hydrogen bond with a nucleotide unit of a second polynucleotide strand. Less than perfect complementarity refers to the situation in which some, but not all, nucleotide units of two strands can form hydrogen bond with each other. For example, for two 20-mers, if only two base pairs on each strand can form hydrogen bond with each other, the polynucleotide strands exhibit 10% complementarity. In the same example, if 18 base pairs on each strand can form hydrogen bonds with each other, the polynucleotide strands exhibit 90% complementarity. As used herein, the term "substantially complementary" means that the siRNA has a sequence (e.g., in the antisense strand) which is

sufficient to bind the desired target mRNA, and to trigger the RNA silencing of the target mRNA.

[0777] *Compound:* Compounds of the present disclosure include all of the isotopes of the atoms occurring in the intermediate or final compounds. "Isotopes" refers to atoms having the same atomic number but different mass numbers resulting from a different number of neutrons in the nuclei. For example, isotopes of hydrogen include tritium and deuterium.

[0778] The compounds and salts of the present disclosure can be prepared in combination with solvent or water molecules to form solvates and hydrates by routine methods.

[0779] *Conditionally active:* As used herein, the term "conditionally active" refers to a mutant or variant of a wild-type polypeptide, wherein the mutant or variant is more or less active at physiological conditions than the parent polypeptide. Further, the conditionally active polypeptide may have increased or decreased activity at aberrant conditions as compared to the parent polypeptide. A conditionally active polypeptide may be reversibly or irreversibly inactivated at normal physiological conditions or aberrant conditions.

[0780] *Conserved*: As used herein, the term "conserved" refers to nucleotides or amino acid residues of a polynucleotide sequence or polypeptide sequence, respectively, that are those that occur unaltered in the same position of two or more sequences being compared. Nucleotides or amino acids that are relatively conserved are those that are conserved amongst more related sequences than nucleotides or amino acids appearing elsewhere in the sequences.

[0781] In some embodiments, two or more sequences are said to be "completely conserved" if they are 100% identical to one another. In some embodiments, two or more sequences are said to be "highly conserved" if they are at least 70% identical, at least 80% identical, at least 90% identical, or at least 95% identical to one another. In some embodiments, two or more sequences are said to be "highly conserved" if they are about 70% identical, about 80% identical, about 90% identical, about 95%, about 98%, or about 99% identical to one another. In some embodiments, two or more sequences are said to be "conserved" if they are at least 30% identical, at least 40% identical, at least 50% identical, at least 60% identical, at least 70% identical, at least 80% identical, at least 90% identical, or at least 95% identical to one another. In some embodiments, two or more sequences are said to be "conserved" if they are about 30% identical, about 40% identical, about 50% identical, about 60% identical, about 70% identical, about 80% identical, about 90% identical, about 95% identical, about 98% identical, or about 99% identical to one another. Conservation of

sequence may apply to the entire length of an polynucleotide or polypeptide or may apply to a portion, region or feature thereof.

[0782] *Control Elements:* As used herein, "control elements", "regulatory control elements" or "regulatory sequences" refers to promoter regions, polyadenylation signals, transcription termination sequences, upstream regulatory domains, origins of replication, internal ribosome entry sites ("IRES"), enhancers, and the like, which provide for the replication, transcription and translation of a coding sequence in a recipient cell. Not all of these control elements need always be present as long as the selected coding sequence is capable of being replicated, transcribed and/or translated in an appropriate host cell.

[0783] *Controlled Release:* As used herein, the term "controlled release" refers to a pharmaceutical composition or compound release profile that conforms to a particular pattern of release to effect a therapeutic outcome.

[0784] *Cytostatic*: As used herein, "cytostatic" refers to inhibiting, reducing, suppressing the growth, division, or multiplication of a cell (*e.g.*, a mammalian cell (*e.g.*, a human cell)), bacterium, virus, fungus, protozoan, parasite, prion, or a combination thereof.

[0785] *Cytotoxic*: As used herein, "cytotoxic" refers to killing or causing injurious, toxic, or deadly effect on a cell (*e.g.*, a mammalian cell (*e.g.*, a human cell)), bacterium, virus, fungus, protozoan, parasite, prion, or a combination thereof.

[0786] *Delivery:* As used herein, "delivery" refers to the act or manner of delivering an AAV particle, a compound, substance, entity, moiety, cargo or payload.

[0787] *Delivery Agent*: As used herein, "delivery agent" refers to any substance which facilitates, at least in part, the *in vivo* delivery of an AAV particle to targeted cells.

[0788] *Destabilized:* As used herein, the term "destable," "destabilize," or "destabilizing region" means a region or molecule that is less stable than a starting, wild-type or native form of the same region or molecule.

[0789] *Detectable label:* As used herein, "detectable label" refers to one or more markers, signals, or moieties which are attached, incorporated or associated with another entity that is readily detected by methods known in the art including radiography, fluorescence, chemiluminescence, enzymatic activity, absorbance and the like. Detectable labels include radioisotopes, fluorophores, chromophores, enzymes, dyes, metal ions, ligands such as biotin, avidin, streptavidin and haptens, quantum dots, and the like. Detectable labels may be located at any position in the peptides or proteins disclosed herein. They may be within the amino acids, the peptides, or proteins, or located at the N- or C- termini.

[0790] *Digest*: As used herein, the term "digest" means to break apart into smaller pieces or components. When referring to polypeptides or proteins, digestion results in the production of peptides.

[0791] *Distal:* As used herein, the term "distal" means situated away from the center or away from a point or region of interest.

[0792] *Dosing regimen*: As used herein, a "dosing regimen" is a schedule of administration or physician determined regimen of treatment, prophylaxis, or palliative care.

[0793] *Encapsulate:* As used herein, the term "encapsulate" means to enclose, surround or encase.

[0794] *Engineered:* As used herein, embodiments of the invention are "engineered" when they are designed to have a feature or property, whether structural or chemical, that varies from a starting point, wild type or native molecule.

[0795] *Effective Amount:* As used herein, the term "effective amount" of an agent is that amount sufficient to effect beneficial or desired results, for example, clinical results, and, as such, an "effective amount" depends upon the context in which it is being applied. For example, in the context of administering an agent that treats cancer, an effective amount of an agent is, for example, an amount sufficient to achieve treatment, as defined herein, of cancer, as compared to the response obtained without administration of the agent.

[0796] *Expression*: As used herein, "expression" of a nucleic acid sequence refers to one or more of the following events: (1) production of an RNA template from a DNA sequence (*e.g.*, by transcription); (2) processing of an RNA transcript (*e.g.*, by splicing, editing, 5′ cap formation, and/or 3′ end processing); (3) translation of an RNA into a polypeptide or protein; and (4) post-translational modification of a polypeptide or protein.

[0797] *Feature:* As used herein, a "feature" refers to a characteristic, a property, or a distinctive element.

[0798] *Formulation*: As used herein, a "formulation" includes at least one AAV particle and a delivery agent.

[0799] *Fragment:* A "fragment," as used herein, refers to a portion. For example, fragments of proteins may comprise polypeptides obtained by digesting full-length protein isolated from cultured cells.

[0800] *Functional*: As used herein, a "functional" biological molecule is a biological molecule in a form in which it exhibits a property and/or activity by which it is characterized.

[0801] *Gene expression*: The term "gene expression" refers to the process by which a nucleic acid sequence undergoes successful transcription and in most instances translation to produce a protein or peptide. For clarity, when reference is made to measurement of "gene expression", this should be understood to mean that measurements may be of the nucleic acid product of transcription, e.g., RNA or mRNA or of the amino acid product of translation, e.g., polypeptides or peptides. Methods of measuring the amount or levels of RNA, mRNA, polypeptides and peptides are well known in the art.

[0802] *Homology*: As used herein, the term "homology" refers to the overall relatedness between polymeric molecules, *e.g.* between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identical or similar. The term "homologous" necessarily refers to a comparison between at least two sequences (polynucleotide or polypeptide sequences). In accordance with the invention, two polynucleotide sequences are considered to be homologous if the polypeptides they encode are at least about 50%, 60%, 70%, 80%, 90%, 95%, or even 99% for at least one stretch of at least about 20 amino acids. In some embodiments, homologous polynucleotide sequences are characterized by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. For polynucleotide sequences less than 60 nucleotides in length, homology is determined by the ability to encode a stretch of at least 4–5 uniquely specified amino acids. In accordance with the invention, two protein sequences are considered to be homologous if the proteins are at least about 50%, 60%, 70%, 80%, or 90% identical for at least one stretch of at least about 20 amino acids.

[0803] *Heterologous Region*: As used herein the term "heterologous region" refers to a region which would not be considered a homologous region.

[0804] *Homologous Region:* As used herein the term "homologous region" refers to a region which is similar in position, structure, evolution origin, character, form or function.

[0805] *Identity*: As used herein, the term "identity" refers to the overall relatedness between polymeric molecules, *e.g.*, between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of the percent identity of two polynucleotide sequences, for example, can be performed by aligning the two sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second nucleic acid sequences for optimal alignment and non-identical sequences

can be disregarded for comparison purposes). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or 100% of the length of the reference sequence. The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. For example, the percent identity between two nucleotide sequences can be determined using methods such as those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; each of which is incorporated herein by reference. For example, the percent identity between two nucleotide sequences can be determined using the algorithm of Meyers and Miller (CABIOS, 1989, 4:11-17), which has been incorporated into the ALIGN program (version 2.0) using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. The percent identity between two nucleotide sequences can, alternatively, be determined using the GAP program in the GCG software package using an NWSgapdna.CMP matrix. Methods commonly employed to determine percent identity between sequences include, but are not limited to those disclosed in Carillo, H., and Lipman, D., SIAM J Applied Math., 48:1073 (1988); incorporated herein by reference. Techniques for determining identity are codified in publicly available computer programs. Exemplary computer software to determine homology between two sequences include, but are not limited to, GCG program package, Devereux, J., *et al.*, *Nucleic Acids Research*, 12(1), 387 (1984)), BLASTP, BLASTN, and FASTA Altschul, S. F. *et al.*, *J. Molec. Biol.*, 215, 403 (1990)).

[0806] *Inhibit expression of a gene:* As used herein, the phrase "inhibit expression of a gene" means to cause a reduction in the amount of an expression product of the gene. The

expression product can be an RNA transcribed from the gene (*e.g.*, an mRNA) or a polypeptide translated from an mRNA transcribed from the gene. Typically a reduction in the level of an mRNA results in a reduction in the level of a polypeptide translated therefrom. The level of expression may be determined using standard techniques for measuring mRNA or protein.

[0807] *In vitro*: As used herein, the term "*in vitro*" refers to events that occur in an artificial environment, *e.g.*, in a test tube or reaction vessel, in cell culture, in a Petri dish, *etc.*, rather than within an organism (*e.g.*, animal, plant, or microbe).

[0808] *In vivo*: As used herein, the term "*in vivo*" refers to events that occur within an organism (*e.g.*, animal, plant, or microbe or cell or tissue thereof).

[0809] *Isolated*: As used herein, the term "isolated" refers to a substance or entity that has been separated from at least some of the components with which it was associated (whether in nature or in an experimental setting). Isolated substances may have varying levels of purity in reference to the substances from which they have been associated. Isolated substances and/or entities may be separated from at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or more of the other components with which they were initially associated. In some embodiments, isolated agents are more than about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more than about 99% pure. As used herein, a substance is "pure" if it is substantially free of other components.

[0810] *Substantially isolated*: By "substantially isolated" is meant that a substance is substantially separated from the environment in which it was formed or detected. Partial separation can include, for example, a composition enriched in the substance or AAV particles of the present disclosure. Substantial separation can include compositions containing at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 97%, or at least about 99% by weight of the compound of the present disclosure, or salt thereof. Methods for isolating compounds and their salts are routine in the art.

[0811] *Linker:* As used herein "linker" refers to a molecule or group of molecules which connects two molecules. A linker may be a nucleic acid sequence connecting two nucleic acid sequences encoding two different polypeptides. The linker may or may not be translated. The linker may be a cleavable linker.

[0812] *MicroRNA (miRNA) binding site:* As used herein, a microRNA (miRNA) binding site represents a nucleotide location or region of a nucleic acid transcript to which at least the "seed" region of a miRNA binds.

[0813] *Modified:* As used herein "modified" refers to a changed state or structure of a molecule of the invention. Molecules may be modified in many ways including chemically, structurally, and functionally.

[0814] *Mutation*: As used herein, the term "mutation" refers to any changing of the structure of a gene, resulting in a variant (also called "mutant") form that may be transmitted to subsequent generations. Mutations in a gene may be caused by the alternation of single base in DNA, or the deletion, insertion, or rearrangement of larger sections of genes or chromosomes.

[0815] *Naturally Occurring:* As used herein, "naturally occurring" or "wild-type" means existing in nature without artificial aid, or involvement of the hand of man.

[0816] *Non-human vertebrate:* As used herein, a "non-human vertebrate" includes all vertebrates except *Homo sapiens*, including wild and domesticated species. Examples of non-human vertebrates include, but are not limited to, mammals, such as alpaca, banteng, bison, camel, cat, cattle, deer, dog, donkey, gayal, goat, guinea pig, horse, llama, mule, pig, rabbit, reindeer, sheep water buffalo, and yak.

[0817] *Off-target:* As used herein, "off target" refers to any unintended effect on any one or more target, gene, or cellular transcript.

[0818] *Open reading frame:* As used herein, "open reading frame" or "ORF" refers to a sequence which does not contain a stop codon in a given reading frame.

[0819] *Operably linked:* As used herein, the phrase "operably linked" refers to a functional connection between two or more molecules, constructs, transcripts, entities, moieties or the like.

[0820] *Particle*: As used herein, a "particle" is a virus comprised of at least two components, a protein capsid and a polynucleotide sequence enclosed within the capsid.

[0821] *Patient:* As used herein, "patient" refers to a subject who may seek or be in need of treatment, requires treatment, is receiving treatment, will receive treatment, or a subject who is under care by a trained professional for a particular disease or condition.

[0822] *Payload:* As used herein, "payload" or "payload region" refers to one or more polynucleotides or polynucleotide regions encoded by or within a viral genome or an expression product of such polynucleotide or polynucleotide region, e.g., a transgene, a

polynucleotide encoding a polypeptide or multi-polypeptide or a modulatory nucleic acid or regulatory nucleic acid.

[0823] *Peptide:* As used herein, "peptide" is less than or equal to 50 amino acids long, e.g., about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

[0824] *Pharmaceutically acceptable*: The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

[0825] *Pharmaceutically acceptable excipients:* The phrase "pharmaceutically acceptable excipient," as used herein, refers any ingredient other than the compounds described herein (for example, a vehicle capable of suspending or dissolving the active compound) and having the properties of being substantially nontoxic and non-inflammatory in a patient. Excipients may include, for example: antiadherents, antioxidants, binders, coatings, compression aids, disintegrants, dyes (colors), emollients, emulsifiers, fillers (diluents), film formers or coatings, flavors, fragrances, glidants (flow enhancers), lubricants, preservatives, printing inks, sorbents, suspensing or dispersing agents, sweeteners, and waters of hydration. Exemplary excipients include, but are not limited to: butylated hydroxytoluene (BHT), calcium carbonate, calcium phosphate (dibasic), calcium stearate, croscarmellose, crosslinked polyvinyl pyrrolidone, citric acid, crospovidone, cysteine, ethylcellulose, gelatin, hydroxypropyl cellulose, hydroxypropyl methylcellulose, lactose, magnesium stearate, maltitol, mannitol, methionine, methylcellulose, methyl paraben, microcrystalline cellulose, polyethylene glycol, polyvinyl pyrrolidone, povidone, pregelatinized starch, propyl paraben, retinyl palmitate, shellac, silicon dioxide, sodium carboxymethyl cellulose, sodium citrate, sodium starch glycolate, sorbitol, starch (corn), stearic acid, sucrose, talc, titanium dioxide, vitamin A, vitamin E, vitamin C, and xylitol.

[0826] *Pharmaceutically acceptable salts*: The present disclosure also includes pharmaceutically acceptable salts of the compounds described herein. As used herein, "pharmaceutically acceptable salts" refers to derivatives of the disclosed compounds wherein the parent compound is modified by converting an existing acid or base moiety to its salt form (e.g., by reacting the free base group with a suitable organic acid). Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic

acids; and the like. Representative acid addition salts include acetate, acetic acid, adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzene sulfonic acid, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptonate, glycerophosphate, hemisulfate, heptonate, hexanoate, hydrobromide, hydrochloride, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like, as well as nontoxic ammonium, quaternary ammonium, and amine cations, including, but not limited to ammonium, tetramethylammonium, tetraethylammonium, methylamine, dimethylamine, trimethylamine, triethylamine, ethylamine, and the like. The pharmaceutically acceptable salts of the present disclosure include the conventional non-toxic salts of the parent compound formed, for example, from non-toxic inorganic or organic acids. The pharmaceutically acceptable salts of the present disclosure can be synthesized from the parent compound which contains a basic or acidic moiety by conventional chemical methods. Generally, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in water or in an organic solvent, or in a mixture of the two; generally, nonaqueous media like ether, ethyl acetate, ethanol, isopropanol, or acetonitrile are preferred. Lists of suitable salts are found in *Remington's Pharmaceutical Sciences*, 17th ed., Mack Publishing Company, Easton, Pa., 1985, p. 1418, *Pharmaceutical Salts: Properties, Selection, and Use*, P.H. Stahl and C.G. Wermuth (eds.), Wiley-VCH, 2008, and Berge et al., *Journal of Pharmaceutical Science*, 66, 1-19 (1977), each of which is incorporated herein by reference in its entirety.

[0827] *Pharmaceutically acceptable solvate*: The term "pharmaceutically acceptable solvate," as used herein, means a compound of the invention wherein molecules of a suitable solvent are incorporated in the crystal lattice. A suitable solvent is physiologically tolerable at the dosage administered. For example, solvates may be prepared by crystallization, recrystallization, or precipitation from a solution that includes organic solvents, water, or a mixture thereof. Examples of suitable solvents are ethanol, water (for example, mono-, di-, and tri-hydrates), *N*-methylpyrrolidinone (NMP), dimethyl sulfoxide (DMSO), *N,N'*-

dimethylformamide (DMF), *N*,*N'*-dimethylacetamide (DMAC), 1,3-dimethyl-2-imidazolidinone (DMEU), 1,3-dimethyl-3,4,5,6-tetrahydro-2-(1H)-pyrimidinone (DMPU), acetonitrile (ACN), propylene glycol, ethyl acetate, benzyl alcohol, 2-pyrrolidone, benzyl benzoate, and the like. When water is the solvent, the solvate is referred to as a "hydrate."

[0828] *Pharmacokinetic:* As used herein, "pharmacokinetic" refers to any one or more properties of a molecule or compound as it relates to the determination of the fate of substances administered to a living organism. Pharmacokinetics is divided into several areas including the extent and rate of absorption, distribution, metabolism and excretion. This is commonly referred to as ADME where: (A) Absorption is the process of a substance entering the blood circulation; (D) Distribution is the dispersion or dissemination of substances throughout the fluids and tissues of the body; (M) Metabolism (or Biotransformation) is the irreversible transformation of parent compounds into daughter metabolites; and (E) Excretion (or Elimination) refers to the elimination of the substances from the body. In rare cases, some drugs irreversibly accumulate in body tissue.

[0829] *Physicochemical:* As used herein, "physicochemical" means of or relating to a physical and/or chemical property.

[0830] *Preventing*: As used herein, the term "preventing" or "prevention" refers to partially or completely delaying onset of an infection, disease, disorder and/or condition; partially or completely delaying onset of one or more symptoms, features, or clinical manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying onset of one or more symptoms, features, or manifestations of a particular infection, disease, disorder, and/or condition; partially or completely delaying progression from an infection, a particular disease, disorder and/or condition; and/or decreasing the risk of developing pathology associated with the infection, the disease, disorder, and/or condition.

[0831] *Proliferate:* As used herein, the term "proliferate" means to grow, expand or increase or cause to grow, expand or increase rapidly. "Proliferative" means having the ability to proliferate. "Anti-proliferative" means having properties counter to or inapposite to proliferative properties.

[0832] *Prophylactic*: As used herein, "prophylactic" refers to a therapeutic or course of action used to prevent the spread of disease.

[0833] *Prophylaxis:* As used herein, a "prophylaxis" refers to a measure taken to maintain health and prevent the spread of disease.

[0834] *Protein of interest:* As used herein, the terms "proteins of interest" or "desired proteins" include those provided herein and fragments, mutants, variants, and alterations thereof.

[0835] *Proximal:* As used herein, the term "proximal" means situated nearer to the center or to a point or region of interest.

[0836] *Purified:* As used herein, "purify," "purified," "purification" means to make substantially pure or clear from unwanted components, material defilement, admixture or imperfection. "Purified" refers to the state of being pure. "Purification" refers to the process of making pure.

[0837] *Region:* As used herein, the term "region" refers to a zone or general area. In some embodiments, when referring to a protein or protein module, a region may comprise a linear sequence of amino acids along the protein or protein module or may comprise a three-dimensional area, an epitope and/or a cluster of epitopes. In some embodiments, regions comprise terminal regions. As used herein, the term "terminal region" refers to regions located at the ends or termini of a given agent. When referring to proteins, terminal regions may comprise N- and/or C-termini. N-termini refer to the end of a protein comprising an amino acid with a free amino group. C-termini refer to the end of a protein comprising an amino acid with a free carboxyl group. N- and/or C-terminal regions may there for comprise the N- and/or C-termini as well as surrounding amino acids. In some embodiments, N- and/or C-terminal regions comprise from about 3 amino acid to about 30 amino acids, from about 5 amino acids to about 40 amino acids, from about 10 amino acids to about 50 amino acids, from about 20 amino acids to about 100 amino acids and/or at least 100 amino acids. In some embodiments, N-terminal regions may comprise any length of amino acids that includes the N-terminus, but does not include the C-terminus. In some embodiments, C-terminal regions may comprise any length of amino acids, which include the C-terminus, but do not comprise the N-terminus.

[0838] In some embodiments, when referring to a polynucleotide, a region may comprise a linear sequence of nucleic acids along the polynucleotide or may comprise a three-dimensional area, secondary structure, or tertiary structure. In some embodiments, regions comprise terminal regions. As used herein, the term "terminal region" refers to regions located at the ends or termini of a given agent. When referring to polynucleotides, terminal regions may comprise 5' and 3' termini. 5' termini refer to the end of a polynucleotide comprising a nucleic acid with a free phosphate group. 3' termini refer to the end of a

polynucleotide comprising a nucleic acid with a free hydroxyl group. 5' and 3' regions may there for comprise the 5' and 3' termini as well as surrounding nucleic acids. In some embodiments, 5' and 3' terminal regions comprise from about 9 nucleic acids to about 90 nucleic acids, from about 15 nucleic acids to about 120 nucleic acids, from about 30 nucleic acids to about 150 nucleic acids, from about 60 nucleic acids to about 300 nucleic acids and/or at least 300 nucleic acids. In some embodiments, 5' regions may comprise any length of nucleic acids that includes the 5' terminus, but does not include the 3' terminus. In some embodiments, 3' regions may comprise any length of nucleic acids, which include the 3' terminus, but does not comprise the 5' terminus.

[0839] *RNA or RNA molecule*: As used herein, the term "RNA" or "RNA molecule" or "ribonucleic acid molecule" refers to a polymer of ribonucleotides; the term "DNA" or "DNA molecule" or "deoxyribonucleic acid molecule" refers to a polymer of deoxyribonucleotides. DNA and RNA can be synthesized naturally, e.g., by DNA replication and transcription of DNA, respectively; or be chemically synthesized. DNA and RNA can be single-stranded (i.e., ssRNA or ssDNA, respectively) or multi-stranded (e.g., double stranded, i.e., dsRNA and dsDNA, respectively). The term "mRNA" or "messenger RNA", as used herein, refers to a single stranded RNA that encodes the amino acid sequence of one or more polypeptide chains.

[0840] *RNA interfering or RNAi:* As used herein, the term "RNA interfering" or "RNAi" refers to a sequence specific regulatory mechanism mediated by RNA molecules which results in the inhibition or interfering or "silencing" of the expression of a corresponding protein-coding gene. RNAi has been observed in many types of organisms, including plants, animals and fungi. RNAi occurs in cells naturally to remove foreign RNAs (e.g., viral RNAs). Natural RNAi proceeds via fragments cleaved from free dsRNA which direct the degradative mechanism to other similar RNA sequences. RNAi is controlled by the RNA-induced silencing complex (RISC) and is initiated by short/small dsRNA molecules in cell cytoplasm, where they interact with the catalytic RISC component argonaute. The dsRNA molecules can be introduced into cells exogenously. Exogenous dsRNA initiates RNAi by activating the ribonuclease protein Dicer, which binds and cleaves dsRNAs to produce double-stranded fragments of 21-25 base pairs with a few unpaired overhang bases on each end. These short double stranded fragments are called small interfering RNAs (siRNAs).

[0841] *Sample:* As used herein, the term "sample" or "biological sample" refers to a subset of its tissues, cells or component parts (e.g. body fluids, including but not limited to

blood, mucus, lymphatic fluid, synovial fluid, cerebrospinal fluid, saliva, amniotic fluid, amniotic cord blood, urine, vaginal fluid and semen). A sample further may include a homogenate, lysate or extract prepared from a whole organism or a subset of its tissues, cells or component parts, or a fraction or portion thereof, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, organs. A sample further refers to a medium, such as a nutrient broth or gel, which may contain cellular components, such as proteins or nucleic acid molecule.

[0842] *Self-complementary viral particle*: As used herein, a "self-complementary viral particle" is a particle comprised of at least two components, a protein capsid and a polynucleotide sequence encoding a self-complementary genome enclosed within the capsid.

[0843] *Sense Strand:* As used herein, the term "the sense strand" or "the second strand" or "the passenger strand" of a siRNA molecule refers to a strand that is complementary to the antisense strand or first strand. The antisense and sense strands of a siRNA molecule are hybridized to form a duplex structure. As used herein, a "siRNA duplex" includes a siRNA strand having sufficient complementarity to a section of about 10-50 nucleotides of the mRNA of the gene targeted for silencing and a siRNA strand having sufficient complementarity to form a duplex with the other siRNA strand.

[0844] *Short interfering RNA or siRNA:* As used herein, the terms "short interfering RNA," "small interfering RNA" or "siRNA" refer to an RNA molecule (or RNA analog) comprising between about 5-60 nucleotides (or nucleotide analogs) which is capable of directing or mediating RNAi. Preferably, a siRNA molecule comprises between about 15-30 nucleotides or nucleotide analogs, such as between about 16-25 nucleotides (or nucleotide analogs), between about 18-23 nucleotides (or nucleotide analogs), between about 19-22 nucleotides (or nucleotide analogs) (e.g., 19, 20, 21 or 22 nucleotides or nucleotide analogs), between about 19-25 nucleotides (or nucleotide analogs), and between about 19-24 nucleotides (or nucleotide analogs). The term "short" siRNA refers to a siRNA comprising 5-23 nucleotides, preferably 21 nucleotides (or nucleotide analogs), for example, 19, 20, 21 or 22 nucleotides. The term "long" siRNA refers to a siRNA comprising 24-60 nucleotides, preferably about 24-25 nucleotides, for example, 23, 24, 25 or 26 nucleotides. Short siRNAs may, in some instances, include fewer than 19 nucleotides, e.g., 16, 17 or 18 nucleotides, or as few as 5 nucleotides, provided that the shorter siRNA retains the ability to mediate RNAi. Likewise, long siRNAs may, in some instances, include more than 26 nucleotides, e.g., 27,

28, 29, 30, 35, 40, 45, 50, 55, or even 60 nucleotides, provided that the longer siRNA retains the ability to mediate RNAi or translational repression absent further processing, e.g., enzymatic processing, to a short siRNA. siRNAs can be single stranded RNA molecules (ss-siRNAs) or double stranded RNA molecules (ds-siRNAs) comprising a sense strand and an antisense strand which hybridized to form a duplex structure called siRNA duplex.

[0845] *Signal Sequences:* As used herein, the phrase "signal sequences" refers to a sequence which can direct the transport or localization of a protein.

[0846] *Single unit dose*: As used herein, a "single unit dose" is a dose of any therapeutic administered in one dose/at one time/single route/single point of contact, i.e., single administration event. In some embodiments, a single unit dose is provided as a discrete dosage form (e.g., a tablet, capsule, patch, loaded syringe, vial, etc.).

[0847] *Similarity*: As used herein, the term "similarity" refers to the overall relatedness between polymeric molecules, *e.g.* between polynucleotide molecules (*e.g.* DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of percent similarity of polymeric molecules to one another can be performed in the same manner as a calculation of percent identity, except that calculation of percent similarity takes into account conservative substitutions as is understood in the art.

[0848] *Split dose*: As used herein, a "split dose" is the division of single unit dose or total daily dose into two or more doses.

[0849] *Stable:* As used herein "stable" refers to a compound that is sufficiently robust to survive isolation to a useful degree of purity from a reaction mixture, and preferably capable of formulation into an efficacious therapeutic agent.

[0850] *Stabilized:* As used herein, the term "stabilize", "stabilized," "stabilized region" means to make or become stable.

[0851] *Subject:* As used herein, the term "subject" or "patient" refers to any organism to which a composition in accordance with the invention may be administered, *e.g.*, for experimental, diagnostic, prophylactic, and/or therapeutic purposes. Typical subjects include animals (*e.g.*, mammals such as mice, rats, rabbits, non-human primates, and humans) and/or plants.

[0852] *Substantially*: As used herein, the term "substantially" refers to the qualitative condition of exhibiting total or near-total extent or degree of a characteristic or property of interest. One of ordinary skill in the biological arts will understand that biological and chemical phenomena rarely, if ever, go to completion and/or proceed to completeness or

achieve or avoid an absolute result. The term "substantially" is therefore used herein to capture the potential lack of completeness inherent in many biological and chemical phenomena.

[0853] *Substantially equal*: As used herein as it relates to time differences between doses, the term means plus/minus 2%.

[0854] *Substantially simultaneously*: As used herein and as it relates to plurality of doses, the term means within 2 seconds.

[0855] *Suffering from*: An individual who is "suffering from" a disease, disorder, and/or condition has been diagnosed with or displays one or more symptoms of a disease, disorder, and/or condition.

[0856] *Susceptible to*: An individual who is "susceptible to" a disease, disorder, and/or condition has not been diagnosed with and/or may not exhibit symptoms of the disease, disorder, and/or condition but harbors a propensity to develop a disease or its symptoms. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition (for example, cancer) may be characterized by one or more of the following: (1) a genetic mutation associated with development of the disease, disorder, and/or condition; (2) a genetic polymorphism associated with development of the disease, disorder, and/or condition; (3) increased and/or decreased expression and/or activity of a protein and/or nucleic acid associated with the disease, disorder, and/or condition; (4) habits and/or lifestyles associated with development of the disease, disorder, and/or condition; (5) a family history of the disease, disorder, and/or condition; and (6) exposure to and/or infection with a microbe associated with development of the disease, disorder, and/or condition. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition will develop the disease, disorder, and/or condition. In some embodiments, an individual who is susceptible to a disease, disorder, and/or condition will not develop the disease, disorder, and/or condition.

[0857] *Sustained release:* As used herein, the term "sustained release" refers to a pharmaceutical composition or compound release profile that conforms to a release rate over a specific period of time.

[0858] *Synthetic*: The term "synthetic" means produced, prepared, and/or manufactured by the hand of man. Synthesis of polynucleotides or polypeptides or other molecules of the present invention may be chemical or enzymatic.

[0859] *Targeting:* As used herein, "targeting" means the process of design and selection of nucleic acid sequence that will hybridize to a target nucleic acid and induce a desired effect.

[0860] *Targeted Cells:* As used herein, "targeted cells" refers to any one or more cells of interest. The cells may be found *in vitro*, *in vivo*, *in situ* or in the tissue or organ of an organism. The organism may be an animal, preferably a mammal, more preferably a human and most preferably a patient.

[0861] *Therapeutic Agent:* The term "therapeutic agent" refers to any agent that, when administered to a subject, has a therapeutic, diagnostic, and/or prophylactic effect and/or elicits a desired biological and/or pharmacological effect.

[0862] *Therapeutically effective amount:* As used herein, the term "therapeutically effective amount" means an amount of an agent to be delivered (*e.g.*, nucleic acid, drug, therapeutic agent, diagnostic agent, prophylactic agent, *etc.*) that is sufficient, when administered to a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition. In some embodiments, a therapeutically effective amount is provided in a single dose. In some embodiments, a therapeutically effective amount is administered in a dosage regimen comprising a plurality of doses. Those skilled in the art will appreciate that in some embodiments, a unit dosage form may be considered to comprise a therapeutically effective amount of a particular agent or entity if it comprises an amount that is effective when administered as part of such a dosage regimen.

[0863] *Therapeutically effective outcome*: As used herein, the term "therapeutically effective outcome" means an outcome that is sufficient in a subject suffering from or susceptible to an infection, disease, disorder, and/or condition, to treat, improve symptoms of, diagnose, prevent, and/or delay the onset of the infection, disease, disorder, and/or condition.

[0864] *Total daily dose:* As used herein, a "total daily dose" is an amount given or prescribed in 24 hour period. It may be administered as a single unit dose.

[0865] *Transfection*: As used herein, the term "transfection" refers to methods to introduce exogenous nucleic acids into a cell. Methods of transfection include, but are not limited to, chemical methods, physical treatments and cationic lipids or mixtures.

[0866] *Treating*: As used herein, the term "treating" refers to partially or completely alleviating, ameliorating, improving, relieving, delaying onset of, inhibiting progression of, reducing severity of, and/or reducing incidence of one or more symptoms or features of a

particular infection, disease, disorder, and/or condition. For example, "treating" cancer may refer to inhibiting survival, growth, and/or spread of a tumor. Treatment may be administered to a subject who does not exhibit signs of a disease, disorder, and/or condition and/or to a subject who exhibits only early signs of a disease, disorder, and/or condition for the purpose of decreasing the risk of developing pathology associated with the disease, disorder, and/or condition.

[0867] *Unmodified*: As used herein, "unmodified" refers to any substance, compound or molecule prior to being changed in any way. Unmodified may, but does not always, refer to the wild type or native form of a biomolecule. Molecules may undergo a series of modifications whereby each modified molecule may serve as the "unmodified" starting molecule for a subsequent modification.

[0868] *Vector*: As used herein, a "vector" is any molecule or moiety which transports, transduces or otherwise acts as a carrier of a heterologous molecule. Vectors of the present invention may be produced recombinantly and may be based on and/or may comprise adeno-associated virus (AAV) parent or reference sequence. Such parent or reference AAV sequences may serve as an original, second, third or subsequent sequence for engineering vectors. In non-limiting examples, such parent or reference AAV sequences may comprise any one or more of the following sequences: a polynucleotide sequence encoding a polypeptide or multi-polypeptide, which sequence may be wild-type or modified from wild-type and which sequence may encode full-length or partial sequence of a protein, protein domain, or one or more subunits of a protein; a polynucleotide comprising a modulatory or regulatory nucleic acid which sequence may be wild-type or modified from wild-type; and a transgene that may or may not be modified from wild-type sequence . These AAV sequences may serve as either the "donor" sequence of one or more codons (at the nucleic acid level) or amino acids (at the polypeptide level) or "acceptor" sequences of one or more codons (at the nucleic acid level) or amino acids (at the polypeptide level).

[0869] *Viral genome*: As used herein, a "viral genome" or "vector genome" is a polynucleotide comprising at least one inverted terminal repeat (ITR) and at least one encoded payload. A viral genome encodes at least one copy of the payload.

VII. EXAMPLES

EXAMPLE 1. Production and Purification of AAV particles

[0870] AAV particles described herein may be produced using methods known in the art, such as, for example, triple transfection or baculovirus mediated virus production. Any suitable permissive or packaging cell known in the art may be employed to produce the vectors. Mammalian cells are often preferred. Also preferred are trans-complementing packaging cell lines that provide functions deleted from a replication-defective helper virus, e.g., 293 cells or other E1a trans-complementing cells.

[0871] The gene cassette may contain some or all of the parvovirus (e.g., AAV) cap and rep genes. Preferably, however, some or all of the cap and rep functions are provided in trans by introducing a packaging vector(s) encoding the capsid and/or Rep proteins into the cell. Most preferably, the gene cassette does not encode the capsid or Rep proteins. Alternatively, a packaging cell line is used that is stably transformed to express the cap and/or rep genes

[0872] Recombinant AAV virus particles are, in some cases, produced and purified from culture supernatants according to the procedure as described in US20160032254, the contents of which are incorporated by reference. Production may also involve methods known in the art including those using 293T cell, sf9 insect cells, triple transfection or any suitable production method.

[0873] In some cases, 293 cells are transfected with CaPO4 with plasmids required for production of AAV, i.e., AAV2 rep, an adenoviral helper construct and a ITR flanked transgene cassette. The AAV2 rep plasmid also contains the cap sequence of the particular virus being studied. Twenty-four hours after transfection, which occurs in serum containing DMEM, the medium is replaced with fresh medium with or without serum. Three (3) days after transfection, a sample is taken from the culture medium of the 293 adherent cells. Subsequently cells are scraped and transferred into a receptacle. After centrifugation to remove cellular pellet, a second sample is taken from the supernatant after scraping. Next, cell lysis is achieved by three consecutive freeze-thaw cycles (-80C to 37C). Cellular debris is removed and sample 3 is taken from the medium. The samples are quantified for AAV particles by DNase resistant genome titration by Taqman.TM. PCR. The total production yield from such a transfection is equal to the particle concentration from sample 3.

[0874] AAV particle titers are measured according to genome copy number (genome particles per milliliter). Genome particle concentrations are based on Taqman.RTM. PCR of the vector DNA as previously reported (Clark et al. (1999) Hum. Gene Ther., 10:1031-1039; Veldwijk et al. (2002) Mol. Ther., 6:272-278).

EXAMPLE 2. Tissue specific expression

[0875] To evaluate the expression of various encoded payloads in tissues, a series of AAV particles carrying the encoded sequences driven by a panel of ubiquitous and tissue-specific promoters are made. These particles are administered to the specific tissue, e.g., systemically, via an appropriate route, e.g., a single intravenous injection and expression is monitored to determine the relative expression potential of the payload as well as of each promoter in this target tissue. Measurement of payload production is performed using standard techniques, for example by ELISA.

[0876] In some cases, the cytomegalovirus immediate early promoter (CMV), chimeric chicken-beta-actin (CAG), and ubiquitin C (UBC), CBA, H1, αMHC, cTnT, and CMV-MLC2k promoters provide robust expression.

EXAMPLE 3. *In Vivo* Mouse Biodistribution and Expression Levels Following Intravenous Treatment with VOY101-GFP vector

[0877] An adeno-associated capsid variant (VOY101) was engineered for widespread gene transfer into the brain and heart. A viral genome comprising AAV2 wild-type inverted terminal repeats (ITR), a synthetic promoter composed of CMV enhancer and chicken beta-actin promoter (CBA), an enhanced green fluorescent protein variant (eGFP) and a rabbit globin polyadenylation sequence was used to generate AAV particles, having a capsid serotype of either VOY101 or AAV9, by triple transfection into HEK293T cells. The ITR to ITR sequence of the viral genome is provided as SEQ ID NO: 1799.

[0878] The single-stranded AAV particles were purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68, and then administered to adult C57Bl/6J mice at 6-7 weeks of age via lateral tail vein injection at ~4 ml/kg, with a vector concentration of 5.0×10^{12} vg/mL. The total dose was 2.0×10^{13} VG/kg. A control group was treated with vehicle (PBS with 0.001% F-68).

[0879] Approximately 28 days following administration, several tissue samples were collected. Tissue samples allocated for GFP protein quantification or vector genome quantification were flash-frozen in liquid nitrogen. Tissue samples allocated for anti-GFP immunohistochemistry were post-fixed in 4% paraformaldehyde overnight. Analysis of the tissue samples by immuno-histochemical staining with an anti-GFP antibody and subsequent DAB substrate development showed that systemic injection with VOY101-GFP particles resulted in increased GFP levels throughout the brain and spinal cord as compared to the administered AAV9-GFP particles.

[0880] GFP protein levels were measured by ELISA and reported in ng GFP/mg of total protein and the results are shown in Table 13. Vector genome digital PCR quantification was performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host TFRC (transferrin receptor protein 1) and expressed in vector genome per diploid cell (VG/DC) and the results are shown in Tables 14 and 15. In Tables 13, 14 and 15, "BLLQ" means below lower limit of quantification.

Table 13. GFP Expression in Mouse after Intravenous Injection

AAV Serotype (Protein SEQ ID NO; Nucleotide SEQ ID NO)	GFP Expression (ng GFP/mg of total protein)				
	Striatum	Lumbar Spinal Cord	Lumbar Dorsal Root Ganglia	Heart	Liver
VOY101 (SEQ ID NO: 1; SEQ ID NO: 1800)	30.4 ± 3.7	111.2 ± 18.2	4.2 ± 2.3	261.8 ± 127.8	428.2 ± 239.2
AAV9 (SEQ ID NO: 136; SEQ ID NO: 135)	0.5 ± 0.1	1.5 ± 0.4	14.3 ± 9.2	453.2 ± 138.1	2115.9 ± 951.0
Vehicle	BLLQ	BLLQ	0.2 ± 0.5	BLLQ	BLLQ

Table 14. Vector Genome Distribution in Mouse after Intravenous Injection

AAV Serotype (Protein SEQ ID NO; Nucleotide SEQ ID NO)	VG Distribution (VG/DC)			
	Striatum	Cortex	Brainstem	Cerebellum cortex
VOY101 (SEQ ID NO: 1; SEQ ID NO: 1800)	27.8 ± 6.2	31.7 ± 8.2	33.5 ± 7.1	4.0 ± 1.2
AAV9 (SEQ ID NO: 136; SEQ ID NO: 135)	0.3 ± 0.1	0.2 ± 0.1	0.5 ± 0.6	0.1 ± 0.1
Vehicle	BLLQ	BLLQ	BLLQ	BLLQ

Table 15. Vector Genome Distribution in Mouse after Intravenous Injection

AAV Serotype (Protein SEQ ID NO; Nucleotide SEQ ID NO)	GFP Expression (ng GFP/mg of total protein)				
	Dentate nucleus	Thoracic Spinal Cord	Thoracic Dorsal Root Ganglia	Heart	Liver
VOY101 (SEQ ID NO: 1; SEQ ID NO: 1800)	34.0 ± 11.6	20.8 ± 2.4	2.1 ± 3.0	1.1 ± 0.6	17.7 ± 7.2
AAV9 (SEQ ID NO: 136; SEQ ID NO: 135)	0.2 ± 0.1	0.2 ± 0.1	0.1 ± 0.02	1.0 ± 0.2	95.8 ± 19.7
Vehicle	BLLQ	BLLQ	BLLQ	BLLQ	BLLQ

[0881] In mouse striatum, 28 days after intravenous injection of 2.0×10^{13} VG/kg, VOY101-GFP resulted in GFP levels 58-fold higher and vector genome distribution 101-fold higher than AAV9-GFP. In mouse spinal cord, 28 days after intravenous injection of 2.0×10^{13} VG/kg, VOY101-GFP resulted in GFP levels 74-fold higher and vector genome

distribution 104-fold higher than AAV9-GFP. In mouse liver, 28 days after intravenous injection of 2.0 x 10^{13} VG/kg, VOY101-GFP resulted in GFP levels 4.9-fold lower and vector genome distribution 5.4-fold lower than AAV9-GFP.

EXAMPLE 4. Intravenous delivery of VOY101-FXN AAV particles

A. In Vivo Mouse Biodistribution and Expression Levels Following Intravenous Treatment with VOY101-FXN AAV particles

[0882] Widespread gene transfer into the brain and heart was also observed when using a viral genome with macaca fascicularis (cynomolgus monkey) frataxin (cFXN) transgene. A viral genome comprising AAV2 wild-type ITRs, a synthetic promoter composed of CMV enhancer and chicken beta-actin promoter (CBA), macaca fascicularis frataxin (cFXN) and a human growth hormone polyadenylation sequence was used to generate AAV particles, having a capsid serotype of either VOY101 or AAV9, by triple transfection into HEK293T cells. The ITR to ITR sequence of the viral genome is provided as SEQ ID NO: 1801.

[0883] The single-stranded AAV particles were purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68, and then administered to adult C57Bl/6J mice at 9 weeks of age via lateral tail vein injection ~4 ml/kg, with a vector concentration of 1.0 × 10^{12} vg/mL. The total dose was 4.2 × 10^{12} VG/kg. A control group was treated with vehicle (PBS with 0.001% F-68).

[0884] Seven days following AAV particle or vehicle administration, several tissue samples were collected. Tissue samples were flash-frozen in liquid nitrogen. Vector genome digital PCR quantification was performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host TFRC, and expressed in vector genome per diploid cell (VG/DC). cFXN protein levels were measured by ELISA and reported in ng cFXN/mg of total protein. cFXN protein levels and vector genome distribution are shown in Tables 16 and 17. In Tables 16 and 17, "BLLQ" means below lower limit of quantification.

Table 16. cFXN Expression in Mouse after Intravenous Injection

AAV Serotype (Protein SEQ ID NO; Nucleotide SEQ ID NO)	cFXN Expression (ng cFXN/mg of total protein)					
	Cortex	Lumbar Spinal Cord	Lumbar Dorsal Root Ganglia	Heart	Liver	Trigeminal ganglion
VOY101 (SEQ ID NO: 1; SEQ ID NO: 1800)	23.4 ± 13.8	64.1 ± 10.2	11.2 ± 2.4	17.8 ± 17.1	69.2 ± 51.1	6.0 ± 3.1
AAV9 (SEQ ID NO: 136; SEQ ID NO: 135)	BLLQ	BLLQ	BLLQ	1.9 ± 3.1	327.8 ± 171.5	0.4 ± 0.5
Vehicle	BLLQ	BLLQ	BLLQ	BLLQ	BLLQ	BLLQ

Table 17. Vector Genome Distribution in Mouse after Intravenous Injection

AAV Serotype (Protein SEQ ID NO; Nucleotide SEQ ID NO)	VG Distribution (VG/DC)					
	Cortex	Lumbar Spinal Cord	Thoracic Dorsal Root Ganglia	Heart	Liver	Trigeminal ganglion
VOY101 (SEQ ID NO: 1; SEQ ID NO: 1800)	14.85 ± 3.58	23.51 ± 1.96	6.49 ± 3.19	0.46 ± 0.13	8.74 ± 5.98	2.45 ± 1.27
AAV9 (SEQ ID NO: 136; SEQ ID NO: 135)	0.09 ± 0.01	0.07 ± 0.02	0.55 ± 0.40	0.17 ± 0.05	56.74 ± 30.60	0.04 ± 0.02
Vehicle	BLLQ	BLLQ	BLLQ	BLLQ	BLLQ	BLLQ

[0885] In mouse cortex, seven days after intravenous injection of 4.2 x 10^{12} vg/kg, VOY101-cFXN resulted in 165-fold higher vector genome than AAV9-cFXN and at least 234-fold higher cFXN protein expression than AAV9-cFXN. In mouse lumbar spinal cord, seven days after intravenous injection of 4.2 x 10^{12} vg/kg, VOY101-cFXN resulted in 336-fold higher vector genome and at least 640-fold higher cFXN protein expression than AAV9-cFXN.

[0886] In dorsal root ganglia, seven days after intravenous injection of 4.2 x 10^{12} vg/kg, VOY101-cFXN resulted in 11.8-fold higher vector genome and 112-fold higher cFXN protein expression than AAV9-cFXN. In trigeminal ganglion, seven days after intravenous injection of 4.2 x 10^{12} vg/kg, VOY101-cFXN resulted in 61-fold higher vector genome and at least 16-fold higher cFXN protein expression than AAV9-cFXN.

[0887] In heart, seven days after intravenous injection of 4.2 x 10^{12} VG/Kg, VOY101-cFXN resulted in 2.7-fold higher vector genome and 9.4-fold higher cFXN protein expression than AAV9-cFXN, indicating significantly higher expression as compared to AAV9.

B. In Vivo Study in Non-Human Primate of cFXN Expression after Treatment with VOY101-FXN-HA AAV Particles

[0888] A study in cynomolgus monkeys (macaca fascicularis) was conducted to evaluate cFXN expression within the CNS after IV dosing of VOY101-cFXN-HA.

[0889] A viral genome comprising HA-tagged cynomolgus frataxin (cFXN-HA) was engineered into a single stranded expression vector. A viral genome comprising AAV2 wild-type ITRs, a synthetic promoter composed of CMV enhancer and chicken beta-actin promoter (CBA), macaca fascicularis frataxin (cFXN) with 3' sequence for HA-tag and a human growth hormone polyadenylation sequence was used to generate AAV particles, having a capsid serotype of VOY101, by triple transfection into HEK293T cells. The ITR to ITR sequence of the viral genome is provided as SEQ ID NO: 1801.

[0890] The single-stranded AAV particles (VOY101-cFXN-HA) were purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68, and then administered to non-human primate (*Macaca* fascicularis) via saphenous vein injection at 5 ml/kg, with a vector concentration of 1.34×10^{12} vg/mL and a total dose of 6.7×10^{12} VG/kg. In addition, a single-stranded AAV9 with a CBA promoter and a viral genome comprising cFXN-HA (AAV9-cFXN-HA) was tested by intravenous injection at a dose of 2×10^{13} VG/kg.

[0891] Approximately 28 days following AAV particle administration, several tissue samples were collected. Tissue samples allocated for cFXN-HA protein quantification or vector genome quantification were snap-frozen. Tissue samples allocated for anti-HA immunohistochemistry were post-fixed in 4% paraformaldehyde for 12 to 72 hours at 2-8°C. Tissue sections (20 μm thickness) were stained with a rabbit monoclonal antibody to HA tag (1:1000 or 1:2000), followed by a goat-anti-rabbit IgG biotinylated secondary antibody (1:1000), and then developed with DAB plus nickel. cFXN-HA staining was observed in multiple CNS regions after IV dosing of VOY101-cFXN. These regions include but are not limited to, the spinal cord (cervical, thoracic and lumbar segments), brainstem nuclei, cerebellum (including cerebellar dentate nucleus), thalamus, caudate nucleus, and cerebral cortex. Homogeneous HA staining was observed along the entire rostral-caudal extent of the spinal cord, particularly in ventral horn motor neurons, after IV dosing of VOY101-cFXN-HA at 6.7×10^{12} VG/kg. The spinal cord and especially ventral horn motor neurons were labeled to a much greater degree with VOY101-cFXN-HA than with AAV9-cFXN-HA, despite the 3-fold lower dose of VOY101-cFXN-HA. Vehicle-treated control non-human primates exhibited essentially no detectable background staining.

[0892] HA staining in the lumbar ventral horn, including motor neurons, was similar after IV VOY101-cFXN-HA (6.7×10^{12} VG/kg) compared with IT administration of a similar dose of a single-stranded rh10 vector and a viral genome comprising cFXN-HA (AAVrh10-FXN-HA).

[0893] Vector genome digital PCR quantification was performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host RnaseP and expressed in vector genome per diploid cell (VG/DC). cFXN-HA protein levels were measured by ELISA. cFXN-HA protein levels (in ng cFXN-HA/mg of total protein) and vector genome distribution (VG/DC) are shown in Table 18. In Table 18, "BLLQ" means below lower limit of quantification and "NA" means not analyzed.

Table 18. cFXN-HA Expression in NHP after Intravenous Injection

Tissue	NHP2001	
	cFXN-HA (ng/mg prot.)	VG (VG/DC)
Frontal Cortex	BLLQ	0.24
Striatum	BLLQ	0.04
Brainstem	112.9	0.50
Cerebellum	BLLQ	0.02
Cervical Spinal Cord	49.2	0.14
Thoracic Spinal Cord	14.1	0.15
Lumbar Spinal Cord	32.4	NA
Cervical Dorsal Root Ganglia	195.4	0.71
Thoracic Dorsal Root Ganglia	88.2	1.18
Lumbar/Sacral Dorsal Root Ganglia	87.4	1.86
Heart Ventricle	212.4	9.1
Heart Atrium	358.0	7.23
Liver	4.48	224.83
Kidney	BLLQ	0.93
Lung	BLLQ	0.58
Soleus	1.1	0.44
Jejunum	2.0	1.86
Spleen	BLLQ	14.65

[0894] These results show that in non-human primates (NHPs) 28 days after intravenous injection of 6.7 x 10^{12} VG/kg, VOY101-cFXN-HA resulted in brain transduction. Significant levels of cFXN-HA protein were detected in many CNS regions including the spinal cord (cervical, thoracic and lumbar segments) and brainstem. Significant levels of vector genomes were detected in many CNS regions including the spinal cord (cervical and thoracic segments), brainstem, and cortex, after IV dosing.

C. In Vivo Biodistribution and Expression Levels of cFXN Expression in Non-Human Primates after Treatment with PHP.B-FXN-HA AAV Particles

[0895] A dose-response study in cynomolgus monkeys (macaca fascicularis) was conducted to evaluate cFXN expression within the CNS after IV dosing of PHP.B-cFXN-HA.

[0896] A viral genome comprising HA-tagged cynomolgus frataxin (cFXN-HA) was engineered into a single stranded expression vector. A viral genome comprising AAV2 wild-type ITRs, a synthetic promoter composed of CMV enhancer and chicken beta-actin promoter (CBA), macaca fascicularis frataxin (cFXN) with 3' sequence for HA-tag, triple repeat of a miR-122 target sequence (to reduce transgene liver expression), and a human growth hormone polyadenylation sequence was used to generate AAV particles, having a capsid serotype of PHP.B, by triple transfection into HEK293T cells. The ITR to ITR sequence of the viral genome is provided as SEQ ID NO: 1802.

[0897] The single-stranded AAV particles were purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68, and then administered to non-human primate (*Macaca* fascicularis) via saphenous vein injection at 5 ml/kg, with a vector concentration of 1.54×10^{11} to 4.75×10^{12} vg/mL. Animals were dosed at 6.32×10^{11}, 2.0×10^{12}, or 2.0×10^{13}, VG/kg.

[0898] Approximately 28 days following AAV particle administration, several tissue samples were collected. Tissue samples allocated for cFXN-HA protein quantification or vector genome quantification were snap frozen. Tissue samples allocated for anti-HA immunohistochemistry were post-fixed in 4% paraformaldehyde for 12 to 72 hours at 2-8 °C. For single labeling, tissue sections (20 μm thickness) were stained with a rabbit monoclonal antibody to HA tag (1:1000 or 1:2000), followed by a goat-anti-rabbit IgG biotinylated secondary antibody (1:1000), and then developed with DAB plus nickel. HA staining was observed in multiple CNS regions after IV dosing of PHP.B-cFXN-HA at 2×10^{13} vg/kg. These regions include but are not limited to, the spinal cord (cervical, thoracic and lumbar segments), cerebellum (including dentate nucleus), thalamus, striatum, substantia nigra, and sensory and motor cortex. Furthermore, HA staining showed transduction of large numbers of neurons in multiple CNS regions, including those of neuronal morphology in the substantia nigra, dentate nucleus and thalamus. In addition, cells of neuronal morphology in the spinal cord, motor and sensory cortices, and striatum were HA-immunoreactive.

[0899] Double labeling for the HA tag and the neuronal marker NeuN was carried out using a chromogenic method. Tissue sections (20 μm thickness) were stained with a rabbit monoclonal antibody to HA tag (1:1000), followed by a goat-anti-rabbit IgG biotinylated secondary antibody (1:1000), and then developed with DAB (without nickel). The sections were then stained with a mouse monoclonal to NeuN second primary antibody, followed by a goat-anti-mouse IgG biotinylated secondary antibody. The NeuN signal was then detected with a green chromogen. Multiple HA+ cells were double-labeled with the neuronal marker NeuN. These results demonstrate that neurons of the cerebellar dentate nucleus were labeled for the HA tag after intravenous injection of PHP.B-cFXN-HA at 2×10^{13} VG/kg. Therefore, after an intravenous dose of 2×10^{13} vg/kg in cynomolgus monkeys, neurons of the cerebellar dentate nucleus are transduced and express the transgene.

[0900] Expression of the HA tag in lumbar dorsal root ganglia was present in both large (>40 um) and small sensory neurons, with the labeling increasing in a dose-dependent

manner with IV injection of PHP.B-cFXN-HA at 6.32×10^{11}, 2.0×10^{12}, or 2.0×10^{13}, VG/kg.

[0901] Vector genome digital PCR quantification was performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host RnaseP and expressed in vector genome per diploid cell (VG/DC). cFXN-HA protein levels were measured by ELISA. cFXN-HA protein levels (in ng cFXN-HA/mg of total protein) and vector genome distribution (VG/DC) for the PHP.B capsid serotype are shown in Table 19. In Table 19, "BLLQ" means below lower limit of quantification and "NA" means not analyzed.

Table 19. cFXN-HA Expression in NHP after Intravenous Injection of PHP.B-cFXN-HA

Tissue	**6.3×10^{11} VG/kg NHP003 NHP004**		**2×10^{12} VG/kg NHP005 NHP009**		**2×10^{13} VG/kg NHP007 NHP008**	
	cFXN-HA (ng/mg prot.)	**VG (VG/DC)**	**cFXN-HA (ng/mg prot.)**	**VG (VG/DC)**	**cFXN-HA (ng/mg prot.)**	**VG (VG/DC)**
Frontal Cortex	NA NA	0.03 0.05	NA NA	0.06 0.03	NA NA	0.27 0.54
Striatum	BLLQ BLLQ	BLLQ BLLQ	BLLQ BLLQ	BLLQ BLLQ	BLLQ BLLQ	0.27 0.81
Brainstem	BLLQ BLLQ	BLLQ BLLQ	BLLQ BLLQ	BLLQ 0.03	29.4 BLLQ	0.73 0.96
Cerebellum	BLLQ 5.1	BLLQ BLLQ	BLLQ BLLQ	BLLQ BLLQ	BLLQ 5.1	0.03 0.22
Cervical Spinal Cord	BLLQ BLLQ	BLLQ 0.02	BLLQ BLLQ	BLLQ BLLQ	63.7 85.0	0.36 0.12
Thoracic Spinal Cord	BLLQ BLLQ	BLLQ 0.06	BLLQ BLLQ	0.02 BLLQ	41.2 44.5	0.32 0.32
Lumbar Spinal Cord	BLLQ BLLQ	0.01 BLLQ	BLLQ BLLQ	0.01 0.01	43.9 49.2	0.37 0.53
Cervical Dorsal Root Ganglia	BLLQ 2.8	BLLQ 0.03	9.29 BLLQ	0.07 0.06	421.5 509.9	2.41 1.87
Thoracic Dorsal Root Ganglia	BLLQ BLLQ	BLLQ 0.01	6.1 BLLQ	0.05 0.02	227.2 866.4	2.92 2.52
Lumbar/Sacral Dorsal Root Ganglia	BLLQ BLLQ	BLLQ 0.03	4.9 BLLQ	0.04 0.04	122.2 138.1	3.68 1.63
Heart Ventricle	BLLQ 6.0	BLLQ 0.2	22.9 BLLQ	0.5 0.4	1034.5 185.6	15.3 7.7
Heart Atrium	7.3 5.2	0.03 0.08	60.5 BLLQ	0.97 0.13	650.5 810.0	26.3 26.6
Liver	BLLQ BLLQ	0.4 7.9	BLLQ BLLQ	30.4 74.8	BLLQ BLLQ	444.1 284.4
Kidney	BLLQ BLLQ	BLLQ 0.1	BLLQ BLLQ	0.3 0.1	6.4 2.8	6.3 2.5
Lung	BLLQ BLLQ	NA NA	BLLQ BLLQ	NA NA	0.9 BLLQ	3.3 3.6

Soleus	BLLQ BLLQ	NA NA	BLLQ BLLQ	NA NA	69.9 12.6	13.4 6.7
Jejunum	BLLQ BLLQ	NA NA	BLLQ BLLQ	NA NA	BLLQ BLLQ	0.6 0.3
Spleen	BLLQ BLLQ	1.3 1.2	BLLQ BLLQ	4.3 4.6	BLLQ 2.1	4.4 2.3

[0902] In summary, in non-human primates (NHPs) 28 days after intravenous injection of PHP.B-cFXN-HA, all three dose levels resulted in brain transduction. Significant levels of cFXN-HA protein were detected in many CNS regions including the spinal cord (cervical, thoracic and lumbar segments), brainstem, and cerebellum. Significant levels of vector genome were detected in many CNS regions including the spinal cord (cervical, thoracic and lumbar segments), striatum, brainstem, cerebellum and frontal cortex after IV dosing. Substantial gene transfer to the NHP CNS was observed, including regions such as spinal cord, brain stem, sensory cortex, motor cortex, cerebellum, thalamus, and substantia nigra, with cells of neuronal morphology in these regions exhibiting transgene expression. In addition, the dorsal root ganglia and the heart showed dose-dependent transgene expression, with sensory neurons of the dorsal root ganglia exhibiting transduction.

D. In Vivo Dose Dependent Study in Non-Human Primate of cFXN Expression after Treatment with VOY101-FXN-HA AAV Particles

[0903] A study in cynomolgus monkeys (macaca fascicularis) was conducted to evaluate cFXN expression within the CNS after two different IV dose levels of single stranded VOY101-cFXN-HA.

[0904] A viral genome comprising HA-tagged cynomolgus frataxin (cFXN-HA) was engineered into a single stranded expression vector. A viral genome comprising AAV2 wild-type ITRs, a synthetic promoter composed of CMV enhancer and chicken beta-actin promoter (CBA), macaca fascicularis frataxin (cFXN) with 3' sequence for HA-tag and a human growth hormone polyadenylation sequence was used to generate AAV particles, having a capsid serotype of VOY101. The ITR to ITR sequence of the viral genome is provided as SEQ ID NO: 1801.

[0905] The single-stranded AAV particles were purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68, and then administered to non-human primate (*Macaca* fascicularis) via saphenous vein injection at 5 ml/kg, with a total dose of 6.7×10^{12} VG/kg or 4.9×10^{13} VG/kg VOY101-cFXN-HA. A vehicle negative control group was also evaluated.

[0906] Approximately 28 days following AAV particle administration, several tissue samples were collected. Tissue samples allocated for cFXN-HA protein quantification or vector genome quantification were snap-frozen. Tissue samples allocated for anti-HA immunohistochemistry were post-fixed in 4% paraformaldehyde for 12 to 72 hours at 2-8 °C. Tissue sections (20 μm thickness) were stained with a rabbit monoclonal antibody to HA tag (1:1000 or 1:2000), followed by a goat-anti-rabbit IgG biotinylated secondary antibody (1:1000), and then developed with DAB plus nickel.

[0907] Vector genome digital PCR quantification was performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host TFRC, and expressed in vector genome per cell (VG/Cell). Vector genome distribution (mean ± standard deviation) is shown in Table 20 for VOY101-cFXN-HA. In Table 20, SC-C is the cervical spinal cord and SC-L is the lumbar spinal cord.

Table 20. Vector Genome Distribution in NHP after Intravenous Injection of VOY101-cFXN-HA

Dose	N	VG Distribution (VG/Cell)			
		SC-C	SC-L	Brainstem	Motor Cortex
6.7×10^{12} VG/kg	3	0.14 ± 0.14	0.17 ± 0.12	0.11 ± 0.09	0.14 ± 0.13
4.9×10^{13} VG/kg	3	1.44 ± 0.37	1.15 ± 0.44	1.32 ± 0.9	1.87 ± 0.41

[0908] Homogeneous HA staining was observed along the entire rostral-caudal extent of the spinal cord, particularly in ventral horn motor neurons after IV dosing of VOY101-cFXN-HA. HA staining in the cervical (C5), thoracic (T12) and lumbar (L4) spinal cord of animals receiving a dose of 4.9×10^{13} VG/kg of VOY101-cFXN-HA revealed robust HA staining at all rostral-caudal levels of the spinal cord, particularly in ventral horn motor neurons (Figure 5). Numerous HA+ cells were observed in animals receiving a dose of 4.9×10^{13} VG/kg of VOY101-cFXN-HA including those of neuronal morphology in the motor cortex, the brainstem including the olivary nucleus, hippocampus, the substantia nigra and lateral geniculate nucleus, and the deep cerebellar nuclei including the dentate nucleus. Vehicle-treated control exhibited essentially no detectable or very low background staining.

EXAMPLE 5. VOY101-FXN for the treatment of Friedreich's Ataxia

A. In Vivo Distribution, Expression and Efficacy Study with Intravenous Dosing of VOY101-FXN in a Mouse Model of Friedreich's Ataxia

[0909] Selected viral genomes comprising a nucleic acid encoding human frataxin are designed and packaged into a single stranded VOY101 capsid.

[0910] The viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter (which includes a CMVie enhancer, a CBA, or a CMV, or a frataxin promoter, or a truncated CBA or a truncated CMV promoter, and a human beta globin intron), hFXN cDNA sequence, a human growth hormone polyA sequence, a fragment of human albumin as a stuffer sequence, and wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0911] Six groups of approximately 10 mice/group, at 7 weeks of age, and balanced for gender and litter, receive vehicle (PBS with 0.001% F-68; two groups), or VOY101-FXN vector at either low (2 groups) or high dose (2 groups) levels (approximately 6.3×10^{12} vg/kg – 2×10^{13} vg/kg body weight) via intravenous injection.

[0912] To test the efficacy, distribution and expression of VOY101-FXN in mice, any test known in the art may be utilized. Non-limiting examples include limb electromyography, notched bar walking test, string hanging test, rotarod test, body weight, and/or survival. Other readouts include FXN protein and mRNA expression in tissues (e.g. dorsal root ganglia, heart, cerebellum, spinal cord) by ELISA, PCR, immunohistochemistry and *in situ* hybridization, and in situ assessment of mitochondrial enzyme function in tissue (dorsal root ganglia) sections. Vector genome levels in different tissues are determined by PCR and ISH.

[0913] Three groups of animals (vehicle, low dose, high dose) are euthanized by 18 weeks. Three remaining groups of animals (vehicle, low dose, high dose) are maintained for 6 months or longer to assess effect on survival. Control groups (n=10/ group) include wild type mice and disease model mice dosed with a reference vector.

[0914] The distribution and expression of human frataxin (hFXN) and vector genome distribution in target tissues such as, but not limited to, DRGs, cerebellum, spinal cord and heart in animals receiving the hFXN vector, is measured by ELISA, PCR, ISH, IHC for hFXN expression and PCR and ISH for vector genome analysis. Human frataxin analysis (by ELISA, PCR, ISH, IHC) demonstrate that upon the delivery of the hFXN vector, expression in target tissues e.g., DRGs, cerebellum, spinal cord and heart occurs with distribution to target tissues. *In situ* assessment of mitochondrial enzyme activity shows that upon delivery of the hFXN vector, increased activity in slices of DRG occurs. Electromyography, notched bar, string hanging and rotarod tests demonstrate improved performance over vehicle control animals.

B. In Vivo Distribution and Expression Study with Intravenous Dosing of VOY101-FXN in Non-Human Primates

[0915] mSelected viral genomes comprising a nucleic acid sequence encoding human frataxin are designed and packaged in a single stranded (ss) VOY101 capsid.

[0916] The single stranded viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a prooter (which includes a CMVie enhancer, a CBA, or a CMV, or a frataxin promoter, or a truncated CBA or a truncated CMV promoter, and a human beta globin intron), hFXN cDNA sequence, a human growth hormone polyA sequence, a fragment of human albumin as a stuffer sequence, and wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0917] Eight groups of approximately 3 cynomolgus monkeys/group, approximately 3 years of age or older, with at least one animal of each gender per group, receive vehicle (PBS with 0.001% F-68; two groups), or VOY101-FXN vector at either low (2 groups) or high dose (2 groups) levels (approximately 6.7×10^{12} vg/kg – 6×10^{13} vg/kg body weight) via intravenous injection.

[0918] To test the efficacy, distribution and expression of VOY101-FXN in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of body weight over time, clinical monitoring, histopathology and blood safety panel testing. Other readouts include FXN protein and mRNA expression in tissues (e.g. dorsal root ganglia, heart, cerebellum, spinal cord) as assessed by ELISA, PCR, immunohistochemistry and in situ hybridization. Vector genome levels in different tissues are determined by PCR and ISH.

[0919] Three groups of animals (vehicle, low dose, high dose) are euthanized by 4 weeks. Three remaining groups of animals (vehicle, low dose, high dose) are maintained for 12 weeks to assess long term gene expression.

[0920] The distribution and expression of human frataxin (hFXN) and vector genome distribution in target tissues such as, but not limited to, DRGs, cerebellum, spinal cord and heart in animals receiving the hFXN vector, are measured by ELISA, PCR, ISH, IHC for hFXN expression and PCR and ISH for vector genome analysis. The primate frataxin expression data are compared to the frataxin expression level which resulted in rescue of the FA disease phenotype in a genetic mouse model of Friedreich's Ataxia. Based on these results, efficacious doses for human trials are calculated.

EXAMPLE 6. VOY101-APOE miRNA for the treatment of Alzheimer's Disease

A. In Vivo Distribution, Expression, and Efficacy Study of Intravenous Dosing of scVOY101-APOE miRNA in Mouse Model of Alzheimer's Disease

[0921] Selected viral genomes comprising pri-miRNA cassettes containing guide strands targeting APOE and passenger strands are engineered into self-complementary (sc) VOY101-miRNA expression vectors.

[0922] The scAAV-miRNA viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, the pri-miRNA cassette containing a guide sequence targeting ApoE and a passenger sequence, a polyA sequence, a stuffer sequence, and a wild type ITR.

[0923] The viral genomes are packaged into VOY101 capsids, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0924] Three groups of P301S mutant tau mice, approximately 20 mice/group, at 2 months of age, are administered vehicle (PBS with 0.001% F-68), or VOY101-APOE miRNA at either high or low dose levels (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) via intravenous tail vein injection.

[0925] Any test known in the art may be utilized to test the efficacy, distribution and expression of VOY101-APOE miRNA in mice. Non-limiting examples include the measurement of body weight, expression of APOE mRNA as measured by qRT-PCR, expression of APOE protein as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of amyloid-beta pathology as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of neurodegeneration as assessed by immunohistochemistry, and vector genome levels as measured by digital droplet PCR.

[0926] All animals are evaluated for body weight and survival. Animals are euthanized at approximately 11 months of age for evaluation of brain, spinal cord, and liver samples for APOE mRNA expression, tau and/or amyloid pathology, and neurodegeneration.

[0927] PCR data will demonstrate the delivery of vector genome throughout the brain in animals receiving intravenous VOY101-APOE miRNA vector. Expression data should indicate widespread reduction of APOE protein and mRNA throughout the brain in animals receiving vector. Brain regions demonstrating significant APOE reduction should be those important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Groups receiving the vector would likely show strong reductions in pathological amyloid-beta and neurodegeneration.

B. In Vivo Distribution and Expression Study of APOE in Non-Human Primates following Intravenous Dosing of scVOY101-APOE miRNA

[0928] Selected viral genomes comprising pri-miRNA cassettes containing guide strands targeting APOE and passenger strands are engineered into self-complementary (sc) VOY101-miRNA expression vectors.

[0929] The scAAV-miRNA viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, the pri-miRNA cassette containing a guide sequence targeting ApoE and a passenger sequence, a polyA sequence, a stuffer sequence, and a wild type ITR.

[0930] The viral genomes are packaged into VOY101 capsid, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0931] Non-human primates (NHPs) (Cynomolgus macaques, adult male, prescreened for AAV neutralizing antibodies) in three groups are administered scVOY101-ApoE miRNA vector with one group a vehicle only control. The NHPs are administered either high or low dose levels (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) using intravenous delivery. 4 weeks post-administration, a saline perfusion is performed and the brain sectioned into 3 mm coronal blocks and snap-frozen.

[0932] To test the efficacy, distribution and expression of VOY101-APOE miRNA in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of expression of APOE mRNA by qRT-PCR, expression of tau protein as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, and vector genome levels as assessed by digital droplet PCR.

[0933] Brain regions demonstrating significant APOE reduction would be expected to cover areas important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Consistent with the expression data, PCR would likely demonstrate widespread distribution of vector genome through the brain.

EXAMPLE 7. VOY101-APOE2 for the treatment of Alzheimer Disease and other tauopathies

A. In Vivo Distribution, Expression, and Efficacy Study of Intravenous Dosing of VOY101-APOE2 in Mouse Model of Alzheimer's Disease and other Tauopathies

[0934] A nucleic acid encoding human APOE2 (apolipoprotein E2 allele) is engineered into an AAV viral genome and packaged in the VOY101 capsid.

[0935] The AAV-APOE2 viral genome, recited 5' to 3' from ITR to ITR, comprises a wild type ITR, a promoter, the nucleic acid encoding human APOE2, a polyA sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and

formulated. The VOY101-APOE2 particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0936] Three groups of APP.PS1-21/TRE4 mice, approximately 20 mice/group, at 9 months of age, are administered vehicle (PBS with 0.001% F-68), or VOY101-APOE2 at either high or low dose levels (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) via intravenous tail vein injection.

[0937] To test the efficacy, distribution and expression of VOY101-APOE2 in mice, any test known in the art may be utilized. Non-limiting examples include measurements of body weight, expression of APOE2 as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of amyloid-beta pathology as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of neurodegeneration as assessed by immunohistochemistry, and vector genome levels as measured by digital droplet PCR.

[0938] All animals are evaluated for body weight and survival. Animals are euthanized at approximately 11 months of age for evaluation of brain, spinal cord, and liver samples for APOE2 expression, amyloid and/or tau pathology, and neurodegeneration.

[0939] Distribution of the vector genome through the brain in animals receiving intravenous VOY101-APOE2 is analyzed by PCR. Expression data will likely show widespread expression of APOE2 throughout the brain in animals receiving VOY101-APOE2 vector. Brain regions demonstrating significant APOE2 expression would likely cover areas important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Groups receiving VOY101-APOE2 vector should show strong reductions in pathological amyloid-beta and/or tau and neurodegeneration.

B. In Vivo Distribution and Expression Study of Intravenous Dosing of VOY101-APOE2 in Non-Human Primates

[0940] A nucleic acid sequence encoding human APOE2 (apolipoprotein E 2 allele) is engineered into an AAV viral genome and packaged in the VOY101 capsid.

[0941] The AAV-APOE2 viral genome, recited 5' to 3' from ITR to ITR, comprises a wild type ITR, a promoter, the nucleic acid encoding human APOE2, a polyA sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-APOE2 particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0942] Non-human primates (NHPs) (Cynomolgus macaques, adult male, prescreened for AAV neutralizing antibodies) in three groups are administered, by intravenous injection, the VOY101-APOE2 vector with one group a vehicle only control (PBS with 0.001% F-68). The NHPs are administered either high or low dose levels (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) using intravenous delivery. 4 weeks post-administration, a saline perfusion is performed and the brain sectioned into 3 mm coronal blocks and snap-frozen.

[0943] Any test known in the art may be utilized to test the efficacy, distribution and expression of VOY101-APOE2 in NHP. Non-limiting examples include measurement of expression of APOE2 as assessed by immunohistochemistry and enzyme-linked immunosorbent assay and vector genome levels as assessed by digital droplet PCR.

[0944] Expression data will likely show widespread expression of APOE2 throughout the brain in animals receiving VOY101-APOE2 vector. Brain regions demonstrating significant APOE2 levels would likely cover areas important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Consistent with the expression data, PCR would likely demonstrate widespread distribution of vector genome through the brain.

EXAMPLE 8. VOY101-HTT miRNA for the treatment of Huntington's Disease

A. In Vivo Efficacy Study of VOY101-miRNA in Mouse Model of Huntington's Disease

[0945] Selected pri-miRNA cassettes containing guide strands targeting HTT and passenger strands are engineered into scAAV-miRNA viral genomes and packaged into VOY101 capsid.

[0946] The viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a CBA promoter (which includes a CMVie enhancer, a CBA promoter and an SV40 intron), the pri-miRNA cassette containing a guide sequence targeting HTT and a passenger sequence, a rabbit globin polyA sequence, a fragment of human alpha-1 antitrypsin as a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-HTT miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0947] Bilateral intrastriatal dosing will be used. Three groups of approximately 12 mice/group, approximately 2 months of age and balanced for sex, will receive vehicle (PBS and 0.001% F-68), or VOY101-HTT miRNA vector at either high or low dose levels (approximately 3×10^{9} vg – 5×10^{10} vg per striatum).

[0948] To test the efficacy of VOY101-HTT miRNA in mice, any test known in the art may be utilized. Non-limiting examples include measurement of body weight, rotarod,

Porsolt swim test, as well as measurement of HTT protein aggregates as assessed by immunohistochemistry.

[0949] All animals will be evaluated for body weight, rotarod, Porsolt swim test and survival. Some animals will be euthanized at 5 months of age (3 months after dosing) for evaluation of striatum tissue samples for HTT mRNA suppression (by RT-qPCR) and HTT protein level by western blot or MSD assay, whereas others will be euthanized at approximately 8 months of age (6 months after dosing) for evaluation of aggregates (by immunohistochemistry).

[0950] HTT measurement data should show widespread reduction of human HTT protein and mRNA throughout the brain in animals receiving HTT miRNA vectors including in primary target areas (striatum and cortex). Groups receiving HTT miRNA vectors would also show reductions in pathological HTT aggregates, and demonstrate significant improvements in lifespan and motor activities.

B. In Vivo Pharmacology and Distribution Study in Non-Human Primates Following Intravenous Dosing of scVOY101-HTT miRNA

[0951] Selected pri-miRNA cassettes containing guide strands targeting HTT and passenger strands are engineered into scAAV-miRNA viral genomes and packaged into VOY101 capsid.

[0952] The scAAV-miRNA viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, the pri-miRNA cassette containing a guide sequence targeting HTT and a passenger sequence, a polyA sequence, a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-HTT miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0953] Non-human primates (NHPs) (rhesus macaque, adult male, prescreened for AAV neutralizing antibodies) in three groups are administered scVOY101-HTT miRNA particles. The NHPs are administered either high, middle or low dose levels (approximately 5×10^{12} vg/kg, 1.5×10^{13}vg/kg and 4.5×10^{13} vg/kg) using intravenous or intracarotid arterial delivery. 4 weeks post-administration, a saline perfusion is performed and part of the spinal cord, brain sections and selected peripheral tissues will be harvested. A subset of tissue will be snap-frozen in liquid nitrogen and a subset will be post-fixed in 4% PFA.

[0954] To test the efficacy of VOY101-HTT miRNA in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of expression of HTT mRNA

as measured by bDNA assay and/or qRT-PCR, expression of HTT protein as assessed by western blot and by immunohistochemistry, and vector genome levels as assessed by digital droplet PCR. In addition, clinical observation, serum and CSF clinical pathology, CSF biomarkers and histopathology of CNS and peripheral tissues will be analyzed.

EXAMPLE 9. VOY101-SOD1 miRNA for treatment of Amyotrophic Lateral Sclerosis

A. In Vivo pharmacology Study of VOY101-SOD1 miRNA in a Mouse Model of ALS

[0955] Selected pri-miRNA cassettes containing guide strands targeting SOD1 and passenger strands are engineered into scAAV-miRNA viral genomes and packaged into a VOY101 capsid.

[0956] The viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a H1 promoter, the pri-miRNA cassette containing a guide sequence targeting SOD1 and a passenger sequence, a rabbit globin polyA sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified, and formulated. The VOY101-SOD1 miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0957] Three groups of approximately 10 mice/group, approximately 40-50 days of age and balanced for sex, age and littermates, will receive vehicle (PBS with 0.001% F-68), or VOY101-SOD1 miRNA vector at either high or low dose levels (approximately 5 x 10^{11}vg/mouse or 2 x 10^{12}vg/mouse). All the animals will be dosed intravenously. All the animals will be euthanized at approximately 4 weeks after intravenous administration.

[0958] Analytical methods known in the art may be used to assess pharmacological profile, primary readouts will include hSOD1 mRNA and protein expression and vector genome biodistribution in multiple CNS regions and selected peripheral tissues. Secondary readouts will include body weights, immunohistochemistry and cage side observations.

B. In Vivo Efficacy Study of VOY101-SOD1 miRNA in a Mouse Model of ALS

[0959] Selected pri-miRNA cassettes containing guide strands targeting SOD1 and passenger strands are engineered into scAAV-miRNA viral genomes and packaged into a VOY101 capsid.

[0960] The scAAV-miRNA viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a H1 promoter, the pri-miRNA cassette containing a guide sequence targeting SOD1 and a passenger sequence, a rabbit globin polyA, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-SOD1 miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0961] Three groups of approximately 36 mice/group, approximately 40-50 days of age and balanced for sex, age and littermates, will receive vehicle, or the vector at either high or low dose levels (approximately $5x10^{11}$ vg/mouse or $2x10^{12}$ vg/mouse). All the animals will be dosed intravenously.

[0962] To assess efficacy of VOY101-SOD1 miRNA in mice, analytical methods known in the art may be used to obtain primary readouts and may include body weight, behavioral NeuroScore, survival and disease onset and duration. Neurological score will be measured daily. Animals will be euthanized when the NeuroScore for that animal reaches 4. Secondary readouts include hSOD1 mRNA/protein expression, vector genome biodistribution and IHC (skeletal muscle and NMJ imaging, spinal cord).

[0963] The data demonstrate that upon delivery of the intravenous VOY101-SOD1 miRNA vector to the motor neurons, brainstem and motor cortex widespread reduction of SOD1 protein and mRNA occurs.

C. In Vivo Efficacy Study of VOY101-SOD1 miRNA in Canine Degenerative Myelopathy as a Disease Model for ALS

[0964] Selected pri-miRNA cassettes containing guide strands targeting SOD1 and passenger strands are engineered into scAAV-miRNA viral genomes designed and packaged in a VOY101 capsid.

[0965] The scAAV-miRNA viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a H1 promoter, the pri-miRNA cassette containing a guide sequence targeting SOD1 and a passenger sequence, a rabbit globin polyA sequence, a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified, and formulated. The VOY101-SOD1 miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0966] Companion DM dogs will be screened for pre-existing immunity to the VOY101 capsid by evaluating serum samples in an in vitro neutralizing antibody assay. Dogs with negative nAb will be candidates for the study. Dogs will be divided into two treatment groups and administered either VOY101-SOD1 miRNA or vehicle (PBS with 0.001% F-68) using intravenous dosing.

[0967] To assess efficacy of VOY101-SOD1 miRNA in dog, any test known in the art may be utilized. Non-limiting examples include longitudinal monitoring of gait and neurologic outcome, DTI and MRS, electrodiagnostic testing, MUNE and electrical Impedance Myography (EIM) at the specified time points.

[0968] Serum and CSF samples will be collected at designated times and at the time of euthanasia for evaluating pNF-H and NFL level in dogs. At the time of euthanasia, CNS and peripheral tissues will be collected for SOD1 mRNA quantification and vector genome biodistribution analysis.

[0969] The data demonstrate that upon delivery of the intravenous VOY101-SOD1 miRNA vector to the motor neurons, brainstem and motor cortex reduction of SOD1 protein and mRNA occurs.

D. In Vivo pharmacology and Distribution Study in Non-Human Primates following Intravenous Dosing of scVOY101-SOD1 miRNA

[0970] Selected pri-miRNA cassettes containing guide strands targeting SOD1 and passenger strands are engineered into scAAV-miRNA viral genomes and packaged into a VOY101 capsid.

[0971] The scAAV-miRNA viral genomes from ITR to ITR, recited 5' to 3', comprise a wild type ITR, a promoter, the pri-miRNA cassette containing a guide sequence targeting SOD1 and a passenger sequence, a polyA sequence, a stuffer sequence, and wild type ITR. The viral genomes are packaged into VOY101 capsids, purified, and formulated. The VOY101-SOD1 miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0972] Non-human primates (NHPs) (Cynomolgus macaques, adult male, prescreened for AAV neutralizing antibodies) in three groups are administered sc VOY101-SOD1 miRNA vector. The NHPs are administered either high, middle or low dose levels (approximately 5 x 10^{12} vg/kg, 1.5 x 10^{13}vg/kg and 4.5 x 10^{13} vg/kg) using intravenous delivery. 4 weeks post-administration, a saline perfusion is performed and part of the spinal cord, brain sections and selected peripheral tissues will be harvested. A subset of the collected tissues will be snap-frozen in liquid nitrogen and another subset will be post-fixed in 4% PFA.

[0973] To determine efficacy and distribution in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of expression of SOD1 mRNA by qRT-PCR, expression of SOD1 protein as assessed by WB and by immunohistochemistry, and vector genome levels as assessed by digital droplet PCR. In addition, clinical observation, serum and CSF clinical pathology, CSF biomarkers and histopathology of CNS and peripheral tissues will be analyzed.

[0974] The data demonstrate that upon intravenous delivery of the VOY101-SOD1 miRNA vector to the spinal cord motor neurons, brainstem and motor cortex, reduction of SOD1 protein and mRNA occurs.

EXAMPLE 10. Anti-tau antibody delivery for the treatment of Alzheimer's Disease and other tauopathies

A. In Vivo Distribution, Expression and Efficacy Study of Intravenous Dosing of VOY101-anti-Tau antibody in a Mouse Model of Alzheimer's Disease and other Tauopathies

[0975] A nucleic acid encoding a monoclonal antibody targeting tau is engineered into an AAV viral genome and produced in the VOY101 capsid.

[0976] The viral genome, recited 5' to 3' from ITR to ITR, comprises a wild type ITR, a promoter, the nucleic acid encoding a monoclonal antibody targeting tau, a polyA sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-anti Tau antibody particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0977] Three groups of P301S mice, approximately 20 mice/group, at 2 months of age, are administered vehicle (PBS with 0.001% F-68), or VOY101-anti Tau antibody vector at either high or low dose levels (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) via intravenous tail vein injection.

[0978] To test the efficacy, distribution and expression of VOY101-anti Tau antibody in mice, any test known in the art may be utilized. Non-limiting examples include measurement of body weight, rotarod, expression of anti-Tau antibody as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of pathogenic tau as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of neurodegeneration as assessed by immunohistochemistry, and vector genome levels as measured by digital droplet PCR. All animals are evaluated for body weight and survival. Animals are euthanized at approximately 5 months of age for evaluation of brain, spinal cord, and liver samples for antibody expression, tau pathology, and neurodegeneration.

[0979] In the case that VOY101-anti Tau antibody delivery for the treatment of Alzheimer Disease and tauopathy is successful, one might anticipate PCR data to demonstrate delivery of vector genome throughout the brain in animals receiving intravenous VOY101-anti-Tau antibody vector. Expression data will also likely show widespread expression of anti-Tau antibody throughout the brain in animals receiving vector, at levels equal to or exceeding that following passive immunization. Brain regions expected to demonstrate significant antibody

levels include areas important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Groups receiving VOY101-anti Tau antibody vector are expected to show strong reductions in pathological tau and neurodegeneration, and demonstrate significant improvements in lifespan and rotarod performance.

B. In Vivo Distribution and Expression Study of Intravenous Dosing of VOY101-anti-Tau antibody in Non-Human Primates

[0980] A nucleic acid encoding a monoclonal antibody targeting tau is engineered into an AAV viral genome and produced in the VOY101 capsid.

[0981] The viral genome, recited 5' to 3' from ITR to ITR, comprises a wild type ITR, a promoter, the nucleic acid encoding a monoclonal antibody targeting tau, a polyA sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-anti Tau particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0982] Non-human primates (NHPs) (Cynomolgus macaques, adult male, prescreened for AAV neutralizing antibodies) in three groups are administered the VOY101-anti-Tau vector with one group a vehicle only control (PBS with 0.001% F-68). The NHPs are administered either high or low dose levels (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) using intravenous delivery. 4 weeks post-administration, a saline perfusion is performed and the brain sectioned into 3 mm coronal blocks and snap-frozen.

[0983] To test the efficacy, distribution and expression of VOY101-anti Tau antibody in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of expression of anti-Tau antibody as assessed by immunohistochemistry and enzyme-linked immunosorbent assay and vector genome levels as assessed by digital droplet PCR.

[0984] One might anticipate expression data to show that anti-Tau antibody is expressed widely in the NHP brain at levels exceeding that following passive immunization. Brain regions expected to demonstrate significant antibody levels include areas important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Consistent with the expression data, PCR would likely demonstrate widespread distribution of vector genome through the brain.

EXAMPLE 11. VOY101-Tau miRNA for treatment of tauopathy

A. In Vivo Distribution, Expression, and Efficacy Study of Intravenous Dosing of scVOY101-Tau miRNA in a Mouse Model of Tauopathy

[0985] Selected pri-miRNA cassettes containing guide strands targeting Tau and passenger strands are engineered into scAAV-miRNA viral genomes and packaged into a VOY101 capsid.

[0986] The scAAV-miRNA viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, the pri-miRNA cassette containing a guide sequence targeting Tau and a passenger sequence, a polyA sequence, a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-Tau miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0987] Three groups of P301S mice, approximately 20 mice/group, at 2 months of age, are administered vehicle (PBS with 0.001% F-68), or VOY101-Tau miRNA vector at either high or low dose levels (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) via intravenous tail vein injection.

[0988] To test the efficacy, distribution and expression of VOY101-Tau miRNA in mice, any test known in the art may be utilized. Non-limiting examples include measurement of body weight, rotarod, expression of tau mRNA as measured by qRT-PCR, expression of total human tau as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of pathogenic tau as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, levels of neurodegeneration as assessed by immunohistochemistry, and vector genome levels as measured by digital droplet PCR.

[0989] All animals are evaluated for body weight and survival. Animals are euthanized at approximately 5 months of age for evaluation of brain, spinal cord, and liver samples for Tau mRNA expression, tau pathology, and neurodegeneration.

[0990] In the case that VOY101-Tau miRNA delivery for the treatment of tauopathy is successful, one might anticipate PCR data to demonstrate delivery of vector genome throughout the brain in animals receiving intravenous VOY101-Tau miRNA vector. Expression data would also be expected to show widespread reduction of human tau protein and mRNA throughout the brain in animals receiving VOY101-Tau miRNA vector. Brain regions likely to demonstrate significant tau reduction include areas important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Groups receiving VOY101-Tau miRNA vector would likely show strong reductions in pathological tau and neurodegeneration, and demonstrate significant improvements in lifespan and rotarod performance.

B. In Vivo Distribution and Expression Study of Tau in Non-Human Primates following Intravenous Dosing of scVOY101-Tau miRNA

[0991] Selected pri-miRNA cassettes containing guide strands targeting Tau and passenger strands are engineered into scAAV-miRNA viral genomes and packaged into a VOY101 capsid.

[0992] The viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, the pri-miRNA cassette containing guide sequence targeting Tau and passenger sequence, a polyA sequence, a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated. The VOY101-Tau miRNA particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0993] Non-human primates (NHPs) (Cynomolgus macaques, adult male, prescreened for AAV neutralizing antibodies) in three groups are administered the scVOY101-Tau miRNA with one group a vehicle only control (PBS with 0.001% F-68). The NHPs are administered either high or low dose levels of VOY101-Tau miRNA (approximately 4×10^{12} vg/kg – 4×10^{13} vg/kg) using intravenous delivery. 4 weeks post-administration, a saline perfusion is performed and the brain sectioned into 3 mm coronal blocks and snap-frozen.

[0994] To test the distribution and expression of VOY101-Tau miRNA in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of expression of tau mRNA by qRT-PCR, expression of tau protein as assessed by immunohistochemistry and enzyme-linked immunosorbent assay, and vector genome levels as assessed by digital droplet PCR.

[0995] One might expect expression data to show that tau protein and mRNA is reduced widely in the brain. Brain regions likely to demonstrate significant tau reduction include areas important for tauopathy related disease, including the entorhinal cortex, hippocampus, and cortex. Consistent with the expression data, PCR would likely demonstrate widespread distribution of vector genome through the brain.

EXAMPLE 12. VOY101-ATP2A2 for the treatment of Cardiovascular Disease (e.g., Heart Failure)

A. In Vivo Distribution, Expression and Efficacy Study with Intravenous Dosing of VOY101-ATP2A2 in a Mouse Model of Cardiovascular Disease

[0996] Selected viral genomes comprising a nucleic acid encoding human ATP2A2 are designed and packaged into a single stranded VOY101 capsid.

[0997] The viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, hATP2A2 cDNA sequence, a human growth hormone polyA sequence, a fragment of human albumin as a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[0998] Six groups of approximately 10 mice/group, at 7 weeks of age, and balanced for gender and litter, receive vehicle (PBS with 0.001% F-68; two groups), or VOY101-ATP2A2 vector at either low (2 groups) or high dose (2 groups) levels (approximately 6.3×10^{12} vg/kg – 2×10^{13} vg/kg body weight) via intravenous injection.

[0999] To test the efficacy, distribution and expression of VOY101-ATP2A2 in mice, any test known in the art may be utilized. Non-limiting examples include limb electromyography, notched bar walking test, string hanging test, rotarod test, body weight, and/or survival. Other readouts include ATP2A2 protein and mRNA expression in tissues (e.g. dorsal root ganglia, heart (e.g., cardiomyocytes), cerebellum, spinal cord) by ELISA, PCR, immunohistochemistry and in situ hybridization, and in situ assessment of mitochondrial enzyme function in tissue (dorsal root ganglia) sections. Vector genome levels in different tissues are determined by PCR and ISH.

[1000] Three groups of animals (vehicle, low dose, high dose) are euthanized by 18 weeks. Three remaining groups of animals (vehicle, low dose, high dose) are maintained for 6 months or longer to assess effect on survival. Control groups (n=10/ group) include wild type mice and disease model mice dosed with a reference vector.

[1001] The distribution and expression of human ATP2A2 and vector genome distribution in target tissues such as, but not limited to, DRGs, cerebellum, spinal cord and heart in animals receiving the hATP2A2 vector, is measured by ELISA, PCR, ISH, IHC for hATP2A2 expression and PCR and ISH for vector genome analysis. Human ATP2A2 analysis (by ELISA, PCR, ISH, IHC) demonstrate that upon the delivery of the hATP2A2 vector, expression in target tissues e.g., heart occurs with distribution of the viral genome to target tissues. *In situ* assessment of mitochondrial enzyme activity shows that upon delivery of the hATP2A2 vector, increased activity in slices of heart occurs. Electromyography, notched bar, string hanging and rotarod tests demonstrate improved performance over vehicle control animals.

B. In Vivo Distribution and Expression Study with Intravenous Dosing of VOY101-ATP2A2 in Non-Human Primates

[1002] Selected viral genomes comprising a nucleic acid sequence encoding human ATP2A2 are designed and packaged in a single stranded (ss) VOY101 capsid.

[1003] The single stranded viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, hATP2A2 cDNA sequence, a human growth hormone polyA sequence, a fragment of human albumin as a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[1004] Eight groups of approximately 3 cynomolgus monkeys/group, approximately 3 years of age or older, with at least one animal of each gender per group, receive vehicle (PBS with 0.001% F-68; two groups), or VOY101-ATP2A2 vector at either low (2 groups) or high dose (2 groups) levels (approximately 6.7×10^{12} vg/kg – 6×10^{13} vg/kg body weight) via intravenous injection.

[1005] To test the efficacy, distribution and expression of VOY101-ATP2A2 in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of body weight over time, clinical monitoring, histopathology and blood safety panel testing. Other readouts include ATP2A2 protein and mRNA expression in tissues (e.g. heart) as assessed by ELISA, PCR, immunohistochemistry and in situ hybridization. Vector genome levels in different tissues are determined by PCR and ISH.

[1006] Three groups of animals (vehicle, low dose, high dose) are euthanized by 4 weeks. Three remaining groups of animals (vehicle, low dose, high dose) are maintained for 12 weeks to assess long term gene expression.

[1007] The distribution and expression of human ATP2A2 (hATP2A2) and vector genome distribution in target tissues such as, but not limited to, heart in animals receiving the hATP2A2 vector, is measured by ELISA, PCR, ISH, IHC for hATP2A2 expression and PCR and ISH for vector genome analysis. The primate ATP2A2 expression data are compared to the ATP2A2 expression level which resulted in rescue of the cardiovascular disease phenotype in a genetic mouse model of cardiovascular disease. Based on these results, efficacious doses for human trials are calculated.

EXAMPLE 13. VOY101-S100A1 for the treatment of Cardiovascular Disease (e.g., Heart Failure)

A. In Vivo Distribution, Expression and Efficacy Study with Intravenous Dosing of VOY101-S100A1 in a Mouse Model of Cardiovascular Disease

[1008] Selected viral genomes comprising a nucleic acid encoding human S100A1 are designed and packaged into a single stranded VOY101 capsid.

[1009] The viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, hS100A1 cDNA sequence, a human growth hormone polyA sequence, a fragment of human albumin as a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[1010] Six groups of approximately 10 mice/group, at 7 weeks of age, and balanced for gender and litter, receive vehicle (PBS with 0.001% F-68; two groups), or VOY101-S100A1 vector at either low (2 groups) or high dose (2 groups) levels (approximately 6.3×10^{12} vg/kg – 2×10^{13} vg/kg body weight) via intravenous injection.

[1011] To test the efficacy, distribution and expression of VOY101-S100A1 in mice, any test known in the art may be utilized. Non-limiting examples include limb electromyography, notched bar walking test, string hanging test, rotarod test, body weight, and/or survival. Other readouts include S100A1 protein and mRNA expression in tissues (e.g. dorsal root ganglia, heart (e.g., cardiomyocytes), cerebellum, spinal cord) by ELISA, PCR, immunohistochemistry and *in situ* hybridization, and in situ assessment of mitochondrial enzyme function in tissue (dorsal root ganglia) sections. Vector genome levels in different tissues are determined by PCR and ISH.

[1012] Three groups of animals (vehicle, low dose, high dose) are euthanized by 18 weeks. Three remaining groups of animals (vehicle, low dose, high dose) are maintained for 6 months or longer to assess effect on survival. Control groups (n=10/ group) include wild type mice and disease model mice dosed with a reference vector.

[1013] The distribution and expression of human S100A1 and vector genome distribution in target tissues such as, but not limited to, DRGs, cerebellum, spinal cord and heart in animals receiving the hS100A1 vector, are measured by ELISA, PCR, ISH, IHC for hS100A1 expression and PCR and ISH for vector genome analysis. Human S100A1 analysis (by ELISA, PCR, ISH, IHC) demonstrate that upon the delivery of the hS100A1 vector, expression in target tissues e.g., heart occurs with distribution of the viral genome to target tissues. *In situ* assessment of mitochondrial enzyme activity shows that upon delivery of the hS100A1 vector, increased activity in slices of heart occurs. Electromyography, notched bar, string hanging and rotarod tests demonstrate improved performance over vehicle control animals.

B. In Vivo Distribution and Expression Study with Intravenous Dosing of VOY101- S100A1 in Non-Human Primates

[1014] Selected viral genomes comprising a nucleic acid sequence encoding human S100A1 are designed and packaged in a single stranded (ss) VOY101 capsid.

[1015] The single stranded viral genome from ITR to ITR, recited 5' to 3', comprises a wild type ITR, a promoter, hS100A1 cDNA sequence, a human growth hormone polyA sequence, a fragment of human albumin as a stuffer sequence, and a wild type ITR. The viral genomes are packaged into VOY101 capsids, purified and formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[1016] Eight groups of approximately 3 cynomolgus monkeys/group, approximately 3 years of age or older, with at least one animal of each gender per group, receive vehicle (PBS with 0.001% F-68; two groups), or VOY101-S100A1 vector at either low (2 groups) or high dose (2 groups) levels (approximately 6.7×10^{12} vg/kg – 6×10^{13} vg/kg body weight) via intravenous injection.

[1017] To test the efficacy, distribution and expression of VOY101-S100A1 in NHP, any test known in the art may be utilized. Non-limiting examples include measurement of body weight over time, clinical monitoring, histopathology and blood safety panel testing. Other readouts include S100A1 protein and mRNA expression in tissues (e.g. heart) as assessed by ELISA, PCR, immunohistochemistry and in situ hybridization. Vector genome levels in different tissues are determined by PCR and ISH.

[1018] Three groups of animals (vehicle, low dose, high dose) are euthanized by 4 weeks. Three remaining groups of animals (vehicle, low dose, high dose) are maintained for 12 weeks to assess long term gene expression.

[1019] The distribution and expression of human S100A1 (hS100A1) and vector genome distribution in target tissues such as, but not limited to, heart in animals receiving the hS100A1 vector, are measured by ELISA, PCR, ISH, IHC for hS100A1 expression and PCR and ISH for vector genome analysis. The primate S100A1 expression data are compared to the S100A1expression level which resulted in rescue of the cardiovascular disease phenotype in a genetic mouse model of cardiovascular disease. Based on these results, efficacious doses for human trials are calculated.

EXAMPLE 14. Anti-tau antibody delivery for the treatment of Alzheimer's Disease and other tauopathies

A. In Vivo Distribution, Expression and Efficacy Study of Intravenous Dosing of VOY101 or VOY201-anti-Tau antibody

[1020] A nucleic acid encoding the monoclonal antibody PHF-1 targeting tau was engineered into an AAV viral genome and produced in the VOY101 capsid (capsid sequence provided as SEQ ID NO: 1809) or VOY201 capsid (capsid sequence provided as SEQ ID NO: 1810).

[1021] The viral genome, recited 5' to 3' from ITR to ITR, comprised a wild type ITR, a promoter, the nucleic acid encoding the monoclonal antibody PHF-1 targeting tau (kozak, heavy chain, linker region, light chain and stop codon provided as SEQ ID NO: 1816), a polyA sequence, and a wild type ITR. The viral genomes were packaged into VOY101 or VOY201 capsids, purified and formulated. The VOY101 or VOY201-anti Tau antibody particles were formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[1022] Three groups of wild type (WT) mice, approximately 5 mice/group, at 2 months of age, were administered vehicle (PBS with 0.001% F-68), VOY101-anti Tau antibody vector at 1.4 x 10^{13} vg/kg, or VOY201-anti Tau antibody vector at 1.4 x 10^{13} vg/kg via intravenous tail vein injection.

[1023] Approximately 28 days following AAV particle administration, several tissue samples were collected. Vector genome digital PCR quantification was performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host TFRC, and expressed in vector genome per cell (VG/Cell). Vector genome distribution is shown in Table 21 for VOY101.PHF-1 and VOY201.PHF-1. In Table 21, Hp is the hippocampus, SC-C is the cervical spinal cord, SC-T is the thoracic spinal cord, and SC-L is the lumbar spinal cord.

Table 21. Viral Genome Distribution in WT Mice after Intravenous Injection

Vector (Dose: 1.4 × 10^{13} VG/kg)	VG/Cell Distribution (Standard Dev. in Parenthesis)				
	Hp	SC-C	SC-T	SC-L	Brainstem
Vehicle	0.06 (0.54)	0.01 (0.13)	0.01 (0.14)	0.003 (0.002)	0.02 (0.19)
VOY101.PHF-1	11.01 (6.22)	15.45 (8.20)	17.82 (9.67)	18.59 (9.49)	29.80 (14.68)
VOY201.PHF-1	4.68 (1.48)	9.30 (2.42)	7.42 (2.6)	9.52 (2.2)	16.16 (4.76)

[1024] The expression levels of PHF-1, present in the soluble fraction of tissue lysates, were also measured in collected tissues by detecting the interaction with PHF tau coated on an ELISA plate. The antibody-antigen complex was visualized and quantified using HRP labeled anti-mouse IgG and its substrate TMB, followed by reading at OD450 on a plate reader and normalized to input tissue protein quantity. PHF1 expression from AAV

transduced cells is shown in Table 22 for VOY101.PHF-1 and VOY201.PHF-1. In Table 22, Hp is the hippocampus and SC spinal cord.

Table 22. PHF-1 Expression Distribution in WT Mice after Intravenous Injection

Vector (Dose: 1.4×10^{13} VG/kg)	PHF-1 Expression (ng/mg protein, Standard Dev. in Parenthesis)			
	Hp	Cortex	SC	Brainstem
Vehicle	0 (0)	0 (0)	0 (0)	0 (0)
VOY101.PHF-1	82 (36.4)	94 (35.6)	718 (440.8)	394.0 (301.3)
VOY201.PHF-1	96 (35.1)	66 (19.6)	361 (147.4)	207.0 (116.3)

[1025] IV dosing of PHF-1 in VOY201 resulted in up to 15-fold higher anti-tau antibody levels in mouse CNS as compared to passive immunization. The passive immunization level of antibody in brain is 20-40 ng/mg of protein, and VOY201 provided 2-5x fold above passive in the hippocampus, 5-10x fold above passive in the brain stem, and 8-16x fold above passive in the spinal cord. IV dosing of VOY101 and VOY201 resulted in widespread CNS biodistribution and transduction of vectorized antibodies.

[1026] Mouse brains were hemisected and tissue samples allocated for antibody immunohistochemistry then post-fixed in 4% paraformaldehyde overnight. PHF-1 antibody was detected by immunohistochemistry using anti-mouse IgG1 antibody (PHF-1 is a mouse IgG1 antibody). In animals dosed with 1.4×10^{13} vg/kg via intravenous tail vein injection of VOY101.PHF-1 or VOY201.PHF-1, staining was observed throughout the brain, including in the hippocampus, cortex, striatum, and thalamus. Numerous PHF1+ cells were observed, including those with neuronal and astroglial morphology. Vehicle-treated control exhibited essentially no detectable background staining

[1027] PHF-1 expression within the CNS after administration of 1.4×10^{13} vg/kg via intravenous tail vein injection of VOY101.PHF-1 or VOY201.PHF-1 was evaluated by mouse anti-IgG1 and anti-NeuN double labeling immunofluorescent staining. PHF-1 is a mouse IgG1 antibody, and is therefore detected by anti-IgG1 antibody staining. Colocalization studies showed multiple PHF1+ cells including those double-labeled with the neuronal marker (NeuN).

[1028] PHF-1 expression within the CNS after administration of 1.4×10^{13} vg/kg via intravenous tail vein injection of VOY101.PHF-1 was evaluated by mouse anti-IgG1 and anti-GFAP (glial fibrillary acidic protein) double labeling immunofluorescent staining. PHF-1 is a mouse IgG1 antibody, and is therefore detected by anti-IgG1 antibody staining.

Colocalization studies showed multiple PHF1+ cells including those double-labeled with the astrocytic marker (GFAP).

B. In Vivo Distribution, Expression and Efficacy Study of Intravenous Dosing of VOY101 or VOY201-anti-Tau antibody in a Mouse Model

[1029] Three groups of P301S mice, approximately 20 mice/group, at 2 months of age, were administered vehicle (PBS with 0.001% F-68), VOY101-anti Tau antibody vector (VOY101.PHF-1) at 1.4 x 10^{13} vg/kg, or VOY201-anti Tau antibody vector (VOY201.PHF-1) at 5.0 x 10^{13} vg/kg via intravenous tail vein injection.

[1030] Approximately 3 months following AAV particle administration, several tissue samples were collected. Vector genome digital PCR quantification was performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host TFRC, and expressed in vector genome per cell (VG/Cell). Vector genome distribution is shown in Table 23 for VOY101.PHF-1 and VOY201.PHF-1. In Table 23, Hp is the hippocampus and SC is the spinal cord.

Table 23. Vector Genome Distribution in P301S Mice after Intravenous Injection

Vector	VG/Cell Distribution (Standard Dev. in Parenthesis)				
	Hp	Cortex	Thalamus	SC	Brainstem
Vehicle	0.09 (0.17)	0.06 (0.07)	0.03 (0.04)	0.07 (0.11)	0.06 (0.06)
VOY101.PHF-1 (Dose: 1.4 × 10^{13} VG/kg)	26.17 (10.01)	32.13 (11.8)	55.16 (20.75)	49.82 (29.57)	59.9 (24.85)
VOY201.PHF-1 (Dose: 5.0 × 10^{13} VG/kg)	16.2 (8.28)	22.29 (11.1)	30.92 (17.9)	27.46 (20.51)	45.86 (30.53)

[1031] The expression levels of PHF1, present in the soluble fraction of tissue lysates, were also measured in collected tissues by detecting the interaction with PHF tau coated on an ELISA plate. The antibody-antigen complex was visualized and quantified using HRP labeled anti- mouse IgG and its substrate TMB, followed by reading at OD450 on a plate reader and normalized to input tissue protein quantity. PHF1 expression from AAV transduced cells is shown in Table 24 for VOY101.PHF-1 and VOY201.PHF-1. In Table 24, Hp is the hippocampus and SC spinal cord.

Table 24. PHF1 Expression in P301S Mice after Intravenous Injection

Vector	PHF1 Expression (ng/mg protein, Standard Dev. in Parenthesis)				
	Hp	Cortex	Thalamus	SC	Brainstem
Vehicle	0.96 (4.07)	0 (0)	0.79 (3.33)	0 (0)	0 (0)
VOY101.PHF-1 (Dose: 1.4 × 10^{13} VG/kg)	193.8 (115.3)	338.1 (176.9)	220.3 (100.9)	1103 (404.8)	1152 (630.3)
VOY201.PHF-1 (Dose: 5.0 × 10^{13} VG/kg)	140.8 (87.45)	238.6 (120.5)	210.6 (103.8)	902.5 (317)	619.3 (386.8)

[1032] IV dosing of VOY101 and VOY201 resulted in high levels of antibody to the CNS of P301 tauopathy mice. AT8 immunoreactivity (IR) is significantly reduced in the PHF1-

treated mice. IV dosing using VOY101 and VOY201 resulted in widespread CNS biodistribution and transduction of vectorized antibodies in P301S tauopathy mice.

EXAMPLE 15. Anti-tau antibody delivery for treatment of tauopathies including Alzheimer's Disease

A. In Vivo Distribution, Expression and Efficacy Study of Intravenous Dosing of VOY101 or VOY201-anti-Tau antibody

[1033] A nucleic acid encoding the monoclonal antibody PHF-1 targeting tau is engineered into an AAV viral genome and produced in the VOY101 capsid (capsid sequence provided as SEQ ID NO: 1809) or VOY201 capsid (capsid sequence provided as SEQ ID NO: 1810).

[1034] The viral genome, recited 5' to 3' from ITR to ITR, comprises a wild type ITR, a promoter, the nucleic acid encoding the monoclonal antibody PHF-1 targeting tau (light chain (SEQ ID NO: 1819), linker region, heavy chain (SEQ ID NO: 1814) and stop codon), a polyA sequence, and a wild type ITR. The viral genomes are packaged into VOY101 or VOY201 capsids, purified and formulated. The VOY101 or VOY201-anti Tau antibody particles are formulated in phosphate buffered saline (PBS) with 0.001% F-68.

[1035] Three groups of wild type (WT) mice, approximately 5 mice/group, at 2 months of age, are administered vehicle (PBS with 0.001% F-68), VOY101-anti Tau antibody vector at 1.4×10^{13} vg/kg, or VOY201-anti Tau antibody vector at 1.4×10^{13} vg/kg via intravenous tail vein injection.

[1036] Approximately 28 days following AAV particle administration, several tissue samples are collected. Vector genome digital PCR quantification is performed using a probe set against the CMV enhancer region of the CBA promoter, normalized to host TFRC, and expressed in vector genome per cell (VG/Cell).

[1037] The expression levels of PHF1, present in the soluble fraction of tissue lysates, are also measured in collected tissues by detecting the interaction with PHF tau coated on an ELISA plate. The antibody-antigen complex is visualized and quantified using HRP labeled anti-mouse IgG and its substrate TMB, followed by reading at OD450 on a plate reader and normalized to input tissue protein quantity.

[1038] Mouse brains are hemisected and tissue samples allocated for antibody immunohistochemistry. The samples are post-fixed in 4% paraformaldehyde overnight. PHF-1 antibody is detected by immunohistochemistry using anti-mouse IgG1 antibody (PHF-1 is a mouse IgG1 antibody).

[1039] PHF-1 expression within the CNS after administration of 1.4 x 10^{13} vg/kg via intravenous tail vein injection of VOY101.PHF1 or VOY201.PHF-1 is evaluated by mouse anti-IgG1 and anti-NeuN or GFAP (glial fibrillary acidic protein) double labeling immunofluorescent staining. PHF-1 is a mouse IgG1 antibody, and is therefore detected by anti-IgG1 antibody staining.

B. In Vivo Distribution, Expression and Efficacy Study of Intravenous Dosing of VOY101 or VOY201-anti-Tau antibody in a Mouse Model

[1040] Three groups of P301S mice, approximately 20 mice/group, at 2 months of age, are administered vehicle (PBS with 0.001% F-68), VOY101-anti Tau antibody vector (VOY101.PHF-1) at 1.4 x 10^{13} vg/kg, or VOY201-anti Tau antibody vector (VOY201.PHF-1) at 5.0 x 10^{13} vg/kg via intravenous tail vein injection.

[1041] Approximately 3 months following AAV particle administration, several tissue samples are collected. Vector genome digital PCR quantification is performed using a probe set against the promoter, normalized to host TFRC, and expressed in vector genome per cell (VG/Cell).

[1042] The expression levels of PHF1, present in the soluble fraction of tissue lysates, are also measured in collected tissues by detecting the interaction with paired helical filamentous tau coated on an ELISA plate. The antibody-antigen complex is visualized and quantified using HRP labeled anti- mouse IgG and its substrate TMB, followed by reading at OD450 on a plate reader and normalized to input tissue protein quantity.

VIII. EQUIVALENTS AND SCOPE

[1043] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments in accordance with the invention described herein. The scope of the present invention is not intended to be limited to the above Description, but rather is as set forth in the appended claims.

[1044] In the claims, articles such as "a," "an," and "the" may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include "or" between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The invention includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The invention

includes embodiments in which more than one, or the entire group members are present in, employed in, or otherwise relevant to a given product or process.

[1045] It is also noted that the term "comprising" is intended to be open and permits but does not require the inclusion of additional elements or steps. When the term "comprising" is used herein, the term "consisting of" is thus also encompassed and disclosed.

[1046] Where ranges are given, endpoints are included. Furthermore, it is to be understood that unless otherwise indicated or otherwise evident from the context and understanding of one of ordinary skill in the art, values that are expressed as ranges can assume any specific value or subrange within the stated ranges in different embodiments of the invention, to the tenth of the unit of the lower limit of the range, unless the context clearly dictates otherwise.

[1047] In addition, it is to be understood that any particular embodiment of the present invention that falls within the prior art may be explicitly excluded from any one or more of the claims. Since such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if the exclusion is not set forth explicitly herein. Any particular embodiment of the compositions of the invention (e.g., any antibiotic, therapeutic or active ingredient; any method of production; any method of use; etc.) can be excluded from any one or more claims, for any reason, whether or not related to the existence of prior art.

[1048] It is to be understood that the words which have been used are words of description rather than limitation, and that changes may be made within the purview of the appended claims without departing from the true scope and spirit of the invention in its broader aspects.

[1049] While the present invention has been described at some length and with some particularity with respect to the several described embodiments, it is not intended that it should be limited to any such particulars or embodiments or any particular embodiment, but it is to be construed with references to the appended claims so as to provide the broadest possible interpretation of such claims in view of the prior art and, therefore, to effectively encompass the intended scope of the invention.

[1050] All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, section headings, the materials, methods, and examples are illustrative only and not intended to be limiting.

CLAIMS

We claim:

1. An adeno-associated viral (AAV) particle comprising a capsid and a viral genome, wherein said capsid penetrates the blood brain barrier following delivery of the AAV particle.

2. The AAV particle of claim 1, wherein the AAV particle comprises a capsid or peptide insert selected from the group consisting of VOY101, VOY201, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5 (G2B5), PHP.S, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25,

AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47, AAVrh.69, AAVrh.45, AAVrh.59, AAVhu.12, AAVH6, AAVLK03, AAVH-1/hu.1, AAVH-5/hu.3, AAVLG-10/rh.40, AAVLG-4/rh.38, AAVLG-9/hu.39, AAVN721-8/rh.43, AAVCh.5, AAVCh.5R1, AAVcy.2, AAVcy.3, AAVcy.4, AAVcy.5, AAVCy.5R1, AAVCy.5R2, AAVCy.5R3, AAVCy.5R4, AAVcy.6, AAVhu.1, AAVhu.2, AAVhu.3, AAVhu.4, AAVhu.5, AAVhu.6, AAVhu.7, AAVhu.9, AAVhu.10, AAVhu.11, AAVhu.13, AAVhu.15, AAVhu.16, AAVhu.17, AAVhu.18, AAVhu.20, AAVhu.21, AAVhu.22, AAVhu.23.2, AAVhu.24, AAVhu.25, AAVhu.27, AAVhu.28, AAVhu.29, AAVhu.29R, AAVhu.31, AAVhu.32, AAVhu.34, AAVhu.35, AAVhu.37, AAVhu.39, AAVhu.40, AAVhu.41, AAVhu.42, AAVhu.43, AAVhu.44, AAVhu.44R1, AAVhu.44R2, AAVhu.44R3, AAVhu.45, AAVhu.46, AAVhu.47, AAVhu.48, AAVhu.48R1, AAVhu.48R2, AAVhu.48R3, AAVhu.49, AAVhu.51, AAVhu.52, AAVhu.54, AAVhu.55, AAVhu.56, AAVhu.57, AAVhu.58, AAVhu.60, AAVhu.61, AAVhu.63, AAVhu.64, AAVhu.66, AAVhu.67, AAVhu.14/9, AAVhu.t 19, AAVrh.2, AAVrh.2R, AAVrh.8, AAVrh.8R, AAVrh.10, AAVrh.12, AAVrh.13, AAVrh.13R, AAVrh.14, AAVrh.17, AAVrh.18, AAVrh.19, AAVrh.20, AAVrh.21, AAVrh.22, AAVrh.23, AAVrh.24, AAVrh.25, AAVrh.31, AAVrh.32, AAVrh.33, AAVrh.34, AAVrh.35, AAVrh.36, AAVrh.37, AAVrh.37R2, AAVrh.38, AAVrh.39, AAVrh.40, AAVrh.46, AAVrh.48, AAVrh.48.1, AAVrh.48.1.2, AAVrh.48.2, AAVrh.49, AAVrh.51, AAVrh.52, AAVrh.53, AAVrh.54, AAVrh.56, AAVrh.57, AAVrh.58, AAVrh.61, AAVrh.64, AAVrh.64R1, AAVrh.64R2, AAVrh.67, AAVrh.73, AAVrh.74, AAVrh8R, AAVrh8R A586R mutant, AAVrh8R R533A mutant, AAAV, BAAV, caprine AAV, bovine AAV, AAVhE1.1, AAVhEr1.5, AAVhER1.14, AAVhEr1.8, AAVhEr1.16, AAVhEr1.18, AAVhEr1.35, AAVhEr1.7, AAVhEr1.36, AAVhEr2.29, AAVhEr2.4, AAVhEr2.16, AAVhEr2.30, AAVhEr2.31, AAVhEr2.36, AAVhER1.23, AAVhEr3.1, AAV2.5T , AAV-PAEC, AAV-LK01, AAV-LK02, AAV-LK03, AAV-LK04, AAV-LK05, AAV-LK06, AAV-LK07, AAV-LK08, AAV-LK09, AAV-LK10, AAV-LK11, AAV-LK12, AAV-LK13, AAV-LK14, AAV-LK15, AAV-LK16, AAV-LK17, AAV-LK18, AAV-LK19, AAV-PAEC2, AAV-PAEC4, AAV-PAEC6, AAV-PAEC7, AAV-PAEC8, AAV-PAEC11, AAV-PAEC12, AAV-2-pre-miRNA-101 , AAV-8h, AAV-8b, AAV-h, AAV-b, AAV SM 10-2 , AAV Shuffle 100-1 , AAV Shuffle 100-3, AAV

Shuffle 100-7, AAV Shuffle 10-2, AAV Shuffle 10-6, AAV Shuffle 10-8, AAV Shuffle 100-2, AAV SM 10-1, AAV SM 10-8 , AAV SM 100-3, AAV SM 100-10, BNP61 AAV, BNP62 AAV, BNP63 AAV, AAVrh.50, AAVrh.43, AAVrh.62, AAVrh.48, AAVhu.19, AAVhu.11, AAVhu.53, AAV4-8/rh.64, AAVLG-9/hu.39, AAV54.5/hu.23, AAV54.2/hu.22, AAV54.7/hu.24, AAV54.1/hu.21, AAV54.4R/hu.27, AAV46.2/hu.28, AAV46.6/hu.29, AAV128.1/hu.43, true type AAV (ttAAV), UPENN AAV 10, Japanese AAV 10 serotypes, AAV CBr-7.1, AAV CBr-7.10, AAV CBr-7.2, AAV CBr-7.3, AAV CBr-7.4, AAV CBr-7.5, AAV CBr-7.7, AAV CBr-7.8, AAV CBr-B7.3, AAV CBr-B7.4, AAV CBr-E1, AAV CBr-E2, AAV CBr-E3, AAV CBr-E4, AAV CBr-E5, AAV CBr-e5, AAV CBr-E6, AAV CBr-E7, AAV CBr-E8, AAV CHt-1, AAV CHt-2, AAV CHt-3, AAV CHt-6.1, AAV CHt-6.10, AAV CHt-6.5, AAV CHt-6.6, AAV CHt-6.7, AAV CHt-6.8, AAV CHt-P1, AAV CHt-P2, AAV CHt-P5, AAV CHt-P6, AAV CHt-P8, AAV CHt-P9, AAV CKd-1, AAV CKd-10, AAV CKd-2, AAV CKd-3, AAV CKd-4, AAV CKd-6, AAV CKd-7, AAV CKd-8, AAV CKd-B1, AAV CKd-B2, AAV CKd-B3, AAV CKd-B4, AAV CKd-B5, AAV CKd-B6, AAV CKd-B7, AAV CKd-B8, AAV CKd-H1, AAV CKd-H2, AAV CKd-H3, AAV CKd-H4, AAV CKd-H5, AAV CKd-H6, AAV CKd-N3, AAV CKd-N4, AAV CKd-N9, AAV CLg-F1, AAV CLg-F2, AAV CLg-F3, AAV CLg-F4, AAV CLg-F5, AAV CLg-F6, AAV CLg-F7, AAV CLg-F8, AAV CLv-1, AAV CLv1-1, AAV Clv1-10, AAV CLv1-2, AAV CLv-12, AAV CLv1-3, AAV CLv-13, AAV CLv1-4, AAV Clv1-7, AAV Clv1-8, AAV Clv1-9, AAV CLv-2, AAV CLv-3, AAV CLv-4, AAV CLv-6, AAV CLv-8, AAV CLv-D1, AAV CLv-D2, AAV CLv-D3, AAV CLv-D4, AAV CLv-D5, AAV CLv-D6, AAV CLv-D7, AAV CLv-D8, AAV CLv-E1, AAV CLv-K1, AAV CLv-K3, AAV CLv-K6, AAV CLv-L4, AAV CLv-L5, AAV CLv-L6, AAV CLv-M1, AAV CLv-M11, AAV CLv-M2, AAV CLv-M5, AAV CLv-M6, AAV CLv-M7, AAV CLv-M8, AAV CLv-M9, AAV CLv-R1, AAV CLv-R2, AAV CLv-R3, AAV CLv-R4, AAV CLv-R5, AAV CLv-R6, AAV CLv-R7, AAV CLv-R8, AAV CLv-R9, AAV CSp-1, AAV CSp-10, AAV CSp-11, AAV CSp-2, AAV CSp-3, AAV CSp-4, AAV CSp-6, AAV CSp-7, AAV CSp-8, AAV CSp-8.10, AAV CSp-8.2, AAV CSp-8.4, AAV CSp-8.5, AAV CSp-8.6, AAV CSp-8.7, AAV CSp-8.8, AAV CSp-8.9, AAV CSp-9, AAV.hu.48R3, AAV.VR-355, AAV3B, AAV4, AAV5, AAVF1/HSC1, AAVF11/HSC11, AAVF12/HSC12, AAVF13/HSC13, AAVF14/HSC14, AAVF15/HSC15, AAVF16/HSC16, AAVF17/HSC17, AAVF2/HSC2, AAVF3/HSC3,

AAVF4/HSC4, AAVF5/HSC5, AAVF6/HSC6, AAVF7/HSC7, AAVF8/HSC8, and/or AAVF9/HSC9 and variants thereof.

3. The AAV particle of claim 2, wherein the capsid is VOY101.

4. The AAV particle of claim 3, wherein the amino acid sequence of the capsid is at least 95% identical to SEQ ID NO: 1.

5. The AAV particle of claim 4, wherein the amino acid sequence of the capsid is at least 99% identical to SEQ ID NO: 1.

6. The AAV particle of claim 5, wherein the amino acid sequence of the capsid is SEQ ID NO: 1.

7. The AAV particle of claim 3, wherein the nucleic acid sequence of the capsid is at least 95% identical to SEQ ID NO: 1809.

8. The AAV particle of claim 7, wherein the nucleic acid sequence of the capsid is at least 99% identical to SEQ ID NO: 1809.

9. The AAV particle of claim 8, wherein the nucleic acid sequence of the capsid is SEQ ID NO: 1809.

10. The AAV particle of claim 2, wherein the capsid is VOY201.

11. The AAV particle of claim 10, wherein the nucleic acid sequence of the capsid is at least 95% identical to SEQ ID NO: 1810.

12. The AAV particle of claim 11, wherein the nucleic acid sequence of the capsid is at least 99% identical to SEQ ID NO: 1810.

13. The AAV particle of claim 12, wherein the nucleic acid sequence of the capsid is SEQ ID NO: 1810.

14. The AAV particle of claim 2, wherein the peptide insert is AAVPHP.N.

15. The AAV particle of claim 2, wherein the peptide insert is AAVPHP.B.

16. The AAV particle of claim 2, wherein the peptide insert is AAVPHP.A.

17. The AAV particle of any of claims 1-16, wherein delivery is by intravenous administration.

18. The AAV particle of claim 17, that transduces CNS structures following intravenous administration.

19. The AAV particle of any of claims 1-16, wherein delivery is by intracarotid artery administration.

20. The AAV particle of claim 19, that transduces CNS structures following intracarotid artery administration.

21. The AAV particle of claim 18 or 20, wherein the CNS structures are one or more regions selected from the group consisting of brain, spinal cord, brainstem nuclei, cerebellum, cerebrum, motor cortex, caudate nucleus, thalamus, hypothalamus, cervical spinal cord, thoracic spinal cord, lumbar spinal cord, striatum, substantia nigra, hippocampus, amygdala and/or cerebral cortex.

22. The AAV particle of any of claims 1-21, wherein the viral genome comprises a nucleic acid sequence positioned between two inverted terminal repeats (ITRs), wherein said nucleic acid when expressed inhibits or suppresses the expression of a gene of interest in a cell, wherein said nucleic acid sequence comprises a sense strand sequence and an antisense strand sequence, and wherein said sense sequence and antisense strand sequence share a region of complementarity of at least four nucleotides in length.

23. The AAV particle of claim 22, wherein the nucleic acid sequence comprises a sense strand sequence and an antisense strand sequence of an siRNA duplex.

24. The AAV particle of claim 22, wherein the gene of interest is selected from the group consisting of SOD1, HTT, APOE and MAPT.

25. The AAV particle of claim 22, wherein the region of complementarity is at least 17 nucleotides in length.

26. The AAV particle of claim 25, wherein the region of complementarity is between 19 and 21 nucleotides in length.

27. The AAV particle of claim 26, wherein the region of complementarity is 19 nucleotides in length.

28. The AAV particle of claim 22, wherein the sense strand sequence and the antisense strand sequence are, independently, 30 nucleotides or less.

29. The AAV particle of claim 22, wherein at least one of the sense strand sequence and the antisense strand sequence comprise a 3' overhang of at least 1 nucleotide.

30. The AAV particle of claim 29, wherein at least one of the sense strand sequence and the antisense strand sequence comprise a 3' overhang of at least 2 nucleotides.

31. The AAV particle of claim 22, wherein the antisense strand is excised from the AAV particle at a rate of at least 80%.

32. The AAV particle of claim 22, wherein the antisense strand is excised from the AAV particle at a rate of at least 90%.

33. The AAV particle of claim 22, wherein the antisense strand is excised from the AAV particle at a rate of at least 95%.

34. The AAV particle of claim 22, wherein the antisense strand is excised from the AAV particle at a rate greater than the rate of excision of the sense strand.

35. The AAV particle of claim 34, where the rate of excision of the antisense strand is at least 2 times greater than the rate of excision of the sense strand.

36. The AAV particle of claim 34, where the rate of excision of the antisense strand is at least 5 times greater than the rate of excision of the sense strand.

37. The AAV particle of claim 34, where the rate of excision of the antisense strand is at least 10 times greater than the rate of excision of the sense strand.

38. The AAV particle of any of claims 1-21, wherein the viral genome comprises a nucleic acid sequence positioned between two inverted terminal repeats (ITRs), wherein said nucleic acid encodes a target protein and wherein when the nucleic acid is expressed the level of the target protein is increased in the cell.

39. The AAV particle of claim 38, wherein the target protein is an antibody, AADC, APOE2, or Frataxin.

40. A pharmaceutical composition comprising an AAV particle, said AAV particle comprising an AAV capsid and a viral genome, wherein said AAV capsid penetrates the blood brain barrier following delivery of the AAV particle.

41. The pharmaceutical composition of claim 40, wherein the AAV capsid is VOY101 or VOY201.

42. The pharmaceutical composition of claim 41, wherein the viral genome comprises a nucleic sequence encoding an siRNA molecule.

43. The pharmaceutical composition of claim 42, wherein the siRNA molecule targets a gene of interest, wherein the gene of interest is selected from the group consisting of SOD1, HTT, APOE, and MAPT.

44. The pharmaceutical composition of claim 41, wherein the viral genome comprises a nucleic acid encoding a target protein.

45. The pharmaceutical composition of claim 44, wherein the target protein is selected from the group consisting of an antibody, AADC, ApoE2, and Frataxin.

46. A method for decreasing or inhibiting the expression of a target gene of interest in a cell comprising administering to the cell a composition comprising an AAV particle of any of claims 1-37 or any of the compositions of claims 40-43.

47. The method of claim 46, wherein the cell is a mammalian cell.

48. The method of claim 47, wherein the mammalian cell is a cell of the CNS.

49. A method for increasing the expression of a gene of interest in a cell comprising administering to the cell a composition comprising an AAV particle of any of claims 38-39 or any of the pharmaceutical compositions of claims 44-45.

50. The method of claim 49, wherein the cell is a mammalian cell.

51. The method of claim 50, wherein the mammalian cell is a cell of the CNS.

52. A method of decreasing the level of a protein of interest in the CNS of a subject comprising administering to the subject a composition comprising an AAV particle of any of claims 1-37 or any of the compositions of claims 40-43.

53. The method of claim 52, wherein the route of administration is intravenous administration.

54. The method of claim 52, wherein the route of administration is intracarotid artery administration.

55. A method of increasing the level of a protein of interest in the CNS of a subject comprising administering to the subject a composition comprising an AAV particle of any of claims 38-39 or any of the pharmaceutical compositions of claims 44-45.

56. The method of claim 55, wherein the route of administration is intravenous administration.

57. The method of claim 55, wherein the route of administration is intracarotid artery administration.

58. A method for treating and/or ameliorating a neurological disease in a subject in need of treatment, the method comprising administering to the subject a therapeutically effective amount of a composition comprising an AAV particle of any of claims 1-39, or any of the pharmaceutical compositions of claims 40-45.

59. The method of claim 58, wherein the subject is administered the composition comprising the AAV particle by intravenous delivery.

60. The method of claim 58, wherein the subject is administered the composition comprising the AAV particle by intracarotid artery delivery.

61. The method of any of claims 58-60, wherein the AAV particle comprises a nucleic acid sequence that encodes a protein of interest.

62. The method of claim 61, wherein the protein of interest is selected from the group consisting of an antibody, AADC, ApoE2, and Frataxin.

63. The method of any of claims 58-60, wherein the AAV particles comprises a nucleic acid sequence that encodes a siRNA molecule.

64. The method of claim 63, wherein the siRNA molecule targets a gene of interest, wherein the gene of interest is selected from the group consisting of SOD1, HTT, APOE, and MAPT.

65. An adeno-associated viral (AAV) particle comprising a capsid and a viral genome, wherein said viral genome transduces cardiomyocytes upon delivery of the AAV particle.

66. The AAV particle of claim 65, wherein the AAV particle comprises a capsid or peptide insert selected from the group consisting of VOY101, VOY201, AAVPHP.B (PHP.B), AAVPHP.A (PHP.A), AAVG2B-26, AAVG2B-13, AAVTH1.1-32, AAVTH1.1-35, AAVPHP.B2 (PHP.B2), AAVPHP.B3 (PHP.B3), AAVPHP.N/PHP.B-DGT, AAVPHP.B-EST, AAVPHP.B-GGT, AAVPHP.B-ATP, AAVPHP.B-ATT-T, AAVPHP.B-DGT-T, AAVPHP.B-GGT-T, AAVPHP.B-SGS, AAVPHP.B-AQP, AAVPHP.B-QQP, AAVPHP.B-SNP(3), AAVPHP.B-SNP, AAVPHP.B-QGT, AAVPHP.B-NQT, AAVPHP.B-EGS, AAVPHP.B-SGN, AAVPHP.B-EGT, AAVPHP.B-DST, AAVPHP.B-DST, AAVPHP.B-STP, AAVPHP.B-PQP, AAVPHP.B-SQP, AAVPHP.B-QLP, AAVPHP.B-TMP, AAVPHP.B-TTP, AAVPHP.S/G2A12, AAVG2A15/G2A3 (G2A3), AAVG2B4 (G2B4), AAVG2B5 (G2B5), PHP.S, AAV1, AAV2, AAV2G9, AAV3, AAV3a, AAV3b, AAV3-3, AAV4, AAV4-4, AAV5, AAV6, AAV6.1, AAV6.2, AAV6.1.2, AAV7, AAV7.2, AAV8, AAV9, AAV9.11, AAV9.13, AAV9.16, AAV9.24, AAV9.45, AAV9.47, AAV9.61, AAV9.68, AAV9.84, AAV9.9, AAV10, AAV11, AAV12, AAV16.3, AAV24.1, AAV27.3, AAV42.12, AAV42-1b, AAV42-2, AAV42-3a, AAV42-3b, AAV42-4, AAV42-5a, AAV42-5b, AAV42-6b, AAV42-8, AAV42-10, AAV42-11, AAV42-12, AAV42-13, AAV42-15, AAV42-aa, AAV43-1, AAV43-12, AAV43-20, AAV43-21, AAV43-23, AAV43-25, AAV43-5, AAV44.1, AAV44.2, AAV44.5, AAV223.1, AAV223.2, AAV223.4, AAV223.5, AAV223.6, AAV223.7, AAV1-7/rh.48, AAV1-8/rh.49, AAV2-15/rh.62, AAV2-3/rh.61, AAV2-4/rh.50, AAV2-5/rh.51, AAV3.1/hu.6, AAV3.1/hu.9, AAV3-9/rh.52, AAV3-11/rh.53, AAV4-8/r11.64, AAV4-9/rh.54, AAV4-19/rh.55, AAV5-3/rh.57, AAV5-22/rh.58, AAV7.3/hu.7, AAV16.8/hu.10, AAV16.12/hu.11, AAV29.3/bb.1, AAV29.5/bb.2, AAV106.1/hu.37, AAV114.3/hu.40, AAV127.2/hu.41, AAV127.5/hu.42, AAV128.3/hu.44, AAV130.4/hu.48, AAV145.1/hu.53, AAV145.5/hu.54, AAV145.6/hu.55, AAV161.10/hu.60, AAV161.6/hu.61, AAV33.12/hu.17, AAV33.4/hu.15, AAV33.8/hu.16, AAV52/hu.19, AAV52.1/hu.20, AAV58.2/hu.25, AAVA3.3, AAVA3.4, AAVA3.5, AAVA3.7, AAVC1, AAVC2, AAVC5, AAV-DJ, AAV-DJ8, AAVF3, AAVF5, AAVH2, AAVrh.72, AAVhu.8, AAVrh.68, AAVrh.70, AAVpi.1, AAVpi.3, AAVpi.2, AAVrh.60, AAVrh.44, AAVrh.65, AAVrh.55, AAVrh.47,

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67. The AAV particle of claim 66, wherein the capsid is VOY101.

68. The AAV particle of claim 67, wherein the amino acid sequence of the capsid is SEQ ID NO. 1.

69. The AAV particle of claim 67, wherein the nucleic acid sequence of the capsid is SEQ ID NO. 1809.

70. The AAV particle of claim 66, wherein the capsid is VOY201.

71. The AAV particle of claim 70, wherein the nucleic acid sequence of the capsid is SEQ ID NO. 1810.

72. The AAV particle of claim 66, wherein the peptide insert is selected from the group consisting of AAVPHP.N, AAVPHP.B and AAVPHP.A.

73. A pharmaceutical composition comprising an AAV particle, said AAV particle comprising an AAV capsid and a viral genome, said viral genome encoding a protein of interest, wherein said protein of interest is selected from the group consisting of ATP2A2 and S100A1.

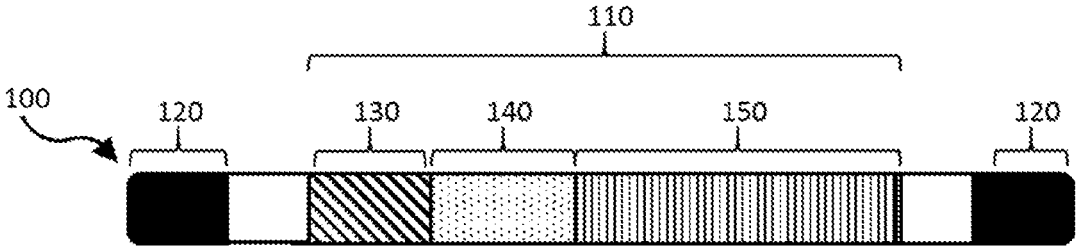
74. A method of increasing the level of a protein of interest in the cardiovascular tissue of a subject comprising administering the pharmaceutical composition of claim 73.

75. A method of treating a cardiovascular disease in a subject in need thereof, said method comprising administering to the subject the pharmaceutical composition of claim 73.

76. A method of treating heart failure in a subject in need thereof, said method comprising administering to the subject the pharmaceutical composition of claim 73.

77. The method of any of claims 74 to 76, wherein the route of administration is intravenous administration.

FIG. 1



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35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
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Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

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Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
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            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
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Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
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Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
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Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
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Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
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Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
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305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
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Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
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Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
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Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
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Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Asp Gly Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
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Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
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Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
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Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
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Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
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Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
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Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
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Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
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Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
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Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
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Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
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Tyr Gly Gln Val Ala Thr Asn His Gln Ser Asp Gly Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
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Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
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Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
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Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
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Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
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35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
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Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
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Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
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Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
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Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
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```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740
```

<210> 4
<211> 2232
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 4
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctctagaact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg taccggcaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaaactttg gcggtgcctt ttaaggcaca ggcgcagacc 1800

ggttgggttc aaaaccaagg aatacttccg ggtatggttt ggcaggacag agatgtgtac 1860

ctgcaaggac ccatttgggc caaaattcct cacacggacg gcaactttca cccttctccg 1920

ctgatgggag ggtttggaat gaagcacccg cctcctcaga tcctcatcaa aaacacacct 1980

gtacctgcgg atcctccaac ggccttcaac aaggacaagc tgaactcttt catcacccag 2040

tattctactg gccaagtcag cgtggagatc gagtgggagc tgcagaagga aaacagcaag 2100

cgctggaacc cggagatcca gtacacttcc aactattaca agtctaataa tgttgaattt 2160

gctgttaata ctgaaggtgt atatagtgaa ccccgcccca ttggcaccag atacctgact 2220

cgtaatctgt aa 2232

<210> 5
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 5
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

```
Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Arg Thr Ile Gln Ser Ser Gln Thr Pro Arg Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 6
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 6
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
```

```
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Ile Leu Gly Thr Gly Thr Ser Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
```

```
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Arg Thr Asn
            580                 585                 590

Pro Glu Ala Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
```

705 710 715 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
725 730 735

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 7
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 7
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Ile Leu Gly Thr Gly Thr Ser Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Asn Gly Gly Thr
            580                 585                 590

Ser Ser Ser Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740
```

<210> 8
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 8
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

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Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Gln Ala Val Arg
            580                 585                 590

Thr Ser Leu Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
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<210> 9
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 9

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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190
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Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
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Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605
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Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 10
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

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tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

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atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

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gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

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<211> 736
<212> PRT
<213> Adeno-associated virus 1

<400> 11
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
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Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
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```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 12
<211> 4718
<212> DNA
<213> Adeno-associated virus serotype 1
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<400> 12
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gcaggcaccc ctgaccgtgg ccgagaagct gcagcgcgac ttcctggtcc aatggcgccg 540

cgtgagtaag gccccggagg ccctcttctt tgttcagttc gagaagggcg agtcctactt 600

ccacctccat attctggtgg agaccacggg ggtcaaatcc atggtgctgg gccgcttcct 660

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ccaccgagcg agcgagcgcg cagagaggga gtgggcaa 4718

<210> 13
<211> 3131
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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agtccgccaa ggccattctc ggcggcagca aggtgcgcgt ggaccaaaag tgcaagtcgt 180

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ttgacgggaa cagcaccacc ttcgagcacc agcagcctct ccaggaccgg atgtttaagt 300

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ccgacaggta ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct 600

gcaaaacgtg cgagagaatg aatcggaatt tcaacatttg cttcacacac ggggtcagag 660

actgctcaga gtgtttcccc ggcgtgtcag aatctcaacc ggtcgtcaga aagaggacgt 720

atcggaaact ccgtgcgatt catcatctgc tggggcgggc tcccgagatt gcttgctcgg 780

cctgcgatct ggtcaacgtg gacctggatg actgtgtttc tgagcaataa atgacttaaa 840

ccaggtatgg ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc 900

attcgcgagt ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag 960

caggacgacg gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga 1020

ctcgacaagg gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggct 1080

tacgaccagc agctgcaggc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc 1140

gagtttcagg agcgtctgca agaagatacg tcttttgggg gcaacctcgg gcgagcagtc 1200

ttccaggcca agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg 1260

gctcctggaa agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg 1320

ggcatcggca agaaaggcca acagcccgcc agaaaaagac tcaattttgg tcagactggc 1380

gactcagagt cagttccaga ccctcaacct ctcggagaac ctccagcagc gccctctggt 1440

gtgggaccta atacaatggc tgcaggcggt ggcgcaccaa tggcagacaa taacgaaggc 1500

gccgacggag tgggtagttc ctcgggaaat tggcattgcg attccacatg gctgggcgac 1560

agagtcatca ccaccagcac ccgaacctgg gccctgccca cctacaacaa ccacctctac 1620

aagcaaatct ccaacgggac atcgggagga gccaccaacg acaacaccta cttcggctac 1680

agcaccccct gggggtattt tgactttaac agattccact gccacctttc accacgtgac 1740

tggcagcgac tcatcaacaa caactgggga ttccgaccca agagactcag cttcaagctc 1800

ttcaacatcc aggtcaagga ggtcacgcag aatgaaggca ccaagaccat cgccaataac 1860

ctcaccagca ccatccaggt gtttacggac tcggagtacc agctgccgta cgttctcggc 1920

tctgtccacc agggctgcct gcctccgttc ccggcggacg tgttcatgat tccccagtac 1980

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gaatactttc cttcgcagat gctgagaacc ggcaacaact tccagtttac ttacaccttc 2100

gaggacgtgc ctttccacag cagctacgcc cacagctaga gcttggaccg gctgatgaat 2160

cctctgattg accagtacct gtactacttg tctcggactc aaacaacagg aggcacggca 2220

aatacgcaga ctctgggctt cagccaaggt gggcctaata caatggccaa tcaggcaaag 2280

aactggctgc caggaccctg ttaccgccaa caacgcgtct caacgacaac cgggcaaaac 2340

aacaatagca actttgcctg gactgctggg accaaatacc atctgaatgg aagaaattca 2400

ttggctaatc ctggcatcgc tatggcaaca cacaaagacg acgaggagcg ttttttccc 2460

agtaacggga tcctgatttt tggcaaacaa aatgctgcca gagacaatgc ggattacagc 2520

gatgtcatgc tcaccagcga ggaagaaatc aaaaccacta accctgtggc tacagaggaa 2580

tacggtatcg tggcagataa cttgcagcag caaaacacgg ctcctcaaat tggaactgtc 2640

aacagccagg gggccttacc cggtatggtc tggcagaacc gggacgtgta cctgcagggt 2700

cccatctggg ccaagattcc tcacacggac ggcaacttcc acccgtctcc gctgatgggc 2760

ggctttggcc tgaaacatcc tccgcctcag atcctgatca agaacacgcc tgtacctgcg 2820

gatcctccga ccaccttcaa ccagtcaaag ctgaactctt tcatcacgca atacagcacc 2880

ggacaggtca gcgtggaaat tgaatgggag ctgcagaagg aaaacagcaa gcgctggaac 2940

cccgagatcc agtacacctc caactactac aaatctataa gtgtggactt tgctgttaat 3000

acagaaggcg tgtactctga accccgcccc attggcaccc gttacctcac ccgtaatctg 3060

taattgcctg ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga 3120

agggcgaatt c 3131

<210> 14
<211> 255
<212> DNA
<213> Adeno-associated virus serotype 10

<400> 14
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 60

accagcaccc gaacctgggt cctgcccacc tacaacaacc acatctacaa gcaaatctcc 120

agcgagacag gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 180

tttgacttta acagattcca ctgccacttt tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattc 255

<210> 15
<211> 738
<212> PRT
<213> Adeno-associated virus 10

<400> 15
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Glu Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670
```

```
Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 16
<211> 738
<212> PRT
<213> Adeno-associated virus 10

<400> 16

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460


Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720
```

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 17
<211> 258
<212> DNA
<213> Adeno-associated virus serotype 11

<400> 17
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 60

accagcaccc gaacctgggc cctgccaacc tacaacaacc acctctacaa acaaatctcc 120

agcgcttcaa cgggggccag caacgacaac cactactttg gctacagcac cccctggggg 180

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc 240

aacaacaact ggggattc 258

<210> 18
<211> 255
<212> DNA
<213> Adeno-associated virus serotype 12

<400> 18
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgaccg agtcattacc 60

accagcaccc ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc 120

agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcacccc ttgggggtat 180

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattc 255

<210> 19
<211> 2208
<212> DNA
<213> Adeno-associated virus serotype 2

<400> 19
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 20
<211> 735
<212> PRT
<213> Adeno-associated virus 2

<400> 20
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525
```

```
Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 21
<211> 621
<212> PRT
<213> Adeno-associated virus 2

<400> 21
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1   5   10   15

Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20   25   30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35   40   45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50   55   60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65   70   75   80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85   90   95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100   105   110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115   120   125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130   135   140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145   150   155   160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

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Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275                 280                 285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
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Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545 550 555 560

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
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Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

595 600 605

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
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35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
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Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg
    130                 135                 140

Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145                 150                 155                 160

Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
                165                 170                 175

Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
            180                 185                 190

Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
        195                 200                 205

Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
    210                 215                 220

Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225                 230                 235                 240

Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
                245                 250                 255

Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
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Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
340 345 350

Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
355 360 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
370 375 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
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Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
420 425 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
435 440 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
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Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465 470 475 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
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Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
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Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met

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Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
                565                 570                 575

Ser Thr Thr Ala Pro Thr Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val
            580                 585                 590

Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
        595                 600                 605

Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
    610                 615                 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625                 630                 635                 640

Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
                645                 650                 655

Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
            660                 665                 670

Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
        675                 680                 685

Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
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35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
115 120 125

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Xaa Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540
```

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 26
<211> 1933
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 26
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cgacgccgag tttcaggagt gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gttgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttctccc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacgccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 27
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 27
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Cys Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65 70 75 80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
85 90 95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
100 105 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Val Ala Gly Gly Gly
115 120 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
130 135 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145 150 155 160

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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365
```

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Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Ser Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575
```

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 28
<211> 1933
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 28
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct ttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 29
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 29

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Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                  10                  15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400
```

```
Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 30
<211> 1933
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 30
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gccagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca cggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctgggccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gaatgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 31
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 31
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg

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1               5                   10                  15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

```
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
```

```
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
```

625 630 635 640

Tyr Ser Glu Pro

<210> 32
<211> 1933
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 32
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct ttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aatagcgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagc ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 33
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 33
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

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Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Ser Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240
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Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445
```

```
Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Leu Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640

Tyr Ser Glu Pro
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<210> 34
<211> 1933
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 34
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggcgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggacc cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat ggaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaaga ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 35
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 35
Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1 5 10 15

Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
20 25 30

Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
35 40 45

Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
50 55 60

```
Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110

Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Pro Glu Tyr Gln Leu Pro
            260                 265                 270
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480
```

```
Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    530                 535                 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545                 550                 555                 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                565                 570                 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Ile Ala Ser Phe Ile Thr
            580                 585                 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        595                 600                 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    610                 615                 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625                 630                 635                 640

Tyr Ser Glu Pro
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<210> 36
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 36
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Thr Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

```
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala Arg Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Gly Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 37
<211> 3121
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 37
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgactg 60

tgtcgacaag atggtgatct ggtgggagga ggggaagatg accgccaagg tcgtggagtc 120

ggccaaagcc attctcggag gaagcaaggt gcgcgtggac cagaaatgca agtcctcggc 180

ccagatagac ccgactcccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaactca acgaccttcg aacaccagca gccgttgcaa gaccggatgt tcaaatttga 300

actcacccgc cgtctggatc atgactttgg gaaggtcacc aagcaggaag tcaaagactt 360

tttccggtgg gcaaaggatc acgtggttga ggtggagcac gaattctacg tcaaaaaggg 420

tggagccaag aaaagacccg cccccagtga cgcagatata agtgagccca aacgggtgcg 480

cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgatcaact acgcagacag 540

gtaccaaaac aaatgttctc gtcacgcggg catgaatctg atgctgtttc cctgcagaca 600

atgcgagaga atgaatcaga attcaaatat ctgcttcact cacggacaga aagactgttt 660

agagtgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcaaaaagg cgtatcagaa 720

actgtgctac attcatcata tcatgggaaa ggtgccagac gcttgcactg cctgcgatct 780

ggtcgatgtg gatttggatg actgcatctt tgaacaataa atgatttaaa tcaggtatgg 840

ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt 900

ggtgggcgct gaaacctgga gccccgaagc ccaaagccaa ccagcaaaag caggacggcg 960

gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga ctcgacaagg 1020

gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc 1080

agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg 1140

agcgtctgca agaagatacg tcttttgggg gcaacctcgg gcgagcagtc ttccaggcca 1200

agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg gctcctggaa 1260

agaagagacc ggtagagcca tcaccccagc gttctccaga ctcctctacg ggcatcggca 1320

agaaaggcca gcagcccgcg aaaaagagac tcaactttgg gcagactggc gactcagagt 1380

cagtgcccga ccctcaacca atcggagaac cccccgcagg cccctctggt ctgggatctg 1440

gtacaatggc tgcaggcggt ggcgctccaa tggcagacaa taacgaaggc gccgacggag 1500

tgggtagttc ctcaggaaat tggcattgcg attccacatg gctgggcgac tgagtcatca 1560

ccaccagcac ccgaacctgg gccctcccca cctacaacaa ccacctctac aagcaaatct 1620

ccaacgggac ttcgggagga agcaccaacg acaacaccta cttcggctac agcacccccc 1680

gggggtattt tgactttaac agattccact gccacttctc accacgtgac tggcagcgac 1740

tcatcaacaa caactgggga ttccggccca agagactcaa cttcaagctc ttcaacatcc 1800

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cgattcaggt ctttacggac tcggaatacc agctcccgta cgtcctcggc tctgcgcacc 1920

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cttattctga gcctcgcccc atcggcaccc gttacctcac ccgtaatctg taattgcttg 3060

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctctgcga agggcgaatt 3120

c 3121

<210> 38
<211> 738

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 38

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

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Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Gly Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Ser Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
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Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asp Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590
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Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
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<210> 39
<211> 3121
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 39

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tgccatctgt gttaacagca aagtccacat ttgtagattt gtagtagttg gaagtgtatt 180

gaatctctgg gttccagcgt ttgctgtttt ctttctgcag ctcccattca atttccacgc 240

tgacctgtcc ggtgctgtac tgcgtgatga acgacgccag cttagcttga ctgaaggtag 300

ttggaggatc cgcgggaaca ggtgtattct taatcaggat ctgaggaggc gggtgtttca 360

gtccaaagcc tcccatcagc ggcgagggat gaaagtttcc gtccgtgtga ggaatcttgg 420

cccagatagg accctgcagg tacacgtccc ggttctgcca gaccatgcca ggtaaggctc 480

cttgactgtt gacggcccct acaataggag cggcgttttg ctgttgcagg ttatcggcca 540

ccacgccgta ctgttctgtg gccactgggt tggtggtttt aatttcttcc tcactggtta 600

gcataacgct gctatagtcc acgttgtctt ttccagctcc ctgtttccca aacattaaga 660

ctccgctgga cggaaaaaat cgctcttcgt cgtccttgtg ggttgccata gcgacaccgg 720

gatttaccag agagtctctg ccattcagat gatacttggt ggcaccggtc caggcaaagt 780

tgctgttgtc attttgcgac agtgtcgtgg agacgcgttg ctgccggtag cagggcccgg 840

gtagccagtt tttggcctga gccgacatgt tattaggccc ggcctgagaa aatagcaact 900

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gcacgtcctc aaactggtag ctgaactcaa agttgttgcc cgttctcagc atttgagaag 1080

gaaagtactc caggcagtag aaggaggaac ggcccacggc ctgactgcca ttgttcagag 1140

tcaggtaccc gtactgagga atcatgaaga cgtccgccgg gaacggaggc aggcagccct 1200

ggtgcgcaga gccgaggacg tacgggagct ggtattccga gtccgtaaag acctgaatcg 1260

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gactccacga ccttggcggt catcttcccc tcctcccacc agatcaccat cttgtcgaca 3060

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c 3121

<210> 40
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 40
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aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

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<210> 41
<211> 736
<212> PRT
<213> Adeno-associated virus 3

<400> 41
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
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    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
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660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 42
<211> 4726
<212> DNA
<213> Adeno-associated virus serotype 3

<400> 42
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gccaactcca tcactagagg tatggcagtg acgtaacgcg aagcgcgcga agcgagacca 180

cgcctaccag ctgcgtcagc agtcaggtga ccctttgcg acagtttgcg acaccacgtg 240

gccgctgagg gtatatattc tcgagtgagc gaaccaggag ctccattttg accgcgaaat 300

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acgtgtcgca gacgcaggag cagaacaaag agaatcagaa ccccaattct gacgcgccgg 960

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ggatcacgtc agaaaagcaa tggattcagg aggaccaggc ctcgtacatc tccttcaacg 1080

ccgcctccaa ctcgcggtcc cagatcaagg ccgcgctgga caatgcctcc aagatcatga 1140

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gctgcgtaaa ctggaccaat gagaactttc ccttcaacga ttgcgtcgac aagatggtga 1440

tctggtggga ggagggcaag atgacggcca aggtcgtgga gagcgccaag gccattctgg 1500

gcggaagcaa ggtgcgcgtg gaccaaaagt gcaagtcatc ggcccagatc gaacccactc 1560

ccgtgatcgt cacctccaac accaacatgt gcgccgtgat tgacgggaac agcaccacct 1620

tcgagcatca gcagccgctg caggaccgga tgtttgaatt tgaacttacc cgccgtttgg 1680

accatgactt tgggaaggtc accaaacagg aagtaaagga ctttttccgg tgggcttccg 1740

atcacgtgac tgacgtggct catgagttct acgtcagaaa gggtggagct aagaaacgcc 1800

ccgcctccaa tgacgcggat gtaagcgagc caaaacggga gtgcacgtca cttgcgcagc 1860

cgacaacgtc agacgcggaa gcaccggcgg actacgcgga caggtaccaa aacaaatgtt 1920

ctcgtcacgt gggcatgaat ctgatgcttt ttccctgtaa aacatgcgag agaatgaatc 1980

aaatttccaa tgtctgtttt acgcatggtc aaagagactg tggggaatgc ttccctggaa 2040

tgtcagaatc tcaacccgtt tctgtcgtca aaaagaagac ttatcagaaa ctgtgtccaa 2100

ttcatcatat cctgggaagg gcacccgaga ttgcctgttc ggcctgcgat ttggccaatg 2160

tggacttgga tgactgtgtt tctgagcaat aaatgactta aaccaggtat ggctgctgac 2220

ggttatcttc cagattggct cgaggacaac ctttctgaag gcattcgtga gtggtgggct 2280

ctgaaacctg gagtccctca acccaaagcg aaccaacaac accaggacaa ccgtcggggt 2340

cttgtgcttc cgggttacaa atacctcgga cccggtaacg gactcgacaa aggagagccg 2400

gtcaacgagg cggacgcggc agccctcgaa cacgacaaag cttacgacca gcagctcaag 2460

gccggtgaca acccgtacct caagtacaac cacgccgacg ccgagtttca ggagcgtctt 2520

caagaagata cgtcttttgg gggcaacctt ggcagagcag tcttccaggc caaaaagagg 2580

atccttgagc ctcttggtct ggttgaggaa gcagctaaaa cggctcctgg aaagaagggg 2640

gctgtagatc agtctcctca ggaaccggac tcatcatctg gtgttggcaa atcgggcaaa 2700

cagcctgcca gaaaaagact aaatttcggt cagactggag actcagagtc agtcccagac 2760

cctcaacctc tcggagaacc accagcagcc cccacaagtt tgggatctaa tacaatggct 2820

tcaggcggtg gcgcaccaat ggcagacaat aacgagggtg ccgatggagt gggtaattcc 2880

tcaggaaatt ggcattgcga ttcccaatgg ctgggcgaca gagtcatcac caccagcacc 2940

agaacctggg ccctgcccac ttacaacaac catctctaca agcaaatctc cagccaatca 3000

ggagcttcaa acgacaacca ctactttggc tacagcaccc cttgggggta ttttgacttt 3060

aacagattcc actgccactt ctcaccacgt gactggcagc gactcattaa caacaactgg 3120

ggattccggc ccaagaaact cagcttcaag ctcttcaaca tccaagttag aggggtcacg 3180

cagaacgatg gcacgacgac tattgccaat aaccttacca gcacggttca agtgtttacg 3240

gactcggagt atcagctccc gtacgtgctc gggtcggcgc accaaggctg tctcccgccg 3300

tttccagcgg acgtcttcat ggtccctcag tatggatacc tcaccctgaa caacggaagt 3360

caagcggtgg gacgctcatc cttttactgc ctggagtact tcccttcgca gatgctaagg 3420

actggaaata acttccaatt cagctatacc ttcgaggatg taccttttca cagcagctac 3480

gctcacagcc agagtttgga tcgcttgatg aatcctctta ttgatcagta tctgtactac 3540

ctgaacagaa cgcaaggaac aacctctgga acaaccaacc aatcacggct gctttttagc 3600

caggctgggc ctcagtctat gtctttgcag gccagaaatt ggctacctgg gccctgctac 3660

cggcaacaga gactttcaaa gactgctaac gacaacaaca acagtaactt tccttggaca 3720

gcggccagca aatatcatct caatggccgc gactcgctgg tgaatccagg accagctatg 3780

gccagtcaca aggacgatga agaaaaattt ttccctatgc acggcaatct aatatttggc 3840

aaagaaggga caacggcaag taacgcagaa ttagataatg taatgattac ggatgaagaa 3900

gagattcgta ccaccaatcc tgtggcaaca gagcagtatg gaactgtggc aaataacttg 3960

cagagctcaa atacagctcc cacgactgga actgtcaatc atcaggggc cttacctggc 4020

atggtgtggc aagatcgtga cgtgtacctt caaggaccta tctgggcaaa gattcctcac 4080

acggatggac actttcatcc ttctcctctg atgggaggct ttggactgaa acatccgcct 4140

cctcaaatca tgatcaaaaa tactccggta ccggcaaatc ctccgacgac tttcagcccg 4200

gccaagtttg cttcatttat cactcagtac tccactggac aggtcagcgt ggaaattgag 4260

tgggagctac agaaagaaaa cagcaaacgt tggaatccag agattcagta cacttccaac 4320

tacaacaagt ctgttaatgt ggactttact gtagacacta atggtgttta tagtgaacct 4380

cgccctattg gaacccggta tctcacacga aacttgtgaa tcctggttaa tcaataaacc 4440

gtttaattcg tttcagttga actttggctc ttgtgcactt ctttatcttt atcttgtttc 4500

catggctact gcgtagataa gcagcggcct gcggcgcttg cgcttcgcgg tttacaactg 4560

ctggttaata tttaactctc gccatacctc tagtgatgga gttggccact ccctctatgc 4620

gcactcgctc gctcggtggg gcctggcgac caaaggtcgc cagacggacg tgctttgcac 4680

gtccggcccc accgagcgag cgagtgcgca tagagggagt ggccaa 4726

<210> 43
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 43
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

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    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Asn Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Glu Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
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            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asp Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
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465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
```

675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 44
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 44
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaagg gggctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgactg gaactgtcaa tcatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 45
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 45
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130   135   140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145   150   155   160

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Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
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Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575
```

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Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 46
<211> 736
<212> PRT
<213> Adeno-associated virus 3A

<400> 46
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445
```

```
Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 47
<211> 624
<212> PRT
<213> Adeno-associated virus 3A

<400> 47
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15

Glu Arg Leu Pro Gly Ile Ser Asn Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Asp Val Pro Pro Asp Ser Asp Met Asp Pro Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60

Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Thr Tyr Phe His Leu His Val Leu Ile Glu
                85                  90                  95
```

```
Thr Ile Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Leu
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Ser Asn
        275                 280                 285

Pro Pro Glu Asp Ile Thr Lys Asn Arg Ile Tyr Gln Ile Leu Glu Leu
    290                 295                 300
```

```
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320


Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335


Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350


Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365


Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380


Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400


Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Glu Pro Thr Pro Val
                405                 410                 415


Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430


Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Glu Phe
        435                 440                 445


Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460


Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Asp Val
465                 470                 475                 480


Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495


Ser Asn Asp Ala Asp Val Ser Glu Pro Lys Arg Glu Cys Thr Ser Leu
            500                 505                 510
```

```
Ala Gln Pro Thr Thr Ser Asp Ala Glu Ala Pro Ala Asp Tyr Ala Asp
        515                 520                 525


Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540


Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Ile Ser Asn Val Cys
545                 550                 555                 560


Phe Thr His Gly Gln Arg Asp Cys Gly Glu Cys Phe Pro Gly Met Ser
                565                 570                 575


Glu Ser Gln Pro Val Ser Val Val Lys Lys Lys Thr Tyr Gln Lys Leu
            580                 585                 590


Cys Pro Ile His His Ile Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser
        595                 600                 605


Ala Cys Asp Leu Ala Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620


<210> 48
<211> 736
<212> PRT
<213> Adeno-associated virus 3B

<400> 48
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 49
<211> 624
<212> PRT
<213> Adeno-associated virus 3B

<400> 49
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15


Glu His Leu Pro Gly Ile Ser Asn Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Pro Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80


Gln Phe Glu Lys Gly Glu Thr Tyr Phe His Leu His Val Leu Ile Glu
                85                  90                  95


Thr Ile Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110


Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125


Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140
```

```
Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Leu
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Ser Asn
        275                 280                 285

Pro Pro Glu Asp Ile Thr Lys Asn Arg Ile Tyr Gln Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350
```

```
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Glu Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Asp Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495

Ser Asn Asp Ala Asp Val Ser Glu Pro Lys Arg Gln Cys Thr Ser Leu
            500                 505                 510

Ala Gln Pro Thr Thr Ser Asp Ala Glu Ala Pro Ala Asp Tyr Ala Asp
        515                 520                 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540

Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Ile Ser Asn Val Cys
545                 550                 555                 560
```

Phe Thr His Gly Gln Arg Asp Cys Gly Glu Cys Phe Pro Gly Met Ser
565 570 575

Glu Ser Gln Pro Val Ser Val Val Lys Lys Lys Thr Tyr Gln Lys Leu
580 585 590

Cys Pro Ile His His Ile Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser
595 600 605

Ala Cys Asp Leu Ala Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 50
<211> 4722
<212> DNA
<213> Adeno-associated virus 3B

<400> 50
tggccactcc ctctatgcgc actcgctcgc tcggtggggc ctggcgacca aaggtcgcca 60

gacggacgtg ctttgcacgt ccggccccac cgagcgagcg agtgcgcata gagggagtgg 120

ccaactccat cactagaggt atggcagtga cgtaacgcga agcgcgcgaa gcgagaccac 180

gcctaccagc tgcgtcagca gtcaggtgac ccttttgcga cagtttgcga caccacgtgg 240

ccgctgaggg tatatattct cgagtgagcg aaccaggagc tccattttga ccgcgaaatt 300

tgaacgagca gcagccatgc cggggttcta cgagattgtc ctgaaggtcc cgagtgacct 360

ggacgagcac ctgccgggca tttctaactc gtttgttaac tgggtggccg agaaggaatg 420

ggagctgccg ccggattctg acatggatcc gaatctgatt gagcaggcac ccctgaccgt 480

ggccgaaaag cttcagcgcg agttcctggt ggagtggcgc cgcgtgagta aggccccgga 540

ggccctcttt tttgtccagt tcgaaaaggg ggagacctac ttccacctgc acgtgctgat 600

tgagaccatc ggggtcaaat ccatggtggt cggccgctac gtgagccaga ttaaagagaa 660

gctggtgacc cgcatctacc gcggggtcga gccgcagctt ccgaactggt tcgcggtgac 720

caaaacgcga aatggcgccg ggggcgggaa caaggtggtg gacgactgct acatccccaa 780

ctacctgctc cccaagaccc agcccgagct ccagtgggcg tggactaaca tggaccagta 840

tttaagcgcc tgtttgaatc tcgcggagcg taaacggctg gtggcgcagc atctgacgca 900

cgtgtcgcag acgcaggagc agaacaaaga gaatcagaac cccaattctg acgcgccggt 960

catcaggtca aaaacctcag ccaggtacat ggagctggtc gggtggctgg tggaccgcgg 1020

gatcacgtca gaaaagcaat ggattcagga ggaccaggcc tcgtacatct ccttcaacgc 1080

cgcctccaac tcgcggtccc agatcaaggc cgcgctggac aatgcctcca agatcatgag 1140

cctgacaaag acggctccgg actacctggt gggcagcaac ccgccggagg acattaccaa 1200

aaatcggatc taccaaatcc tggagctgaa cgggtacgat ccgcagtacg cggcctccgt 1260

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ctgcgtaaac tggaccaatg agaactttcc cttcaacgat tgcgtcgaca agatggtgat 1440

ctggtgggag gagggcaaga tgacggccaa ggtcgtggag agcgccaagg ccattctggg 1500

cggaagcaag gtgcgcgtgg accaaaagtg caagtcatcg gcccagatcg aacccactcc 1560

cgtgatcgtc acctccaaca ccaacatgtg cgccgtgatt gacgggaaca gcaccacctt 1620

cgagcatcag cagccgctgc aggaccggat gtttaaattt gaacttaccc gccgtttgga 1680

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tcacgtgact gacgtggctc atgagttcta cgtcagaaag ggtggagcta agaaacgccc 1800

cgcctccaat gacgcggatg taagcgagcc aaaacggcag tgcacgtcac ttgcgcagcc 1860

gacaacgtca gacgcggaag caccggcgga ctacgcggac aggtaccaaa acaaatgttc 1920

tcgtcacgtg ggcatgaatc tgatgctttt tccctgtaaa acatgcgaga gaatgaatca 1980

aatttccaat gtctgtttta cgcatggtca aagagactgt ggggaatgct tccctggaat 2040

gtcagaatct caacccgttt ctgtcgtcaa aaagaagact tatcagaaac tgtgtccaat 2100

tcatcatatc ctgggaaggg cacccgagat tgcctgttcg gcctgcgatt tggccaatgt 2160

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aagaagatac gtcttttggg ggcaaccttg gcagagcagt cttccaggcc aaaaagagga 2580

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gagcttcaaa cgacaaccac tactttggct acagcacccc ttgggggtat tttgacttta 3060

acagattcca ctgccacttc tcaccacgtg actggcagcg actcattaac aacaactggg 3120

gattccggcc caagaaactc agcttcaagc tcttcaacat ccaagttaaa gaggtcacgc 3180

agaacgatgg cacgacgact attgccaata accttaccag cacggttcaa gtgtttacgg 3240

actcggagta tcagctcccg tacgtgctcg ggtcggcgca ccaaggctgt ctcccgccgt 3300

ttccagcgga cgtcttcatg gtccctcagt atggatacct caccctgaac aacggaagtc 3360

aagcggtggg acgctcatcc ttttactgcc tggagtactt cccttcgcag atgctaagga 3420

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aagaagggac aacggcaagt aacgcagaat tagataatgt aatgattacg gatgaagaag 3900

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gccctattgg aacccggtat ctcacacgaa acttgtaatc ctggttaatc aataaaccgt 4440

ttaattcgtt tcagttgaac tttggctctt gtgcacttct tatcttatct tgtttccatg 4500

gctactgcgt agataagcag cggcctgcgg cgcttgcgct tcgcggttta caactgctgg 4560

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ggccccaccg agcgagcgag tgcgcataga gggagtggcc aa 4722

<210> 51
<211> 1800
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> modified_base
<222> (342)..(342)
<223> a, c, g, or t

<400> 51
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ggtatcggca aaaaaggcaa gcagccggct aaaaagaagc tcgttttcga agacgaaact 120

ggagcaggcg acggaccccc tgagggatca acttccggag ccatgtctga tgacagtgag 180

atgcgtgcag cagctggcgg agctgcagtc gagggsggac aaggtgccga tggagtgggt 240

aatgcctcgg gtgattggca ttgcgattcc acctggtctg agggccacgt cacgaccacc 300

agcaccagaa cctgggtctt gcccacctac aacaaccacc tntacaagcg actcggagag 360

agcctgcagt ccaacaccta caacggattc tccacccccc ggggatactt tgacttcaac 420

cgcttccact gccacttctc accacgtgac tggcagcgac tcatcaacaa caactggggc 480

atgcgaccca aagccatgcg ggtcaaaatc ttcaacatcc aggtcaagga ggtcacgacg 540

tcgaacggcg agacaacggt ggctaataac cttaccagca cggttcagat ctttgcggac 600

tcgtcgtacg aactgccgta cgtgatggat gcgggtcaag agggcagcct gcctcctttt 660

cccaacgacg tctttatggt gccccagtac ggctactgtg gactggtgac cggcaacact 720

tcgcagcaac agactgacag aaatgccttc tactgcctgg agtactttcc ttcgcagatg 780

ctgcggactg gcaacaactt tgaaattacg tacagttttg agaaggtgcc tttccactcg 840

atgtacgcgc acagccagag cctggaccgg ctgatgaacc ctctcatcga ccagtacctg 900

tggggactgc aatcgaccac caccggaacc accctgaatg ccgggactgc caccaccaac 960

tttaccaagc tgcggcctac caacttttcc aactttaaaa agaactggct gcccgggcct 1020

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ttgggagccg tgcctggaat ggtctggcaa aacagagaca tttactacca gggtcccatt 1440

tgggccaaga ttcctcatac cgatggacac tttcacccct caccgctgat tggtgggttt 1500

gggctgaaac acccgcctcc tcaaattttt atcaagaaca ccccggtacc tgcgaatcct 1560

gcaacgacct tcagctctac tccggtaaac tccttcatta ctcagtacag cactggccag 1620

gtgtcggtgc agattgactg ggagatccag aaggagcggt ccaaacgctg gaaccccgag 1680

gtccagttta cctccaacta cggacagcaa aactctctgt tgtgggctcc cgatgcggct 1740

gggaaataca ctgagcctag ggctatcggt acccgctacc tcacccacca cctgtaataa 1800

<210> 52
<211> 2208
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> modified_base
<222> (750)..(750)
<223> a, c, g, or t

<400> 52
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gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggsggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctn tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaataa 2208

<210> 53
<211> 1872
<212> DNA
<213> Adeno-associated virus 4

<400> 53
atgccggggt tctacgagat cgtgctgaag gtgcccagcg acctggacga gcacctgccc 60

ggcatttctg actcttttgt gagctgggtg gccgagaagg aatgggagct gccgccggat 120

tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

ccggactacc tggtgggcca gaacccgccg gaggacattt ccagcaaccg catctaccga 900

atcctcgaga tgaacgggta cgatccgcag tacgcggcct ccgtcttcct gggctgggcg 960

caaaagaagt tcgggaagag gaacaccatc tggctctttg ggccggccac gacgggtaaa 1020

accaacatcg cggaagccat cgcccacgcc gtgcccttct acggctgcgt gaactggacc 1080

aatgagaact ttccgttcaa cgattgcgtc gacaagatgg tgatctggtg ggaggagggc 1140

aagatgacgg ccaaggtcgt agagagcgcc aaggccatcc tgggcggaag caaggtgcgc 1200

gtggaccaaa agtgcaagtc atcggcccag atcgacccaa ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

ctccaggacc ggatgttcaa gttcgagctc accaagcgcc tggagcacga ctttggcaag 1380

gtcaccaagc aggaagtcaa agacttttc cggtgggcgt cagatcacgt gaccgaggtg 1440

actcacgagt tttacgtcag aaagggtgga gctagaaaga ggcccgcccc caatgacgca 1500

gatataagtg agcccaagcg ggcctgtccg tcagttgcgc agccatcgac gtcagacgcg 1560

gaagctccgg tggactacgc ggacaggtac caaaacaaat gttctcgtca cgtgggtatg 1620

aatctgatgc tttttccctg ccggcaatgc gagagaatga atcagaatgt ggacatttgc 1680

ttcacgcacg gggtcatgga ctgtgccgag tgcttccccg tgtcagaatc tcaacccgtg 1740

tctgtcgtca gaaagcggac gtatcagaaa ctgtgtccga ttcatcacat catggggagg 1800

gcgcccgagg tggcctgctc ggcctgcgaa ctggccaatg tggacttgga tgactgtgac 1860

atggaacaat aa 1872

<210> 54
<211> 1611
<212> DNA
<213> Adeno-associated virus 4

<400> 54
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tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

ccggactacc tggtgggcca gaacccgccg gaggacattt ccagcaaccg catctaccga 900

atcctcgaga tgaacgggta cgatccgcag tacgcggcct ccgtcttcct gggctgggcg 960

caaaagaagt tcgggaagag gaacaccatc tggctctttg ggccggccac gacgggtaaa 1020

accaacatcg cggaagccat cgcccacgcc gtgcccttct acggctgcgt gaactggacc 1080

aatgagaact ttccgttcaa cgattgcgtc gacaagatgg tgatctggtg ggaggagggc 1140

aagatgacgg ccaaggtcgt agagagcgcc aaggccatcc tgggcggaag caaggtgcgc 1200

gtggaccaaa agtgcaagtc atcggcccag atcgacccaa ctcccgtgat cgtcacctcc 1260

aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

ctccaggacc ggatgttcaa gttcgagctc accaagcgcc tggagcacga ctttggcaag 1380

gtcaccaagc aggaagtcaa agacttttc cggtgggcgt cagatcacgt gaccgaggtg 1440

actcacgagt tttacgtcag aaagggtgga gctagaaaga ggcccgcccc caatgacgca 1500

gatataagtg agcccaagcg ggcctgtccg tcagttgcgc agccatcgac gtcagacgcg 1560

gaagctccgg tggactacgc ggacagattg gctagaggac aacctctctg a 1611

<210> 55
<211> 1872
<212> DNA
<213> Adeno-associated virus 4

<400> 55
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ggcatttctg actcttttgt gagctgggtg gccgagaagg aatgggagct gccgccggat 120

tctgacatgg acttgaatct gattgagcag gcacccctga ccgtggccga aaagctgcaa 180

cgcgagttcc tggtcgagtg gcgccgcgtg agtaaggccc cggaggccct cttctttgtc 240

cagttcgaga agggggacag ctacttccac ctgcacatcc tggtggagac cgtgggcgtc 300

aaatccatgg tggtgggccg ctacgtgagc cagattaaag agaagctggt gacccgcatc 360

taccgcgggg tcgagccgca gcttccgaac tggttcgcgg tgaccaagac gcgtaatggc 420

gccggaggcg ggaacaaggt ggtggacgac tgctacatcc ccaactacct gctccccaag 480

acccagcccg agctccagtg ggcgtggact aacatggacc agtatataag cgcctgtttg 540

aatctcgcgg agcgtaaacg gctggtggcg cagcatctga cgcacgtgtc gcagacgcag 600

gagcagaaca aggaaaacca gaaccccaat tctgacgcgc cggtcatcag gtcaaaaacc 660

tccgccaggt acatggagct ggtcgggtgg ctggtggacc gcgggatcac gtcagaaaag 720

caatggatcc aggaggacca ggcgtcctac atctccttca acgccgcctc caactcgcgg 780

tcacaaatca aggccgcgct ggacaatgcc tccaaaatca tgagcctgac aaagacggct 840

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aacaccaaca tgtgcgcggt catcgacgga aactcgacca ccttcgagca ccaacaacca 1320

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ttcacgcacg gggtcatgga ctgtgccgag tgcttccccg tgtcagaatc tcaacccgtg 1740

tctgtcgtca gaaagcggac gtatcagaaa ctgtgtccga ttcatcacat catggggagg 1800

gcgcccgagg tggcctgctc ggcctgcgaa ctggccaatg tggacttgga tgactgtgac 1860

atggaacaat aa 1872

<210> 56
<211> 1617
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> modified_base
<222> (162)..(162)
<223> a, c, g, or t

<400> 56
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agcaccagaa cctgggtctt gcccacctac aacaaccacc tntacaagcg actcggagag 180

agcctgcagt ccaacaccta caacggattc tccacccccct ggggatactt tgacttcaac 240

cgcttccact gccacttctc accacgtgac tggcagcgac tcatcaacaa caactggggc 300

atgcgaccca aagccatgcg ggtcaaaatc ttcaacatcc aggtcaagga ggtcacgacg 360

tcgaacggcg agacaacggt ggctaataac cttaccagca cggttcagat ctttgcggac 420

tcgtcgtacg aactgccgta cgtgatggat gcgggtcaag agggcagcct gcctcctttt 480

cccaacgacg tctttatggt gccccagtac ggctactgtg gactggtgac cggcaacact 540

tcgcagcaac agactgacag aaatgccttc tactgcctgg agtactttcc ttcgcagatg 600

ctgcggactg gcaacaactt tgaaattacg tacagttttg agaaggtgcc tttccactcg 660

atgtacgcgc acagccagag cctggaccgg ctgatgaacc ctctcatcga ccagtacctg 720

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tttaccaagc tgcggcctac caacttttcc aactttaaaa agaactggct gcccgggcct 840

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gcaacgacct tcagctctac tccggtaaac tccttcatta ctcagtacag cactggccag 1440

gtgtcggtgc agattgactg ggagatccag aaggagcggt ccaaacgctg gaaccccgag 1500

gtccagttta cctccaacta cggacagcaa aactctctgt tgtgggctcc cgatgcggct 1560

gggaaataca ctgagcctag ggctatcggt acccgctacc tcacccacca cctgtaa 1617

<210> 57
<211> 939
<212> DNA
<213> Adeno-associated virus 4

<400> 57
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gaggaccagg cgtcctacat ctccttcaac gccgcctcca actcgcggtc acaaatcaag 120

gccgcgctgg acaatgcctc caaaatcatg agcctgacaa agacggctcc ggactacctg 180

gtgggccaga acccgccgga ggacatttcc agcaaccgca tctaccgaat cctcgagatg 240

aacgggtacg atccgcagta cgcggcctcc gtcttcctgg gctgggcgca aaagaagttc 300

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gaagccatcg cccacgccgt gcccttctac ggctgcgtga actggaccaa tgagaacttt 420

ccgttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc 480

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tgcaagtcat cggcccagat cgacccaact cccgtgatcg tcacctccaa caccaacatg 600

tgcgcggtca tcgacggaaa ctcgaccacc ttcgagcacc aacaaccact ccaggaccgg 660

atgttcaagt tcgagctcac caagcgcctg gagcacgact ttggcaaggt caccaagcag 720

gaagtcaaag actttttccg gtgggcgtca gatcacgtga ccgaggtgac tcacgagttt 780

tacgtcagaa agggtggagc tagaaagagg cccgccccca atgacgcaga tataagtgag 840

cccaagcggg cctgtccgtc agttgcgcag ccatcgacgt cagacgcgga agctccggtg 900

gactacgcgg acagattggc tagaggacaa cctctctga 939

<210> 58
<211> 1197
<212> DNA
<213> Adeno-associated virus 4

<400> 58
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gaggaccagg cgtcctacat ctccttcaac gccgcctcca actcgcggtc acaaatcaag 120

gccgcgctgg acaatgcctc caaaatcatg agcctgacaa agacggctcc ggactacctg 180

gtgggccaga acccgccgga ggacatttcc agcaaccgca tctaccgaat cctcgagatg 240

aacgggtacg atccgcagta cgcggcctcc gtcttcctgg gctgggcgca aaagaagttc 300

gggaagagga acaccatctg gctctttggg ccggccacga cgggtaaaac caacatcgcg 360

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ccgttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgacggcc 480

aaggtcgtag agagcgccaa ggccatcctg ggcggaagca aggtgcgcgt ggaccaaaag 540

tgcaagtcat cggcccagat cgacccaact cccgtgatcg tcacctccaa caccaacatg 600

tgcgcggtca tcgacggaaa ctcgaccacc ttcgagcacc aacaaccact ccaggaccgg 660

atgttcaagt tcgagctcac caagcgcctg gagcacgact ttggcaaggt caccaagcag 720

gaagtcaaag actttttccg gtgggcgtca gatcacgtga ccgaggtgac tcacgagttt 780

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tttccctgcc ggcaatgcga gagaatgaat cagaatgtgg acatttgctt cacgcacggg 1020

gtcatggact gtgccgagtg cttccccgtg tcagaatctc aacccgtgtc tgtcgtcaga 1080

aagcggacgt atcagaaact gtgtccgatt catcacatca tggggagggc gcccgaggtg 1140

gcctgctcgg cctgcgaact ggccaatgtg gacttggatg actgtgacat ggaacaa 1197

<210> 59
<211> 245
<212> DNA
<213> Adeno-associated virus 4

<400> 59
ctccatcatc taggtttgcc cactgacgtc aatgtgacgt cctagggtta gggaggtccc 60

tgtattagca gtcacgtgag tgtcgtattt cgcggagcgt agcggagcgc ataccaagct 120

gccacgtcac agccacgtgg tccgtttgcg acagtttgcg acaccatgtg gtcaggaggg 180

tatataaccg cgagtgagcc agcgaggagc tccattttgc ccgcgaattt tgaacgagca 240

gcagc 245

<210> 60
<211> 313
<212> PRT
<213> Adeno-associated virus 4

<220>
<221> MOD_RES
<222> (313)..(313)
<223> Any naturally occurring amino acid

<400> 60
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1 5 10 15

```
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
        35                  40                  45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
    50                  55                  60

Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
65                  70                  75                  80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220
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Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240


Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
                245                 250                 255


Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
            260                 265                 270


Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285


Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
    290                 295                 300


Arg Leu Ala Arg Gly Gln Pro Leu Xaa
305                 310


<210> 61
<211> 399
<212> PRT
<213> Adeno-associated virus 4

<400> 61
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1               5                   10                  15


Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30


Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
        35                  40                  45


Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
    50                  55                  60


Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
65                  70                  75                  80
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
                245                 250                 255

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
            260                 265                 270

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285
```

```
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
    290                 295                 300


Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305                 310                 315                 320


Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
                325                 330                 335


Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
            340                 345                 350


Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
        355                 360                 365


Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
    370                 375                 380


Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
385                 390                 395


<210> 62
<211> 623
<212> PRT
<213> Adeno-associated virus 4

<400> 62
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15


Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30


Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45


Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60


Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80
```

```
Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285
```

```
Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495
```

```
Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510


Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
        515                 520                 525


Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540


Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
545                 550                 555                 560


Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
                565                 570                 575


Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
            580                 585                 590


Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
        595                 600                 605


Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
    610                 615                 620


<210> 63
<211> 537
<212> PRT
<213> Adeno-associated virus 4


<220>
<221> MOD_RES
<222> (537)..(537)
<223> Any naturally occurring amino acid

<400> 63
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15


Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30
```

```
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60

Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240
```

```
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285

Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445
```

```
Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495

Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
        515                 520                 525

Arg Leu Ala Arg Gly Gln Pro Leu Xaa
    530                 535


<210> 64
<211> 623
<212> PRT
<213> Adeno-associated virus 4

<400> 64
Met Pro Gly Phe Tyr Glu Ile Val Leu Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Glu Phe Leu
    50                  55                  60

Val Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80
```

```
Gln Phe Glu Lys Gly Asp Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Val Gly Val Lys Ser Met Val Val Gly Arg Tyr Val Ser Gln Ile
            100                 105                 110

Lys Glu Lys Leu Val Thr Arg Ile Tyr Arg Gly Val Glu Pro Gln Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Asp Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Asp Gln Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
            260                 265                 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Asn
        275                 280                 285
```

```
Pro Pro Glu Asp Ile Ser Ser Asn Arg Ile Tyr Arg Ile Leu Glu Met
    290                 295                 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Lys Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Thr His Glu Phe Tyr Val Arg Lys Gly Gly Ala Arg Lys Arg Pro Ala
                485                 490                 495
```

```
Pro Asn Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510


Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Pro Val Asp Tyr Ala Asp
        515                 520                 525


Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
    530                 535                 540


Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Val Asp Ile Cys
545                 550                 555                 560


Phe Thr His Gly Val Met Asp Cys Ala Glu Cys Phe Pro Val Ser Glu
                565                 570                 575


Ser Gln Pro Val Ser Val Val Arg Lys Arg Thr Tyr Gln Lys Leu Cys
            580                 585                 590


Pro Ile His His Ile Met Gly Arg Ala Pro Glu Val Ala Cys Ser Ala
        595                 600                 605


Cys Glu Leu Ala Asn Val Asp Leu Asp Asp Cys Asp Met Glu Gln
    610                 615                 620


<210> 65
<211> 544
<212> PRT
<213> Adeno-associated virus 4

<400> 65
Met Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val
1               5                   10                  15


Glu Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp
            20                  25                  30


His Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr
        35                  40                  45


Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu
    50                  55                  60
```

```
Gly Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp
65                  70                  75                  80

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
                85                  90                  95

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met
            100                 105                 110

Arg Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
        115                 120                 125

Gly Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
    130                 135                 140

Ala Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
145                 150                 155                 160

Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
                165                 170                 175

Gly Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp
            180                 185                 190

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
        195                 200                 205

Thr Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe
    210                 215                 220

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
225                 230                 235                 240

Leu Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr
                245                 250                 255

Thr Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro
            260                 265                 270
```

```
Thr Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile
        275                 280                 285

Lys Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro
    290                 295                 300

Ala Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu
305                 310                 315                 320

Asp Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala
                325                 330                 335

Gly Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly
            340                 345                 350

Pro Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe
        355                 360                 365

Thr Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met
    370                 375                 380

Trp Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr
385                 390                 395                 400

Val Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln
                405                 410                 415

Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
            420                 425                 430

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
        435                 440                 445

Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
    450                 455                 460

Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr
465                 470                 475                 480
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln
                485                 490                 495

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
            500                 505                 510

Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys
        515                 520                 525

Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
    530                 535                 540


<210> 66
<211> 734
<212> PRT
<213> Adeno-associated virus 4

<400> 66
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110
```

```
Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320
```

```
Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525
```

```
Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 67
<211> 598
<212> PRT
<213> Adeno-associated virus 4

<400> 67

```
Thr Ala Pro Gly Lys Lys Arg Pro Leu Ile Glu Ser Pro Gln Gln Pro
1               5                  10                  15

Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Lys Gln Pro Ala Lys Lys
            20                  25                  30

Lys Leu Val Phe Glu Asp Glu Thr Gly Ala Gly Asp Gly Pro Pro Glu
        35                  40                  45

Gly Ser Thr Ser Gly Ala Met Ser Asp Asp Ser Glu Met Arg Ala Ala
    50                  55                  60

Ala Gly Gly Ala Ala Val Glu Gly Gly Gln Gly Ala Asp Gly Val Gly
65                  70                  75                  80

Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly His
                85                  90                  95

Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn
            100                 105                 110

His Leu Tyr Lys Arg Leu Gly Glu Ser Leu Gln Ser Asn Thr Tyr Asn
        115                 120                 125

Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
    130                 135                 140

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
145                 150                 155                 160

Met Arg Pro Lys Ala Met Arg Val Lys Ile Phe Asn Ile Gln Val Lys
                165                 170                 175

Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ala Asn Asn Leu Thr
            180                 185                 190
```

```
Ser Thr Val Gln Ile Phe Ala Asp Ser Ser Tyr Glu Leu Pro Tyr Val
        195                 200                 205

Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe Pro Asn Asp Val
    210                 215                 220

Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val Thr Gly Asn Thr
225                 230                 235                 240

Ser Gln Gln Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
                245                 250                 255

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Ile Thr Tyr Ser
            260                 265                 270

Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
        275                 280                 285

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Trp Gly Leu Gln
    290                 295                 300

Ser Thr Thr Thr Gly Thr Thr Leu Asn Ala Gly Thr Ala Thr Thr Asn
305                 310                 315                 320

Phe Thr Lys Leu Arg Pro Thr Asn Phe Ser Asn Phe Lys Lys Asn Trp
                325                 330                 335

Leu Pro Gly Pro Ser Ile Lys Gln Gln Gly Phe Ser Lys Thr Ala Asn
            340                 345                 350

Gln Asn Tyr Lys Ile Pro Ala Thr Gly Ser Asp Ser Leu Ile Lys Tyr
        355                 360                 365

Glu Thr His Ser Thr Leu Asp Gly Arg Trp Ser Ala Leu Thr Pro Gly
    370                 375                 380

Pro Pro Met Ala Thr Ala Gly Pro Ala Asp Ser Lys Phe Ser Asn Ser
385                 390                 395                 400
```

```
Gln Leu Ile Phe Ala Gly Pro Lys Gln Asn Gly Asn Thr Ala Thr Val
                405                 410                 415

Pro Gly Thr Leu Ile Phe Thr Ser Glu Glu Glu Leu Ala Ala Thr Asn
            420                 425                 430

Ala Thr Asp Thr Asp Met Trp Gly Asn Leu Pro Gly Gly Asp Gln Ser
        435                 440                 445

Asn Ser Asn Leu Pro Thr Val Asp Arg Leu Thr Ala Leu Gly Ala Val
    450                 455                 460

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
465                 470                 475                 480

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
                485                 490                 495

Ile Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
            500                 505                 510

Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro
        515                 520                 525

Val Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Gln
    530                 535                 540

Ile Asp Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu
545                 550                 555                 560

Val Gln Phe Thr Ser Asn Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala
                565                 570                 575

Pro Asp Ala Ala Gly Lys Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg
            580                 585                 590

Tyr Leu Thr His His Leu
        595
```

<210> 68
<211> 129
<212> DNA
<213> Adeno-associated virus 4

<400> 68
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctgcggcca gaggccggca 60

gtctggagac ctttggtgtc cagggcaggg ccgagtgagt gagcgagcgc gcatagaggg 120

agtggccaa 129

<210> 69
<211> 125
<212> DNA
<213> Adeno-associated virus 4

<400> 69
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctggagacc aaaggtctcc 60

agactgccgg cctctggccg gcagggccga gtgagtgagc gagcgcgcat agagggagtg 120

gccaa 125

<210> 70
<211> 4768
<212> DNA
<213> Adeno-associated virus 4

<220>
<221> modified_base
<222> (3009)..(3009)
<223> a, c, g, or t

<400> 70
ttggccactc cctctatgcg cgctcgctca ctcactcggc cctggagacc aaaggtctcc 60

agactgccgg cctctggccg gcagggccga gtgagtgagc gagcgcgcat agagggagtg 120

gccaactcca tcatctaggt ttgcccactg acgtcaatgt gacgtcctag ggttagggag 180

gtccctgtat tagcagtcac gtgagtgtcg tatttcgcgg agcgtagcgg agcgcatacc 240

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<211> 3098
<212> DNA
<213> Adeno-associated virus

<400> 71
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ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gctgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

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acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

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<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu

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                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
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    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
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580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
595 600 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 73
<211> 2495
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

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gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

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<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255
```

```
Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460
```

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Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Thr Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670
```

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 75
<211> 2504
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 75
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcatcacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccaagagact caacttcaag ctcttcaaca tccaggtcaa ggaggtcacg 1200

cagaatgaag gcaccaagac catcgccaat aaccttacca gcacgattca ggtctttacg 1260

gactcggaat accggctccc gtacgtcctc ggctctgcgc accagggctg cctgcctccg 1320

ttcccggcgg acgtcttcat gattcctcag tacgggtacc tgactctgaa caacggcagt 1380

caggccgtgg gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga 1440

acgggcaaca actttgagtt cagctaccag tttgaggacg tgccttttca cagcagctac 1500

gcgcacagcc aaagcctgga ccggctgatg aacccccctca tcgaccagta cctgtactac 1560

ctgtctcgga ctcagtccac gggaggtacc gcaggaactc agcagttgct attttctcag 1620

gccgggccta ataacatgtc ggctcaggcc aaaaactggc tacccgggcc ctgctaccgg 1680

cagcaacgcg tctccacgac actgtcgcaa aataacaaca gcaactttgc ttggaccggt 1740

gccaccaagt atcatctgaa tggcagagac tctctggtaa atcccggtgt cgctatggca 1800

acgcacaagg acgacgaaga gcgatttttt ccatccagcg gagtcttgat gtttgggaaa 1860

cagggagctg gaaaagacaa cgtggactat agcagcgtta tgctaaccag tgaggaagaa 1920

atcaaaacca ccaacccagt ggccacagaa cagtacggcg tggtggccga taacctgcaa 1980

cagcaaaacg ccgctcctat tgtaggggcc gtcaacagtc aaggagcctt acctggcatg 2040

gtctggcaga accgggacgt gtacctgcag ggtcctatct gggccaagat tcctcacacg 2100

gacggcaact ttcatccttc gccgctgatg ggaggctttg gactgaaaca cccgcctcct 2160

cagatcctga ttaagaatac acctgttccc gcggatcctc caactacctt cagtcaagcc 2220

aagccggcgt cgttcatcac gcagtacagc accggacagg tcagcgtgga aattgaatgg 2280

gagctgcaga aagagaacag caagcgctgg aacccagaga ttcagtatac ttccaactac 2340

tacaaatcta caaatgtgga ctttgctgtc aatactgagg gtacttattc agagcctcgc 2400

cccattggca cccgttacct cacccgtaac ctgtaattgc ctgttaatca ataaaccggt 2460

taattcgttt cagttgaact ttggtctctg cgaagggcga attc 2504

<210> 76
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 76
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Ser Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335
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Gln Val Phe Thr Asp Ser Glu Tyr Arg Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
        435                 440                 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540
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Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560


Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575


Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590


Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605


Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620


His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640


Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
                645                 650                 655


Phe Ser Gln Ala Lys Pro Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670


Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685


Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
    690                 695                 700


Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705                 710                 715                 720


Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 77
<211> 3128
<212> DNA
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 77
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctag ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggctaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 78
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 78
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

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Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 79
<211> 3084
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 79
gaattcgccc tttctacggc tgcatcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacgtgcga gaaaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact 660

gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc 720

agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

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caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320

atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380

tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620

caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680

acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt ccccggctct 1920

gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040

tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag 2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct 2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt 2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtcggctca ggccaagaac 2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340

aacagcaatt ttgcttggac cggtgccacc aagtatcacc tgaatggcag agactccctg 2400

gttaatcccg gcgttgccat ggctacccac aaggacgacg aggagcgctt cttcccgtca 2460

agcggagttc taatgtttgg caagcagggg gctggaaaag acaatgtgga ctacagcagc 2520

gtgatgctca ccagcgaaga agaaattaaa actactaacc cagtggctac agagcagtat 2580

ggtgtggtgg cagacaacct gcagcagacc aacggagctc ccattgtggg aactgtcaac 2640

agccaggggg ccttacctgg tatggtctgg caaaaccggg acgtgtacct gcagggcccc 2700

atctgggcca aaattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctggtgaaaa acactcctgt tcctgcggat 2820

cctccgacca ccttcagcca ggccaagctg gcttctttta tcacgcagta cagcaccgga 2880

caggtcagcg tggaaatcga atgggagctg cagaaagaaa acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

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<210> 80
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 80
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
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Asn Leu

<210> 81
<211> 3123
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 81
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aaggccattc tcggcggcag caaggtgcgc gtggaccaaa agtgcaagtc gtccgcccag 180

atcgacccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa gttcgaactc 300

acccgccgtc tggagcacga ctttggcaag gtgaccaagc aggaagtcaa agagttcttc 360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tctacgtcag aaagggcgga 420

gccagcaaaa gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc 480

tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg 540

taccaaaaca aatgttctcg tcacgcgggc atgctccaga tgctgtttcc ctgcaaaacg 600

tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acggggtcag agactgctca 660

gaatgtttcc ccggtgcatc agaatctcaa ccggtcgtca gaaaaaaaac gtatcagaaa 720

ctgtgtgcca ttcatcatct gctggggcgg gcacccgaga ttgcttgctc ggcctgcgat 780

ctggtcaacg tggacctgga cgactgtgtt tctgagcaat aaatgactta aaccaggtat 840

ggctgccgat ggttatcttc cagattggct tgaggacaac ctctctgagg gcattcgcga 900

gtggtgggac ctgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga 960

cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020

gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaagg cctacgacca 1080

gcagctcaaa gcgggtgaca atccgtacct gcggtataac cacgccgacg ccgagtttca 1140

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caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260

aaagaagaga ccggtagagc catcacctca gcgttccccc gactcctcca cgggcatcgg 1320

caagaaaggc caccagcccg cgagaaagag actgaacttt gggcagactg gcgactcgga 1380

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 1440

tggtacaatg gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg 1500

agtgggtagt tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 1560

caccaccagc acccgaacct gggccctgcc cacctacaac aaccatctct acaagcaaat 1620

ctccaacggg acatcgggag gaagcactaa cgacaacacc tactttggct acagcacccc 1680

ctgggggtat tttgacttca acagattcca ctgccacttc tcaccacgtg actggcagcg 1740

actcatcaac aataactggg gattccggcc caagagactc aacttcaagc tcttcaacat 1800

ccaggtcaag gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag 1860

cacgattcag gtgtttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca 1920

ccagggctgc ctccctccgt tcccggcgga cgtcttcatg attcctcagt acgggtatct 1980

gaccctaaac aatggcagtc aggctgtggg ccgttcctcc ttctactgcc tggaatactt 2040

cccttctcaa atgctgagga cgggcaacaa ctttgaattc agctacacct tcgaggacgt 2100

gcctttccac agcagctacg cgcacagcca gagcctggac cggctgatga accctctcat 2160

cgaccagtac ctgtattact tatccagaac tcagtccaca ggaggaactc aaggtactca 2220

gcaattgtta ttttctcaag ccgggcccgc aaacatgtcg gctcaggcca agaactggct 2280

acctggaccg tgttaccgtc agcaacgagt ttccacgaca ctgtcgcaaa acaacaacag 2340

caattttgct tggaccggtg ccaccaagta tcacctgaat ggcagagact ccctggttaa 2400

tcccggcgtt gccatggcta cccacaagga cgacgaggag cgcttcttcc cgtcaagcgg 2460

agttctaatg tttggcaagc agggggctgg aaaagacaat gtggactaca gcagcgtgat 2520

gctcaccagc gaagaagaaa ttaaaactac taacccagtg gctacagagc agtatggtgt 2580

ggtggcagac aacctgcagc agaccaacgg agctcccatt gtgggaactg tcaacagcca 2640

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gggggcctta cctggtatgg tctggcaaaa ccgggacgtg tacctgcagg gccccatctg     2700

ggccaaaatt cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg     2760

actgaaacac ccgcctcctc agatcctggt gaaaaacact cctgttcctg cggatcctcc     2820

gaccaccttc agccaggcca agctggcttc ttttatcacg cagtacagca ccggacaggt     2880

cagcgtggaa atcgaatggg agctgcagaa agaaaacagc aagcgctgga acccagagat     2940

tcagtatact tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg     3000

tacttattca gagcctcgcc ccattggcac tcgttatctc acccgtaatc tgtaattgct     3060

tgttaatcaa taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa     3120

ttc                                                                   3123
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<210> 82
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 82

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
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```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
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Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 83
<211> 3122
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 83
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ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag cgccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

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cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

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ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg 2700

gccaaaattc ctcacacgga cggcaacttt cacccgtctc ccctgatggg cggctttgga 2760

ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggacccgccg 2820

cttaccttca accaggccaa gctgaactct ttcatcacgc agtacagcac cggacaggtc 2880

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt 2940

caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggaagga 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

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tc 3122

<210> 84
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 84
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

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65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Leu Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
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        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
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485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
500 505 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
515 520 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
530 535 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
580 585 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn

690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 85
<211> 3117
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 85
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc 60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc tcggcggcag caaggtgcgt gtggaccaaa agtgcaagtc ttccgcccag 180

atcgatccca cccccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg 240

aacagcacca ccttcgagca ccagcagccg ttgcaggacc ggatgttcaa atttgaactc 300

acccgccgtc tggagcatga ctttggcaag gtgacgaagc aggaagtcaa agagttcttc 360

cgctgggcgc aggatcacgt gaccgaggtg gcgcatgagt tccacgtcag aaagggtgga 420

gccaacaaga gacccgcccc cgatgacgcg gatataagcg agcccaagcg ggcctgcccc 480

tcagtcgcgg atccatcgac gtcagacgcg gaaggagctc cggtggactt tgccgacagg 540

taccaaaaca aatgttctcg tcacgcgggc atgcttcaga tgctgtttcc ctgcaagaca 600

tgcgagagaa tgaatcagaa tttcaacatt tgcttcacgc acgggaccag agactgttca 660

gaatgtttcc ccggcgtgtc agaatctcaa ccggtcgtca gaaagaggac gtatcggaaa 720

ctctgtgcga ttcatcatct gctggggcgg gctcccgaga ttgcttgctc ggcctgcgat 780

ctggtcaacg tggacctgga tgactgtgtt tctgagcaat aaatgactta aaccaggtat 840

ggctgccgat ggttatcttc cagattggct cgaggacaac ctctctgagg gcattcgcga 900

gtggtgggac ttgaaacctg gagccccgaa acccaaagcc aaccagcaaa agcaggacga 960

cggccggggt ctggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 1020

gggggagccc gtcaacgcgg cggacgcagc ggccctcgag cacgacaaag cctacgacca 1080

gcagctcaaa gcgggtgaca atccgtacct gcggtataat cacgccgacg ccgagtttca 1140

ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 1200

caagaagcgg gttctcgaac ctctcggtct ggttgaggaa ggcgctaaga cggctcctgg 1260

aaagaagaga ccggtagagc agtcgccaca agagccagac tcctcctcgg gcatcggcaa 1320

gacaggccag cagcccgcta aaaagagact caattttggt cagactggcg actcagagtc 1380

agtccccgac ccacaacctc tcggagaacc tccagcagcc ccctcaggtc tgggacctaa 1440

tacaatggct tcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt 1500

gggtaattcc tcgggaaatt ggcattgcga ttccacatgg ctgggggaca gagtcatcac 1560

caccagcacc cgaacctggg ccctgcccac ctacaacaac cacctctaca agcaaatctc 1620

caacggcacc tcgggaggaa gcaccaacga caacacctat tttggctaca gcacccctg 1680

ggggtatttt gacttcaaca gattccactg tcacttttca ccacgtgact ggcaacgact 1740

catcaacaac aattggggat tccggcccaa aagactcaac ttcaagctgt tcaacatcca 1800

ggtcaaggaa gtcacgacga acgaaggcac caagaccatc gccaataatc tcaccagcac 1860

cgtgcgggtc tttacggact cggagtacca gttaccgtac gtgctaggat ccgctcacca 1920

gggatgtctg cctccgttcc cggcggacgt cttcatggtt cctcagtacg gctatttaac 1980

tttaaacaat ggaagccaag ccctgggacg ttcctccttc tactgtctgg agtatttccc 2040

atcgcagatg ctgagaaccg gcaacaactt tcagttcagc tacaccttcg aggacgtgcc 2100

tttccacagc agctacgcgc acagccagag cctggacagg ctgatgaatc ccctcatcga 2160

ccagtacctg tactacctgg tcagaacgca aacgactgga actggaggga cgcagactct 2220

ggcattcagc caagcgggtc ctagctcaat ggccaaccag gctagaaatt gggtgcccgg 2280

accttgctac cggcagcagc gcgtctccac gacaaccaac cagagcaaca acagcaactt 2340

tgcctggacg ggagctgcca agtttaagct gaacggccga gactctctaa tgaatccggg 2400

cgtggcaatg gcttcccaca aggatgacga cgaccgcttc ttcccttcga gcggggtcct 2460

gatttttggc aagcaaggag ccgggaacga tggagtggat tacagccaag tgctgattac 2520

agatgaggaa gaaatcaagg ctaccaaccc cgtggccaca gaagaatatg gagcagtggc 2580

catcaacaac caggccgcca atacgcaggc gcagaccgga ctcgtgcaca accaggggt 2640

gattcccggc atggtgtggc agaatagaga cgtgtacctg cagggtccca tctgggccaa 2700

aattcctcac acggacggca actttcaccc gtctcccctg atgggcggct ttggactgaa 2760

gcacccgcct cctcaaattc tcatcaagaa cacaccggtt ccagcggacc cgccgcttac 2820

cttcaaccag gccaagctga actctttcat cacgcagtac agcaccggac aggtcagcgt 2880

ggaaatcgag tgggagctgc agaaagaaaa cagcaaacgc tggaatccag agattcaata 2940

cacttccaac tactacaaat ctacaaatgt ggactttgct gtcaacacgg aaggagttta 3000

tagcgagcct cgccccattg gcacccgtta cctcacccgc aacctgtaat tacatgttaa 3060

tcaataaacc ggttaattcg tttcagttga actttggtct ctgcgaaggg cgaattc 3117

<210> 86
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 86
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
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Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Arg Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Ser
                485                 490                 495
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Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 87
<211> 3121
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 87
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg 60

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120

cgccaaggcc attctcggcg gcagcaaggt gcgtgtggac caaaagtgca agtcttccgc 180

ccagatcgat cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggtgacg aagcaggaag tcaaagagtt 360

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttccacg tcagaaaggg 420

tggcgccaac aagagacccg cccccgatga cgcggatata agcgagccca agcgggcctg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

gacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gcgattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaaggggga gcccgtcaac gcggcggacg cagcggccct cgagcacgac aaagcctacg 1080

accagcagct caaagcgggt gacaatccgt acctgcggta taatcacgcc gacgccgagt 1140

ttcaggagcg tctgcaagaa gatacgtcct ttgggggcaa cctcgggcga gcagtcttcc 1200

aggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 1260

ctggaaagaa gagaccggta gagcagtcgc cacaagagcc agactcctcc tcgggcatcg 1320

gcaagacagg ccagcagccc gctaaaaaga gactcaattt tggtcagact ggcgactcag 1380

agtcagtccc cgacccacaa cctctcggag aacctccagc agccccctca ggtctgggac 1440

ctaatacaat ggcttcaggc ggtggcgctc caatggcaga caataacgaa ggcgccgacg 1500

gagtgggtaa ttcctcggga aattggcatt gcgattccac atggctgggg gacagagtca 1560

tcaccaccag cacccgaacc tgggccctgc ccacctacaa caaccacctc tacaagcaaa 1620

tctccaacgg cacctcggga ggaagcacca acgacaacac ctattttggc tacagcaccc 1680

cctgggggta ttttgacttc aacagattcc actgtcactt ttcaccacgt gactggcaac 1740

gactcatcaa caacaattgg ggattccggc ccaaaagact caacttcaag ctgttcaaca 1800

tccaggtcaa ggaagtcacg acgaacgaag gcaccaagac catcgccaat aatctcacca 1860

gcaccgtgca ggtctttacg gacttggagt accagttacc gtacgtgcta ggatccgctc 1920

accagggatg tctgcctccg ttcccggcgg acgtcttcat ggttcctcag tacggctatt 1980

taactttaaa caatggaagc caagccctgg gacgttcctc cttctactgt ctggagtatt 2040

tcccatcgca gatgccgaga accggcaaca actttcagtt cagctacacc ttcgaggacg 2100

tgcctttcca cagcagctac gcgcacagcc agagcctgga caggctgatg aatcccctca 2160

tcgaccagta cctgtactac ctggtcagaa cgcaaacgac tggaactgga gggacgcaga 2220

ctctggcatt cagccaagcg ggtcctagct caatggccaa ccaggctaga aattgggtgc 2280

ccggaccttg ctaccggcag cagcgcgtct ccacgacaac caaccagaac aacaacagca 2340

actttgcctg gacgggagct gccaagttta agctgaacgg ccgagactct ctaatgaatc 2400

cgggcgtggc aatggcttcc cacaaggatg acgacgaccg cttcttccct tcgagcgggg 2460

tcctgatttt tggcaagcaa ggagccggga acgatggagt ggattacagc caagtgctga 2520

ttacagatga ggaagaaatc aaggctacca accccgtggc cacagaagaa tatggagcag 2580

tggccatcaa caaccaggcc gccaatacgc aggcgcagac cggactcgtg cacaaccagg 2640

gggtgattcc cggcatggtg tggcagaata gagacgtgta cctgcagggt cccatctggg 2700

ccaaaattcc tcacacggac ggcaactttc acccgtctcc cctgatgggc ggctttggac 2760

tgaagcaccc gcctcctcaa attctcatca agaacacacc ggttccagcg gacccgccgc 2820

ttaccttcaa ccaggccaag ctgaactctt tcatcacgca gtacagcacc ggacaggtca 2880

gcgtggaaat cgagtgggag ctgcagaaag aaaacagcaa acgctggaat ccagagattc 2940

aatacacttc caactactac aaatctacaa atgtggactt tgctgtcaac acggaaggag 3000

tttatagcga gcctcgcccc attggcaccc gttacctcac ccgcaacctg taattacatg 3060

ttaatcaata aaccggttaa ttcgtttcag ttgaactttg gtctctgcga agggcgaatt 3120

c 3121

<210> 88
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 88
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

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65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
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        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Pro Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
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485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
500 505 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
515 520 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
530 535 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
580 585 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn

690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 89
<211> 3122
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 89
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgtgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac gaagcaggaa gtcaaagggt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttccac gtgcgagccc 420

aagcgggcct gcccctcagt cgcggatcca tcgacgtcag accagaaagg gtggagccaa 480

caagagaccc gcccccgatg acgcggatat aagcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaagcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataatcacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagcagtcg ccacaagagc cagactcctc ctcgggcatc 1320

ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 1380

gagtcagtcc ccgacccaca acctctcgga gaacctccag cagccccctc aggtctggga 1440

cctaatacaa tggcttcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 1500

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 1560

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 1620

atctccaacg gcacctcggg aggaagcacc aacgacaaca cctattttgg ctacagcacc 1680

ccctgggggt attttgactt caacagattc cactgtcact tttcaccacg tgactggcaa 1740

cgactcatca acaacaattg gggattccgg cccaaaagac tcaacttcaa gctgttcaac 1800

atccaggtca aggaagtcac gacgaacgaa ggcaccaaga ccatcgccaa taatctcacc 1860

agcaccgtgc aggtctttac ggactcggag taccagttac cgtacgtgct aggatccgct 1920

caccagggat gtctgcctcc gttcccggcg gacgtcttca tggttcctca gtacggctat 1980

ttaactttaa acaatggaag ccaagccctg ggacgttcct ccttctactg tctggagtat 2040

ttcccatcgc agatgctgag aaccggcaac aactttcagt tcagctacac cttcgaggac 2100

gtgcctttcc acagcagcta cgcgcacagc cagagcctgg acaggctgat gaatcccctc 2160

atcgaccagt acctgtacta cctggtcaga acgcaaacga ctggaactgg agggacgcag 2220

actctggcat tcagccaagc gggtcctagc tcaatggcca accaggctag aaattgggtg 2280

cccggacctt gctaccggca gcagcgcgtc tccacgacaa ccaaccagaa caacaacagc 2340

aactttgcct ggacgggagc tgccaagttt aagctgaacg gccgagactc tctaatgaat 2400

ccgggcgtgg caatggcttc ccacaaggat gacgacgacc gcttcttccc ttcgagcggg 2460

gtcctgattt ttggcaagca aggagccggg aacgatggag tggattacag ccaagtgctg 2520

attacagatg aggaagaaat caaggctacc aaccccgtgg ccacagaaga atatggagca 2580

gtggccatca acaaccaggc cgccaatacg caggcgcaga ccggactcgt gcacaaccag 2640

ggggtgattc ccggcatggt gtggcagaat agagacgtgt acctgcaggg tcccatctgg 2700

gccaaaattc ctcacacgga cggcaacttt cacccgtctc ccctgatggg cggctttgga 2760

ctgaagcacc cgcctcctca aattctcatc aagaacacac cggttccagc ggacccgccg 2820

cttaccttca accaggccaa gctgaactct ttcatcacgc agtacagcac cggacaggtc 2880

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca aacgctggaa tccagagatt 2940

caatacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg 3000

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaattacat 3060

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 90
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 90
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270
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Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480
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Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
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Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 91
<211> 2370
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 91
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagttcg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac caagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gcggagccag caaaagaccc gcccccgatg acgcggatat aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagacgctg tttccctgca 600

aaacgtgcga gagaatgaat cagaatttca acatttgctt cacgcacggg gtcagagact 660

gctcagaatg tttccccggt gcatcagaat ctcaaccggt cgtcagaaaa aaaacgtatc 720

agaaactgtg tgccattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggacgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggcttgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacctgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

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caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca cctcagcgtt cccccgactc ctccacgggc 1320

atcggcaaga aaggccacca gcccgcgaga aagagactga actttgggca gactggcgac 1380

tcggagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca tctctacaag 1620

caaatctcca acgggacatc gggaggaagc actaacgaca acacctactt tggctacagc 1680

acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaataa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtgtt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctccc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tatctgaccc taaacaatgg cagtcaggct gtgggccgtt cctccttcta ctgcctggaa 2040

tacttccctt ctcaaatgct gaggacgggc aacaactttg aattcagcta caccttcgag 2100

gacgtgcctt tccacagcag ctacgcgcac agccagagcc tggaccggct gatgaaccct 2160

ctcatcgacc agtacctgta ttacttatcc agaactcagt ccacaggagg aactcaaggt 2220

actcagcaat tgttattttc tcaagccggg cccgcaaaca tgtyggctca ggccaagaac 2280

tggctacctg gaccgtgtta ccgtcagcaa cgagtttcca cgacactgtc gcaaaacaac 2340

aacagcaatt ttgctggacc ggtgccacca 2370

<210> 92
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 92
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln

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                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
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    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
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580 585 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 93
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 93
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggaccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

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tttatggtgc cccagtacgg ctactgtgga ctggtgaccg gcaacacttc gcagcaacag 1140

actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 94
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 94
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

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Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270
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Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480
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Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685
```

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 95
<211> 3128
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 95
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gcgtcgacaa gatgttgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagccgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgcg ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact gtaaatcccg gtgtcgctat ggcaacccac aaggacgacg aagagcgatt 2400

ttgcctggac cggtgccacc aagtatcatc tgaatggcag agactctctg ttttccgtcc 2460

agcggagtct taatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac ggaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccca 2940

gagattcaat acacttccaa ctactacaaa tctacaaatg tggacttcgc tgttaacaca 3000

gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

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gcgaattc 3128

<210> 96
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 96
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
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Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480
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Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 97
<211> 3128
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 97
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gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt tgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg ggcgggcacc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctagatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga aaggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacttc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gacccaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

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tacctgactc tgaacaatgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

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aacagcaact ttgcctggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacccac aaggacgacg aagagcgatt ttttccgtcc 2460

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gttatgctaa ccagtgagga agaaattaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacgga aactttcatc cctcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agctaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaaa acagcaaacg ctggaaccca 2940

gagattcaat acacttccaa ctactacaaa tctacaaatg tggactttgc tgttaacaca 3000

gatggcactt attctgagcc tcgccccatt ggcacccgtt acctcacccg taatctgtaa 3060

ttgcttgtta atcaataaac cggttgattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 98
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 98
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
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Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Pro Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
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Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670
```

```
Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 99
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 99
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 100
<211> 2172
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 100
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tt 2172

<210> 101
<211> 720
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 101
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

```
Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400
```

```
Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605
```

```
Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
```

<210> 102
<211> 724
<212> PRT
<213> Adeno-associated virus 5

<400> 102

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Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60
```

```
Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270
```

```
Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480
```

```
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685
```

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 103
<211> 2175
<212> DNA
<213> Adeno-associated virus

<400> 103
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 104
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 104
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

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tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

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<211> 736
<212> PRT
<213> Adeno-associated virus 6

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
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Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510
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Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720
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Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 106
<211> 623
<212> PRT
<213> Adeno-associated virus 6

<400> 106
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
165 170 175

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Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala His Asp
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380
```

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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
                485                 490                 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
    530                 535                 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560

Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565                 570                 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580                 585                 590
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Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 107
<211> 4683
<212> DNA
<213> Adeno-associated virus 6

<400> 107
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gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240

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ggtttgaacg cgcagcgcca tgccggggtt ttacgagatt gtgattaagg tccccagcga 360

ccttgacgag catctgcccg gcatttctga cagctttgtg aactgggtgg ccgagaagga 420

atgggagttg ccgccagatt ctgacatgga tctgaatctg attgagcagg caccctgac 480

cgtggccgag aagctgcagc gcgacttcct ggtccagtgg cgccgcgtga gtaaggcccc 540

ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc tccatattct 600

ggtggagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc agattaggga 660

caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact ggttcgcggt 720

gaccaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt gctacatccc 780

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caa 4683

<210> 108
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

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gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

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tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

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<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
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Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 110
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 110
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
```

```
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 111
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 111
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210> 112
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 112
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 113
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 113
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

gcaaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacag tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

attaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg aaactgcagg tagtaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020

acgattcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca atggcagtca gtctgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac tttgagttca gctacagctt cgaggacgtg 1260

cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcccctcatc 1320

gaccagtact tgtactacct ggccagaaca cagagtaacc caggaggcac agctggcaat 1380

cgggaactgc agttttacca gggcgggcct tcaactatgg ccgaacaagc caagaattgg 1440

ttacctggac cttgcttccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt 1560

aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca actaacaaaa ctacattgga aaatgtgtta 1680

atgacaaatg aagaagaaat tcgtcctact aatcctgtag ccacggaaga atacgggata 1740

gtcagcagca acttacaagc ggctaatact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg 1980

gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc 2040

agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt 2100

cagtacacct ccaactttga aaagcagact ggtgtggact ttgccgttga cagccagggt 2160

gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct gtaa 2214

<210> 114
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 114
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

```
Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 115
<211> 737
<212> PRT
<213> Adeno-associated virus 7

<400> 115

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

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Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700
```

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 116
<211> 623
<212> PRT
<213> Adeno-associated virus 7

<400> 116
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110

Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Val Glu Pro Thr Leu
115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140

```
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275                 280                 285

Leu Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350
```

```
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
                485                 490                 495

Pro Asp Asp Ala Asp Ile Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Ile Gln Met
    530                 535                 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560
```

Cys Phe Thr His Gly Val Arg Asp Cys Leu Glu Cys Phe Pro Gly Val
565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Lys Thr Tyr Arg Lys Leu Cys
580 585 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 117
<211> 4721
<212> DNA
<213> Adeno-associated virus 7

<400> 117
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gccaactcca tcactagggg taccgcgaag cgcctcccac gctgccgcgt cagcgctgac 180

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attttgaccg cgaaatttga acgagcagca gccatgccgg gtttctacga gatcgtgatc 360

aaggtgccga gcgacctgga cgagcacctg ccgggcattt ctgactcgtt tgtgaactgg 420

gtggccgaga aggaatggga gctgcccccg gattctgaca tggatctgaa tctgatcgag 480

caggcacccc tgaccgtggc cgagaagctg cagcgcgact tcctggtcca atggcgccgc 540

gtgagtaagg ccccggaggc cctgttcttt gttcagttcg agaagggcga gagctacttc 600

caccttcacg ttctggtgga gaccacgggg gtcaagtcca tggtgctagg ccgcttcctg 660

agtcagattc gggagaagct ggtccagacc atctaccgcg gggtcgagcc cacgctgccc 720

aactggttcg cggtgaccaa gacgcgtaat ggcgccggcg gggggaacaa ggtggtggac 780

gagtgctaca tccccaacta cctcctgccc aagacccagc ccgagctgca gtgggcgtgg 840

actaacatgg aggagtatat aagcgcgtgt ttgaacctgg ccgaacgcaa acggctcgtg 900

gcgcagcacc tgacccacgt cagccagacg caggagcaga acaaggagaa tctgaacccc 960

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tacatctcct tcaacgccgc ctccaactcg cggtcccaga tcaaggccgc gctggacaat 1140

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cacgattcag gtattctcgg actcggaata ccagctgccg tacgtcctcg gctctgcgca 3300

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cgctcgctcg gtggggcctg cggaccaaag gtccgcagac ggcagagctc tgctctgccg 4680

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<210> 118
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

gcaaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

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ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga 1920

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gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc 2040

agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt 2100

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<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
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Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
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```
Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
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<210> 120
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

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gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

cagggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 121
<211> 2213
<212> DNA
<213> Adeno-associated virus 8

<400> 121
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

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atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

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caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

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attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

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caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

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atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt aatacagaag 2160

gcgtgtactc tgaaccccgc cccattggca cccgttacct cacccgtaat ctg 2213

<210> 122
<211> 4393
<212> DNA
<213> Adeno-associated virus 8

<400> 122
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tgcttttgcg gcattttgcg acaccacgtg gccatttgag gtatatatgg ccgagtgagc 180

gagcaggatc tccattttga ccgcgaaatt tgaacgagca gcagccatgc cgggcttcta 240

cgagatcgtg atcaaggtgc cgagcgacct ggacgagcac ctgccgggca tttctgactc 300

gtttgtgaac tgggtggccg agaaggaatg ggagctgccc ccggattctg acatggatcg 360

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ccaatggcgc cgcgtgagta aggccccgga ggccctcttc tttgttcagt tcgagaaggg 480

cgagagctac tttcacctgc acgttctggt cgagaccacg ggggtcaagt ccatggtgct 540

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ggggaacaag gtggtggacg agtgctacat ccccaactac ctcctgccca agactcagcc 720

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ctatatggag ctggtcgggt ggctggtgga ccggggcatc acctccgaga agcagtggat 960

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ggccaaggtc gtggagtccg ccaaggccat tctcggcggc agcaaggtgc gcgtggacca 1440

aaagtgcaag tcgtccgccc agatcgaccc cacccccgtg atcgtcacct ccaacaccaa 1500

catgtgcgcc gtgattgacg ggaacagcac caccttcgag caccagcagc ctctccagga 1560

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gatgctgttt ccctgcaaaa cgtgcgagag aatgaatcag aatttcaaca tttgcttcac 1920

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gcaagcgctg gaaccccgag atccagtaca cctccaacta ctacaaatct acaagtgtgg 4260

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tcacccgtaa tctgtaattg cctgttaatc aataaaccgg ttgattcgtt tcagttgaac 4380

tttggtctct gcg 4393

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<211> 738
<212> PRT
<213> Adeno-associated virus 8

<400> 123
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
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Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560
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Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590


Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
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<210> 124
<211> 737
<212> PRT
<213> Adeno-associated virus 8

<400> 124
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180   185   190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195   200   205

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Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415
```

```
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Ile Gln Lys
705                 710                 715                 720

Ala Cys Thr Leu Asn Pro Ala Pro Leu Ala Pro Val Thr Ser Pro Val
                725                 730                 735

Ile
```

<210> 125
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 125
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 126
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 126
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgcc tgagcggacg gcgatgagtc ttccgggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 127
<211> 738

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 127
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

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Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
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Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Pro Glu Arg Thr Ala Met
            580                 585                 590
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```
Ser Leu Pro Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 128
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 128

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgag ttttagtcgt gcggttcttt gtgatggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 129
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 129
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
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Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495
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Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Ser Phe Ser Arg Ala Val
            580                 585                 590

Leu Cys Asp Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 130
<211> 4385
<212> DNA
<213> Adeno-associated virus 9

<400> 130
cagagaggga gtggccaact ccatcactag gggtaatcgc gaagcgcctc ccacgctgcc 60

gcgtcagcgc tgacgtagat tacgtcatag gggagtggtc ctgtattagc tgtcacgtga 120

gtgcttttgc gacattttgc gacaccacat ggccatttga ggtatatatg gccgagtgag 180

cgagcaggat ctccattttg accgcgaaat ttgaacgagc agcagccatg ccgggcttct 240

acgagattgt gatcaaggtg ccgagcgacc tggacgagca cctgccgggc atttctgact 300

cttttgtgaa ctgggtggcc gagaaggaat gggagctgcc cccggattct gacatggatc 360

ggaatctgat cgagcaggca cccctgaccg tggccgagaa gctgcagcgc gacttcctgg 420

tccaatggcg ccgcgtgagt aaggccccgg aggccctctt ctttgttcag ttcgagaagg 480

gcgagagcta ctttcacctg cacgttctgg tcgagaccac gggggtcaag tccatggtgc 540

taggccgctt cctgagtcag attcgggaga agctggtcca gaccatctac cgcgggatcg 600

agccgaccct gcccaactgg ttcgcggtga ccaagacgcg taatggcgcc ggcgggggga 660

acaaggtggt ggacgagtgc tacatcccca actacctcct gcccaagact cagcccgagc 720

tgcagtgggc gtggactaac atggaggagt atataagcgc gtgcttgaac ctggccgagc 780

gcaaacggct cgtggcgcag cacctgaccc acgtcagcca gacgcaggag cagaacaagg 840

agaatctgaa ccccaattct gacgcgcccg tgatcaggtc aaaaacctcc gcgcgctaca 900

tggagctggt cgggtggctg gtggaccggg gcatcacctc cgagaagcag tggatccagg 960

aggaccaggc ctcgtacatc tccttcaacg ccgcctccaa ctcgcggtcc cagatcaagg 1020

ccgcgctgga caatgccggc aagatcatgg cgctgaccaa atccgcgccc gactacctgg 1080

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ctgcg 4385

<210> 131
<211> 4382
<212> DNA
<213> Adeno-associated virus 9

<400> 131
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gtgcttttgc gacattttgc gacaccacat ggccatttga ggtatatatg gccgagtgag 180

cgagcaggat ctccattttg accgcgaaat ttgaacgagc agcagccatg ccgggcttct 240

acgagattgt gatcaaggtg ccgagcgacc tggacgagca cctgccgggc atttctgact 300

cttttgtgaa ctgggtggcc gagaaggaat gggagctgcc cccggattct gacatggatc 360

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cg 4382

<210> 132
<211> 736
<212> PRT
<213> Adeno-associated virus 9

<400> 132
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

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Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

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Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 133
<211> 736
<212> PRT
<213> Adeno-associated virus 9

<400> 133
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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Glu Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415
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Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 134
<211> 623
<212> PRT
<213> Adeno-associated virus 9

<400> 134
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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Arg Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

```
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Val Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Glu Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ser
        275                 280                 285
```

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Leu Pro Val Asp Ile Thr Gln Asn Arg Ile Tyr Arg Ile Leu Gln Leu
    290                 295                 300

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Ser Asp His Val Thr Glu Val
465                 470                 475                 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Ser Lys Arg Pro Ala
                485                 490                 495
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Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
530 535 540

Leu Leu Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545 550 555 560

Cys Phe Thr His Gly Val Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
580 585 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 135
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 135
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 136
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 136
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

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            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
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305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
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        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 137
<211> 2460
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 137
ggtaattcct ccggaaattg gcattgcgat tccacatggc tgggcgaccg agtcattacc 60

accagcaccc ggacttgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc 120

agccaatcgg gtgccaccaa cgacaaccac tacttcggct acagcacccc ttgggggtat 180

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 240

aacaactggg gattcatggc tgccgatggt tatcttccag attggctcga ggacactctc 300

tctgaaggaa tcagacagtg gtggaagctc aaacctggcc caccaccgcc gaaacctaac 360

caacaacacc gggacgacag taggggtctt gtgcttcctg ggtacaagta cctcggaccc 420

ttcaacggac tcgacaaagg agagccggtc aacgaggcag acgccgcggc cctcgagcac 480

gacaaagcct acgaccacca gctcaagcaa ggggacaacc cgtacctcaa atacaaccac 540

gcggacgctg aatttcagga gcgtcttcaa gaagatacgt ctttcggggg caacctcggg 600

cgagcagtct tccaggccaa aaagagggta ctcgagcctc ttggtctggt tgaggaagct 660

gttaagacgg ctcctggaaa aaagagacct atagagcagt ctcctgcaga accggactct 720

tcctcgggca tcggcaaatc aggccagcag cccgctaaga aaagactcaa ttttggtcag 780

actggcgaca cagagtcagt cccagaccct caaccaatcg gagaaccccc cgcagccccc 840

tctggtgtgg gatctaatac aatggcttca ggcggtgggg caccaatggc agacaataac 900

gaaggcgccg acggagtggg taattcctcg ggaaattggc attgcgattc cacatggatg 960

ggcgacagag ttatcaccac cagcacaaga acctgggccc tccccaccta caataatcac 1020

ctctacaagc aaatctccag cgaatcggga gccaccaacg acaaccacta cttcggctac 1080

agcaccccct gggggtattt tgactttaac agattccact gtcacttctc accacgtgac 1140

tggcagcgac tcatcaacaa caactgggga tttagaccca agaaactcaa tttcaagctc 1200

ttcaacatcc aagtcaagga ggtcacgcag aatgatggaa ccacgaccat cgccaataac 1260

cttaccagca cggtgcaggt cttcacagac tctgagtacc agctgcccta cgtcctcggt 1320

tcggctcacc agggctgcct tccgccgttc ccagcagacg tcttcatgat tcctcagtac 1380

ggctacttga ctctgaacaa tggcagccaa gcggtaggac gttcttcatt ctactgtcta 1440

gagtattttc cctctcagat gctgaggacg ggaaacaact tcaccttcag ctacactttt 1500

gaagacgtgc ctttccacag cagctacgcg cacagccaga gtctggatcg gctgatgaat 1560

cctctcattg accagtacct gtattacctg agcaaaactc agggtacaag tggaacaacg 1620

cagcaatcga gactgcagtt cagccaagct gggcctagct ccatggctca gcaggccaaa 1680

aactggctac cgggacccag ctaccgacag cagcgaatgt ctaagacggc taatgacaac 1740

aacaacagtg aatttgcttg gactgcagcc accaaatatt acctgaatgg aagaaattct 1800

ctggtcaatc ccgggccccc aatggccagt cacaaggacg atgaggaaaa gtatttcccc 1860

atgcacggaa atctcatctt tggaaaacaa ggcacaggaa ctaccaatgt ggacattgaa 1920

tcagtgctta ttacagacga agaagaaatc agaacaacta atcctgtggc tacagaacaa 1980

tacggacagg ttgccaccaa ccatcagagt cagaacacca cagcttccta tggaagtgtg 2040

gacagccagg gaatcttacc tggaatggtg tggcaggacc gcgatgtcta tcttcaaggt 2100

cccatttggg ccaaaactcc tcacacggac ggacactttc atccttctcc gctcatggga 2160

ggctttggac tgaaacaccc tcctccccag atcctgatca aaaacacacc tgtgccagcg 2220

aatcccgcga ccactttcac tcctggaaag tttgcttcgt tcattaccca gtattccacc 2280

ggacaggtca gcgtggaaat agagtgggag ctgcagaaag aaaacagcaa acgctggaac 2340

ccagaaattc agtacacctc caactacaac aagtcggtga atgtggagtt taccgtggac 2400

gcaaacggtg tttattctga accccgccct attggcactc gttaccttac ccggaacttg 2460

<210> 138
<211> 3123
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 138
gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat 120

ctgccaaagc cattctgggt ggaggcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg 300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact 360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg 420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc 480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcggaca 540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac 600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt 660

tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga 720

aactttgtta cattcatcat atcatgggaa aagtaccaga cgcctgcact gcctgcgacc 780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg 840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag 900

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcaaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccaggcc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cgcggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcagccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccagtggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccatcaga gtcagaacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760

cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatcccgc gaccactttc 2820

actcctggaa agtttgcttc gttcattacc cagtattcca cctgacaggt cagcgtggaa 2880

atagagtggg agctgcagaa agaaaacagc aaacgctgga acccagaaat tcagtacacc 2940

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gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taagccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttcgtttaaa 3120

cct 3123

<210> 139
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 139
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Gly Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Ala Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
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Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Val Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560
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```
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 140
<211> 3123
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 140

gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat 120

ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg 300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact 360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg 420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc 480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcgggca 540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac 600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt 660

tggaatgctt tcccgtgtca gaatctcaac ccgtttctgt cgtcagaaaa acgtatcaga 720

aactttgtta cattcatcat atcatgggaa aagaaccaga cgcctgcact gcctgcgacc 780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg 840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag 900

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcgaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacgata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cacggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcagccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacctgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacaac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccatcaga gtcaggacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760

cctcctcccc agatcctgat caaaaacaca cctgtgccag cgaatcccgc gaccactttc 2820

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tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct 3000

gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttcgcggccg 3120

cta 3123

<210> 141
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 141
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg

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    130                 135                 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Glu Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asp Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
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            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
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545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asp Thr Thr Ala Ser Tyr
580 585 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 142
<211> 3113
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 142
gaattcgccc tttctacggc tgcgtcaact ggaccaatga aaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggaaagat gaccgccaag gtcgtggaat 120

ctgccaaagc cattctgggt ggaagcaagg ttcgtgtgga ccagaaatgc aagtcttcgg 180

cccagatcga cccgactccg gtgattgtca cctctaacac caacatgtgc gccgtgattg 240

acggaaactc gaccaccttc gagcaccagc agccgttgca agaccggatg ttcaaatttg 300

aacttacccg ccgtttggat catgactttg ggaaggtcac caagcaggaa gtcaaagact 360

ttttccggtg ggctcaagat cacgtgactg aggtggagca tgagttctac gtcaaaaagg 420

gtggagccaa gaaaaggccc gcccccgatg atgtatatat aaatgagccc aagcgggcgc 480

gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc ttcgataaac tacgcggaca 540

ggtaccaaaa caaatgttct cgtcacgtgg gcatgaatct gatgctgttt ccctgtcgac 600

aatgcgaaag aatgaatcag aattcaaata tctgcttcac acacgggcaa aaagactgtt 660

tggaatgctt tcccgtgtca gaatctcaac ccgttcctgt cgtcagaaaa acgtatcaga 720

aactttgtta cattcatcat atcatgggaa aagtaccaga cgcctgcact gcctgcgacc 780

tggtaaatgt ggacttggat gactgtattt ctgagcaata aatgacttaa atcaggtatg 840

gctgctgacg gttatcttcc agattggctc gaggacactc tctctgaagg aatcagacag 900

tggtggaagc tcaaacctgg cccaccaccg ccgaaaccta accaacaaca ccgggacgac 960

agtaggggtc ttgtgcttcc tgggtacaag tacctcggac ccttcaacgg actcgacaaa 1020

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaagc ctacgaccac 1080

cagctcaagc aaggggacaa cccgtacctc aaatacaacc acgcggacgc tgaatttcag 1140

gagcgtcttc aagaagatac gtctttcggg ggcaacctcg ggcgagcagt cttccaggcc 1200

aaaaagaggg tactcgagcc tcttggtctg gttgaggaag ctgttaagac ggctcctgga 1260

aaaaagagac ctatagagca gtctcctgca gaaccggact cttcctcggg catcggcaaa 1320

tcaggccagc agcccgctaa gaaaagactc aattttggtc agactggcga cacagagtca 1380

gtcccagacc ctcaaccaat cggagaaccc cccgcagccc cctctggtgt gggatctaat 1440

acaatggctt caggcggtgg ggcaccaatg gcagacaata acgaaggcgc cgacggagtg 1500

ggtaattcct cgggaaattg gcattgcgat tccacatgga tgggcgacag agttatcacc 1560

accagcacaa gaacctgggc cctccccacc tacaataatc acctctacaa gcaaatctcc 1620

agcgaatcgg gagccaccaa cgacaaccac tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgtcacttc tcaccacgtg actggcagcg actcatcaat 1740

aacaactggg gatttagacc caagaaactc aatttcaagc tcttcaacat ccaagtcaag 1800

gaggtcacgc agaatgatgg aaccacgacc atcgccaata accttaccag cacggtgcag 1860

gtcttcacag actctgagta ccagctgccc tacgtcctcg gttcggctca ccagggctgc 1920

cttccgccgt tcccagcaga cgtcttcatg attcctcagt acggctactt gactctgaac 1980

aatggcagcc aagcggtagg acgttcttca ttctactgtc tagagtattt tccctctcag 2040

atgctgagga cgggaaacaa cttcaccttc agctacactt ttgaagacgt gcctttccac 2100

agcagctacg cgcacagcca gagtctggat cggctgatga atcctctcat tgaccagtac 2160

ctgtattacc tgagcaaaac tcagggtaca agtggaacaa cgcagcaatc gagactgcag 2220

ttcaaccaag ctgggcctag ctccatggct cagcaggcca aaaactggct accgggaccc 2280

agctaccgac agcagcgaat gtctaagacg gctaatgaca acaacaacag tgaatttgct 2340

tggactgcag ccaccaaata ttacccgaat ggaagaaatt ctctggtcaa tcccgggccc 2400

ccaatggcca gtcacaagga cgatgaggaa aagtatttcc ccatgcacgg aaatctcatc 2460

tttggaaaac aaggcacagg aactaccaat gtggacattg aatcagtgct tattacagac 2520

gaagaagaaa tcagaacgac taatcctgtg gctacagaac aatacggaca ggttgccacc 2580

aaccgtcaga gtcagaacac cacagcttcc tatggaagtg tggacagcca gggaatctta 2640

cctggaatgg tgtggcagga ccgcgatgtc tatcttcaag gtcccatttg ggccaaaact 2700

cctcacacgg acggacactt tcatccttct ccgctcatgg gaggctttgg actgaaacac 2760

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actcctggaa agtttgcttc gttcattacc cagtattcca ccggacaggt cagcgtggaa 2880

atagagtggg agctgcagaa agaaaacagc aaacgctgga acccggaaat tcagtacacc 2940

tccaactaca acaagtcggt gaatgtggag tttaccgtgg acgcaaacgg tgtttattct 3000

gaaccccgcc ctattggcac tcgttacctt acccggaact tgtaatttcc tgttaatgaa 3060

taaaccgatt tatgcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 143
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 143
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
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Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Asn Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Pro Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545                 550                 555                 560
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Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn Arg Gln Ser Gln Asn Thr Thr Ala Ser Tyr
            580                 585                 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 144
<211> 3122
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 144
agcggccgcg aattcgccct ttctacggct gcgtcaactg gaccaatgaa aactttccct 60

tcaacgattg cgtcgacaag atggtgatct ggtgggagga gggaaagatg accgccaagg 120

tcgtggaatc tgccaaagcc attctgggtg gaagcaaggt tcgtgtggac cagaaatgca 180

ggtcttcggc ccagatcgac ccgactccgg tgattgtcac ctctaacacc aacatgtgcg 240

ccgtgattga cggaaactcg accaccttcg agcaccagca gccgttgcaa gaccggatgt 300

tcaaatttga acttacccgc cgtttggatc atgactttgg gaaggtcacc aagcaggaag 360

tcaaagactt tttccggtgg gctcaagatc acgtgactga ggtggagcat gagttctacg 420

tcaaaaaggg tggagccaag aaaaggcccg cccccgatga tgtatatata aatgagccca 480

agcgggcgcg cgagtcagtt gcgcagccat cgacgtcaga cgcggaagct tcgataaact 540

acgcggacag gtaccaaaac aaatgttctc gtcacgtggg catgaatctg atgctgtttc 600

cctgtcgaca atgcgaaaga atgaatcaga attcaaatat ctgcttcaca cacgggcaaa 660

aagactgttt ggaatgcttt cccgtgtcag aatctcaacc cgtttctgtc gtcagaaaaa 720

cgtatcagaa actttgttac attcatcata tcatgggaaa agtaccagac gcctgcactg 780

cctgcgacct ggtaaatgtg gacttggatg actgtatttc tgagcaataa atgacttaaa 840

tcaggtatgg ctgctgacgg ttatcttcca gattggctcg aggacactct ctctgaagga 900

atcagacagt ggtggaagct caaacctggc ccaccaccgc cgaaacctaa ccaacaacac 960

cgggacgaca gtaggggtct tgtgcttcct gggtacaagt acctcggacc cttcaacgga 1020

ctcgacaaag gagagccggt caacgaggca gacgccgcgg ccctcgagca cgacaaagcc 1080

tacgaccacc agctcaagca aggggacaac ccgtacctca aatacaacca cgcggacgct 1140

gaatttcagg agcgtcttca agaagatacg tctttcgggg gcaacctcgg gcgagcagtc 1200

ttccaggcca aaaagagggt actcgagcct cttggtctgg ttgaggaagc tgttaagacg 1260

gctcctggaa aaaagagacc tatagagcag tctcctgcag aaccggactc ttcctcgggc 1320

atcggcaaat caggccagca gcccgctaag aaaagactca attttggtca gactggcgac 1380

acagagtcag tcccagaccc tcaaccaatc ggagaacccc ccgcagcccc ctctggtgtg 1440

ggatctaata caatggcttc aggcggtggg gcaccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtaattcctc gggaaattgg cattgcgatt ccacatggat gggcgacaga 1560

gttatcacca ccagcacaag aacctgggcc ctccccacct acaataatcg cctctacaag 1620

caaatctcca gcgaatcggg agccaccaac gacaaccact acttcggcta cagcaccccc 1680

tgggggtatt ttgactttaa cagattccac tgtcacttct caccacgtga ctggcagcga 1740

ctcatcaaca acaactgggg atttagaccc aagaaactca atttcaagct cttcaacatc 1800

caagtcaagg aggtcacgca gaatgatgga accacgacca tcgccaataa ccttaccagc 1860

acggtgcagg tcttcacaga ctctgagtac cagctgccct acgtcctcgg ttcggctcac 1920

cagggctgcc ttccgccgtt cccagcagac gtcttcatga ttcctcagta cggctacttg 1980

actctgaaca atggcagcca agcggtagga cgttcttcat tctactgtct agagtatttt 2040

ccctctcaga tgctgaggac gggaaacaac ttcaccttca gctacacttt tgaagacgtg 2100

cctttccaca gcagctacgc gcacagccag agtctggatc ggctgatgaa tcctctcatt 2160

gaccagtacc tgtattacct gagcaaaact cagggtacaa gtggaacaac gcagcaatcg 2220

agactgcagt tcagccaagc tgggcctagc tccatggctc agcaggccaa aaactggcta 2280

ccgggaccca gctaccgaca gcagcgaatg tctaagacgg ctaatgacaa caacaacagt 2340

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cccgggcccc caatggccag tcacaaggac gatgaggaaa agtatttccc catgcacgga 2460

aatctcatct ttggaaaaca aggcacagga actaccaatg tggacattga atcagtgctt 2520

attacagacg aagaagaaat cagaacaact aatcctgtgg ctacagaaca atacggacag 2580

gttgccacca accatcagag tcagaacacc acagcttcct atggaagtgt ggacagccag 2640

ggaatcttac ctggaatggt gtggcaggac cgcgatgtct atcttcaagg tcccatttgg 2700

gccaaaactc ctcacacgga cggacacttt catccttctc cgctcatggg aggctttgga 2760

ctgaaacacc ctcctcccca gatcctgatc aaaaacacac ctgtgccagc gaatcccgcg 2820

accactttca ctcctggaaa gtttgcttcg ttcattaccc agtattccac cggacaggtc 2880

agcgtggaaa tagagtggga gctgcagaaa gaaaacagca aacgctggaa cccagaaatt 2940

cagtacacct ccaactacaa caagtcggtg aatgtggagt ttaccgtgga cgcaaacggt 3000

gtttattctg aaccccgccc tattggcact cgttacctta cccggaactt gtaatttcct 3060

gttaatgaat aaaccgattt atgcgtttca gttgaacttt ggtctctgcg aagggcgaat 3120

tc 3122

<210> 145
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 145
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg

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    130                 135                 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
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            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
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545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
580 585 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Thr Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 146
<211> 3121
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 146
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgggtgccga tggggcgagg ctcagaataa 120

gtgccatctg tgttaacagc aaagtccaca tttgtagatt tgtagtagtt ggaagtgtat 180

tgaatctctg ggttccagcg tttgctgttt tctttctgca gctcccattc aatttccacg 240

ctgacctgtc cggtgctgta ctgcgtgatg aacgacgcca gcttagcttg actgaaggta 300

gttggaggat ccgcgggaac aggtgtattc ttaatcagga tctgaggagg cgggtgtttc 360

agtccaaagc cccccatcag cggcgaggga tgaaagtttc cgtccgtgtg aggaatcttg 420

gcccagatag gaccctgcag gtacacgtcc cggttctgcc agaccatgcc aggtaaggct 480

ccttgactgt tgacggcccc tacaatagga gcggcgtttt gctgttgcag gttatcggcc 540

accacgccgt actgttctgt ggccactggg ttggtggttt taatttcttc ctcactggtt 600

agcataacgc tgctatagtc cacgttgcct tttccagctc cctgtttccc aaacattaag 660

actccgctgg acggaaaaaa tcgctcttcg tcgtccttgt gggttgccat agcgacaccg 720

ggatttacca gagagtctct gccattcaga tgatacttgg tggcaccggt ccaggcaaag 780

ttgctgttgt tattttgcga cagtgtcgtg gagacgcgtt gctgccggta gcagggcccg 840

ggtagccagt ttttggcctg agccgacatg ttattaggcc cggcctgaga aaatagcaac 900

tgctgagttc ctgcggtacc tcccgtggac tgagtccgag acaggtagta caggtactgg 960

tcgatgaggg ggttcatcag ccggtccagg ctttggctgt gcgcgtagct gctgtgaaaa 1020

ggcacgtcct caaactggta gctgaactca aagttgttgc ccgttctcag catttgagaa 1080

ggaaagtact ccaggcagta gaaggaggaa cggcccacgg cctgactgcc attgttcaga 1140

gtcaggtacc cgtactgagg aatcatgaag acgtccgccg ggaacggagg caggcagccc 1200

tggcgcgcag agccgaggac gtacgggagc tggtattccg agtccgtaaa gacctgaatc 1260

gtgctggtaa ggttattggc gatggtcttg gtgccttcat tctgcgtgac ctccttgacc 1320

tggatgttga agagcttgaa gttgagtctc ttgggccgga atccccagtt gttgttgatg 1380

agtcgctgcc agtcacgtgg tgagaagtgg cagtggaatc tgttaaagtc aaaatacccc 1440

caggggggtgc tgtagccgaa gtaggtgttg tcgttggtgc ttcctcccga agtcccgttg 1500

gagatttgct tgtagaggtg gttgttgtag gtggggaggg cccaggttcg ggtgctggtg 1560

gtgatgactc tgtcgcccag ccatgtggaa tcgcaatgcc aatttcctga ggaactaccc 1620

actccgtcgg cgccttcgtt attgtctgcc attggagcgc caccgcctgc agccattgta 1680

ccagatccca gaccagaggg gcctgcgggg ggttctccga ttggttgagg gtcgggcact 1740

gactctgagt cgccagtctg cccaaagttg agtctctttt tcgcgggctg ctggcctttc 1800

ttgccgatgc ccgtagtgga gtctggagaa cgctggggtg atggctctac cggtctcttc 1860

tttccaggag ccgtcttagc gccttcctca accagaccga gaggttcgag aacccgcttc 1920

ttggcctgga agactgctcg tccgaggttg cccccaaaag acgtatcttc ttgcagacgc 1980

tcctgaaact cggcgtcggc gtggttatac cgcaggtacg gattgtcacc cgctttgagc 2040

tgctggtcgt aggccttgtc gtgctcgagg gccgctgcgt ccgccgcgtt gacgggctcc 2100

cccttgtcga gtccgttgaa gggtccgagg tacttgtagc caggaagcac cagaccccgg 2160

ccgtcgtcct gcttttgctg gttggctttg ggcttcgggg ctccaggttt cagcgcccac 2220

cactcgcgaa tgccctcaga gaggttgtcc tcgagccaat ctggaagata accatcggca 2280

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cagatcgcag gcagtgcaag cgtctggcac ctttcccatg atatgatgaa tgtagcacag 2400

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taaacagtct ttctgtccgt gagtgaagca gatatttgaa ttctgattca ttctctcgca 2520

ttgtctgcag ggaaacagca tcagattcat gcccacgtga cgagaacatt tgttttggta 2580

cctgtccgcg tagttgatcg aagcttccgc gtctgacgtc gatggctgcg caactgactc 2640

gcgcacccgt ttgggctcac ttatatctgc gtcactgggg gcgggtcttt tcttggctcc 2700

acccttttg acgtagaatt catgctccac ctcaaccacg tgatcctttg cccaccggaa 2760

aaagtctttg acttcctgct tggtgacctt cccaaagtca tgatccagac ggcgggtgag 2820

ttcaaatttg aacatccggt cttgcaacgg ctgctggtgt tcgaaggtcg ttgagttccc 2880

gtcaatcacg gcgcacatgt tggtgttgga ggtgacgatc acgggagtcg ggtctatctg 2940

ggccgaggac ttgcatttct ggtccacgcg caccttgctt cctccgagaa tggctttggc 3000

cgactccacg accttggcgg tcatcttccc ctcctcccac cagatcacca tcttgtcgac 3060

acagtcgttg aagggaaagt tctcattggt ccagttgacg cagccgtaga agggcgaatt 3120

c 3121

<210> 147
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 147
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Leu
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe His Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
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Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540
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Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560


Gly Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575


Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590


Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605


Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620


His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655


Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685


Ser Lys Arg Arg Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700


Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720


Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730


<210> 148
<211> 735
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 148
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Asn Gln Gln His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

His Gln Leu Lys Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Glu Ser Gly Ala Thr Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
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385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
435 440 445

Gln Gly Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465 470 475 480

Pro Ser Tyr Arg Gln Gln Arg Met Ser Lys Thr Ala Asn Asp Asn Asn
485 490 495

Asn Ser Glu Phe Ala Trp Thr Ala Ala Thr Lys Tyr Tyr Leu Asn Gly
500 505 510

Arg Asn Ser Leu Val Asn Pro Gly Pro Pro Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Tyr Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
530 535 540

Gln Gly Thr Gly Thr Thr Asn Val Asp Ile Glu Ser Val Leu Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Gln Val Ala Thr Asn His Gln Ser Gln Asn Thr Thr Ala Ser Tyr
580 585 590

Gly Ser Val Asp Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp

595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Glu Phe Thr Val Asp Ala Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 149
<211> 3127
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 149
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac atgcaattac agattacggg tgaggtaacg agtgccaata gggcgaggct 120

cagagtaaac accctggctg tcaacggcaa agtccacacc agtctgcttt tcaaagttgg 180

aggtgtactg aatctccggg tcccagcgct tgctgttttc cttctgcagc tcccactcga 240

tttccacgct gacttgtccg gtgctgtact gtgtgatgaa cgaagcaaac ttggcaggag 300

taaacacctc cggaggatta gcgggaacgg gagtgttctt gatcaggatc tgaggaggcg 360

gatgtttaag tccaaagccg cccatcaaag gagacgggtg aaagttgcca tccgtgtgag 420

gaatcttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccag 480

gtaaggctcc ctggttgttg acaacttgtg tctgggctgc agtattagcc gcttgtaagt 540

tgctgctgac tatcccgtat tcttccgtgg ctacaggatt agtaggacga atttcttctt 600

catttgtcat taacacattt tccaatgtag ttttgttagt tgctccagtt tttccaaaaa 660

tcaggactcc gctggatggg aaaaagcggt cctcgtcgtc cttgtgagtt gccatggcga 720

cgccgggatt aaccaacgag tttctgccgt tcaggtgata tttggtggca ccagtccaag 780

caaagttgct gttgttgttt tgatccagcg ttttggagac cctttgttgc cggaagcagg 840

gtccaggtaa ccaattcttg gcttgttcgg ccatagttga aggcccgccc tggtaaaact 900

gcagttcccg attgccagct gtgcctcctg ggtcactctg tgttctggcc aggtagtaca 960

agtactggtc gatgagggga ttcatcagcc ggtccaggct ctggctgtgt gcgtagctgc 1020

tgtggaaagg cacgtcctcg aagctgtagc tgaactcaaa gttgttgccc gttctcagca 1080

tctgagaggg gaagtactcc aggcagtaga aggaggaacg tcccacagac tgactgccat 1140

tgttgagagt caggtagccg tactgaggaa tcatgaagac gtccgccggg aacggaggca 1200

ggcagccctg gtgcgcagag ccgaggacgt acggcagctg gtattccgag tccgagaata 1260

cctgaatcgt gctggtaagg ttattagcga tggtcgtaac gccgtcattc gtcgtgacct 1320

ccttgacctg gatgttgaag agcttgaacc gcagcttctt gggccggaat ccccagttgt 1380

tgttgatgag tcgctgccag tcacgtggtg agaagtggca gtggaatctg ttaaagtcaa 1440

aatacccca gggggtgctg tagccgaagt aggtgttgtc gttggtacta cctgcagttt 1500

cactggagat ttgctcgtag aggtggttgt tgtaggtggg cagggcccag gttcgggtgc 1560

tggtggtaat gactctgtcg cccagccatg tggaatcgca atgccaattt cctgaggcat 1620

tacccactcc gtcggcacct tcgttattgt ctgccattgg tgcgccaccg cctgcagcca 1680

ctgtaccaga tcccacacta gagggcgctg ctggaggttc tccgagaggt tgagggtcgg 1740

ggactgactc tgagtcgcca gtctgaccga aattgagtct ctttctggcg ggctgctggc 1800

ccttcttgcc gatgcccgtg gaggagtcgg gggaacgctg aggtgacggc tctaccggtc 1860

tcttctttgc aggagccgtc ttagcgcctt cctcaaccag accgagaggt tcgagaaccc 1920

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cccggccgtt gtcctgcttt tgctggttgg ctttgggttt cggggctcca ggtttcaggt 2220

cccaccactc gcgaatgccc tcagagaggt tgtcctcgag ccaatctgga agataaccat 2280

cggcagccat acctgattta aatcatttat tgttcaaaga tgcagtcatc caaatccaca 2340

ttgaccagat cgcaggcagt gcaagcgtct ggcacctttc ccatgatatg atgaatgtag 2400

cacagtttct gatacgcctt tttgacgaca gaaacgggtt tagattctga cacgggaaag 2460

cactctaaac agtctttctg tccgtgagtg aagcagatat ttgaattctg attcattctc 2520

tcgcattgtc tgcagggaaa cagcatcaga ttcatgccca cgtgacgaga acatttgttt 2580

tggtacctgt ctgcgtagtt gatcgaagct tccgcgtctg acgtcgatgg ctgcgcaact 2640

gactcgcgca cccgtttggg ctcacttata tctgcgtcac tgggggcggg tcttttcttg 2700

gctccaccct ttttgacgta gaattcatgc tccacctcaa ccacgtaatc ctttgcccac 2760

cggaaaaagt ctttgacttc ctgcttggtg accttcccaa agtcatgatc cagacggcgg 2820

gtgagttcaa atttgaacat ccggtcttgc aacggctgct ggtgttcgaa ggtcgttgag 2880

ttcccgtcga tcacggcgca catgttggtg ttggagatga cgatcgcggg agtcgggtct 2940

atctgggccg aggacttgca tttctggtcc acgcgcacct tgcttcctcc gagaatggct 3000

ttggccgact ccacgacctt ggcggtcatc ttcccctcct cccaccagat caccatcttg 3060

tcgacacagt cgttgaaggg aaagttctca ttggtccagt tgacgcagcc gtagaaaggg 3120

cgaattc 3127

<210> 150
<211> 728
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 150
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Arg Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Val Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

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Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Ser Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380
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Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Val His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590
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Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Cys Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 151
<211> 3106
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 151
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt       60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct      120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg      180
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aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaattttggc ccagatggga ccctgcaggc acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtctaggc tctggctgtg cacatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagctgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg ctgctggcct ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcga 1860

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cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtctgaggta cttgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

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tattgctcag aaacacagtc atccaggtcc acgttgacca gatcgcaggc cgagcaagca 2340

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aacccatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaacct tttgacttcc 2760

tgctttgtca ccttgccaaa gttatgctcc agacggcggg tgggttcaaa tttgaacatc 2820

cggtcctgca acggctgctg gtgctcgaag gtggcgctgt tcccgtcaat cacggcgcac 2880

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gccgtcatct tgccctcctc ccaccagatc accatcttgt cggcgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc 3106

<210> 152
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 152
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Ser Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser

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            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Cys Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
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385 390 395 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
405 410 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
420 425 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
435 440 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Val
450 455 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465 470 475 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
485 490 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
500 505 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Leu
515 520 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
530 535 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545 550 555 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
565 570 575

Gln Ser Ser Thr Ala Gly Pro Arg Thr Gln Thr Val Asn Ser Gln Gly
580 585 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly

595 600 605

Pro Ile Trp Ala Glu Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
610 615 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 153
<211> 3102
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 153
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat caaccggttt 60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct 120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg 180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga 240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag 300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg 360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag 420

gaatttcggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg 480

gcagagcccc ctggctgttg acagtctgtg tccggggtcc ggccgtagac gattgcaggt 540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct 600

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aggaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccacggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtccaggc tctggctgtg cgcatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttattgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagcag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

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aactcatgcg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc 2760

tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc 2820

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ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatct tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg aagggcgaat tc 3102

<210> 154
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 154

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160


Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175


Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190
```

```
Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400
```

```
Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605
```

```
Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 155
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 155

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240
```

```
Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445
```

```
Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655
```

```
Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 156
<211> 3106
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 156
gcggccgcga attcgccctt cgcagagacc aaagttcaac tgaaacgaat cagccggttt       60

attgattaac aagtaattac aggttacggg tgaggtaacg ggtgccaatg gggcgaggct      120

cagtataaac cccttcgttg ttgacagcaa attccacatt attagacttg gcataatttg      180

aggtgtactg aatctctgga ttccagcgtt tgctgttttc tttctgcagt tcccactcga      240

tctccacgct gacctggccg gtgctgtact gcgtgataaa tgaggcaaac ttggcaggag      300

taaacacctc tggaggatta gcaggtaccg gggtgttttt gatgagaatt tgaggaggcg      360

ggtgtttgag tccaaatccg cccatcaggg gagacgggtg aaagttgccg tccgtgtgag      420

gaattttggc ccagatggga ccctgcaggt acacgtcccg gttctgccag accatgccgg      480

gcagagcccc ctggctgttg acagtctgtg tctggggtcc ggccgtagac gattgcaggt      540

tgctggagac cacaccgtat tcttctgtag ccacgggatt ggtggttttg atctcctcct      600
```

cgctggtcat tagcacgttt tccagcgttg tcttgttggc agcccccgtt ttgccaaaaa 660

ccagcactcc gttgatggga aagaactggt cctcgtcgtc cttgttggtg gccatggcta 720

cgcccgggtt ggttaatgaa tttctaccat tcagatggta tttagtggcc ccggtccagg 780

caaagttact gttgttgttg ctgtctatgt tttttgacag tctctgctgc cgataacagg 840

gtccgggcag ccagttcttt gattgctcgg ccatggtgtt gggcccagcc tgatggaact 900

gcagctccct tgtggacccc gtagtgctct gggtccgggc caggtagtac aggtactggt 960

cgatgagggg attcatcagc cggtccaggc tctggctgtg cgcatagctg ctgtggaaag 1020

gcacttcctc aaaggtgtag ctgaattcaa agttatcgcc cgttctcagc atctgagaag 1080

gaaagtactc caggcagtag aaggaggaac gtcccacaga ctgactgccg ttgtttagag 1140

tcagatatcc gtactgagga atcatgaaca cgtccgcagg gaacggaggg aggcagccct 1200

ggtgcgcaga gccgaggacg tacggcagtt ggtactccga gtccgagaag acctgaatcg 1260

tgctggtaag gttattagcg atggtcgtaa cgccgtcgtt cgtcgtgacc tccttgacct 1320

ggatgttgaa caacttgaac cgcagctttc tgggccggaa tccccagttg ttgttgatga 1380

gtcgctgcca gtcacgtggt gagaagtggc agtggaatct gttgaagtca aaatagcccc 1440

agggggtgct gtagccgaag aagtggttgt cgttggtagc cccgctctga cttgatatct 1500

gcttgtagag gtggttgttg taggtgggca gggcccaggt gcgggtgctg gtggtgatga 1560

ctctgtcgcc cagccatgtg gaatcgcaat gccaatttcc ggaggcatta cccactccgt 1620

cggcgccttc gttattgtct gccattggtg cgccaccgcc tgcagccatt gtaccagatc 1680

ccagacctga gggcgcggcg ggaggttctc cgagaggttg ggggtcgggc actgactctg 1740

agtcgccagt ctgcccaaag ttgagcttct ttttagcggg cggctggccg ttcttgccga 1800

tgcccgtgga ggagtcgggg gattctatgg gtctcttctt tccaggagcc gtcttagcgc 1860

cttcctcaac cagaccgaga ggttcgagaa cccgcttctt ggcctggaag actgctcgcc 1920

cgaggttgcc cccaaaagac gtatcttctt gaagacgctc ctgaaactcg gcgtcggcgt 1980

ggttgtactt gaggtacggg ttgtcccccc gctcgagctg cttgtcgtag gccttgtcgt 2040

gctcgagggc cgcggcgtct gcctcgttga ccggctctcc cttgtcgagt ccgttgaagg 2100

gtccgaggta cctgtagcca ggaagcacca gaccccggcc gtcgtcctgc ttttgctggt 2160

tggctttggg tttcggggct ccaggtttca agtcccacca ctcgcgaatg ccctcagaga 2220

ggttgccctc gagccaatct ggaagataac catcggcagc catacctggt ttaagtcatt 2280

tattgctcag aaacacagtc atccaggtcc acgttggcca gatcgcaggc cgagcaagca 2340

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atctgaagca tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc 2580

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tcgcttttat ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag 2700

aactcatacg ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc 2760

tgctttgtca ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc 2820

cggtcttgta acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac 2880

atgttggtgt tggaagtgac gatcacgggg gtgggatcga tctgggcgga cgacttgcac 2940

ttttggtcca cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg 3000

gccgtcatcc tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga 3060

aagttctcat tggtccagtt gacgcagccg tagaaagggc gaattc 3106

<210> 157
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 157
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240
```

```
Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Met Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445
```

```
Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Gly Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Gly Val Phe Thr Pro
                645                 650                 655
```

Ala Leu Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 158
<211> 3098
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 158
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagtaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa 120

acccccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac 180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg 240

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa actaggcagg agtaaacacc 300

cctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360

agtccaaatc cgcccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg 420

gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc 480

ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag 540

accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc 600

attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact 660

ccgttgatgg gaaagaactg gccctcgtcg tccttgttgg tggccatggc tacgcccggg 720

ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta 780

ctgttgttgt tgctgtctat gttttttgac agtctctgct gccgataaca gggtccgggc 840

agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc 900

cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg 960

ggattcatca gccggtccag gctctggctg tgcgcatagc tgctgtggaa aggcacttcc 1020

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tccaggcagt agaaggagga acgtcccata gactgactgc cgttgtttag agtcagatat 1140

ccgtactgag gaatcatgaa cacgtccgca gggaacggag ggaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta 1260

aggttattag cgatggtcgt aacgccgtcg ttcgtcgtga cctccttgac ctggatgttg 1320

aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttgaagt caaaatagcc ccaggggtg 1440

ctgtagccga agaagtggtt gtcgttggta gccccgctct gacttgatat ctgcttgtag 1500

aggtggttgt tgtaggtggg cagggcccag gtgcgggtgc tggtggtgat gactctgtcg 1560

cccagccatg tggaatcgca atgccaattt ccggaggcat tacccactcc gtcggcgcct 1620

tcgttattgt ctgccattgg tgcgccaccg cctgcagcca ttgtaccaga tcccagacct 1680

gagggcgcgg cgggaggttc tccgagaggt tgggggtcgg gcactgactc tgagtcgcca 1740

gtctgcccaa agttgagctt ctttttagcg ggctgctggc ctttcttgcc gatgcccgtg 1800

gaggagtcgg gggattctat gggtctcttc tttccaggag ccgtcttagc gccttcctca 1860

accagaccga gaggttcgag aacccgcttc ttggcctgga agactgctcg cccgaggttg 1920

cccccaaaag acgtatcttc ttgaagacgc tcctgaaact cagcgtcggc gtggttgtac 1980

ttgaggtacg ggttgtcccc ctgctcgagc tgcttgtcgt aggccttgtc gtgctcgagg 2040

gccgcggcgt ctgcctcgtt gaccggctct cccttgtcga gtccgttgaa gggtccgagg 2100

tacttgtagc caggaagcac cagaccccgg ccgtcgtcct gcttttgctg gttggctttg 2160

ggtttcgggg ctccaggttt caagtcccac cactcgcgaa tgccctcaga gaggttgtcc 2220

tcgagccaat ctggaagata accatcggca gccatacctg gtttaagtca tttattgctc 2280

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agcccgcccc agcagatgat gaatggcaca gagtttccga tacgtcctct ttctgacgac 2400

cggttgagat tctgacacgc cggggaaaca ttctgaacag tctctggtcc cgtgcgtgaa 2460

gcaaatgttg aaattctgat tcattctctc gcatgtcttg cagggaaaca gcatctgaag 2520

catgcccgcg tgacgagaac atttgttttg gtacctgtcg gcaaagtcca ccggagctcc 2580

ttccgcgtct gacgtcgatg gatccgcgac tgaggggcag gcccgcttgg gctcgctttt 2640

atccgcgtca tcgggggcgg gcctcttgtt ggctccaccc tttctgacgt agaactcatg 2700

cgccacctcg gtcacgtgat cctgcgccca gcggaagaac tctttgactt cctgctttgt 2760

caccttgcca aagtcctgct ccagacggcg ggtgagttca aatttgaaca tccggtcttg 2820

taacggctgc tggtgctcga aggtggtgct gttcccgtca atcacggcgc acatgttggt 2880

gttggaagtg acgatcacgg gggtgggatc gatctgggcg gacgacttgc acttttggtc 2940

cacgcgcacc ttgctgccgc cgagaatggc cttggcggac tccacgacct tggccgtcat 3000

cttgccctcc tcccaccaga tcaccatctt gtcgacgcaa tcgttgaagg gaaagttctc 3060

attggtccag ttgacgcagc cgtagaaagg gcgaattc 3098

<210> 159
<211> 2187
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 159
atggctgccg atggttatct tccagattgg ctcgagggca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaacggccag 480

ccgcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1200

acgggcgata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

gccggacccc agacacagac tgtcaacagc cagggggctc tgcccggcat ggtctggcag 1800

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 1860

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 1920

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 1980

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2160

acccgttacc tcacccgtaa cctgtaa 2187

<210> 160
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 160
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Gly Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320
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```
Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525
```

```
Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 161
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 161
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145 150 155 160

```
Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365
```

```
Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asp Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575
```

```
Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590


Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 162
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 162
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
```

```
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
```

```
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
```

625 630 635 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
645 650 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
660 665 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
675 680 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
690 695 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 163
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 163
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Asn Gly Gln
145                 150                 155                 160

Pro Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270
```

```
Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480
```

```
Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685
```

```
Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725

<210> 164
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 164
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320
```

```
Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525
```

```
Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 165
<211> 2215
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 165
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ctgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agttttttc ctcagagcgg 1620

ggttctcatc tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggtcat 1680

gattacagac gaagaggaaa tcaggacaac caatcccgtg gctacggagc agtatggttc 1740

tgtatctacc aacctccaga gaggcaacag acaagcagct accgcagatg tcaacacaca 1800

aggcgttctt ccaggcatgg tctggcagga cagagatgtg taccttcagg ggcccatctg 1860

ggcaaagatt ccacacacgg acggacattt tcacccctct cccctcatgg gtggattcgg 1920

acttaaacac cctccgcctc agatcctgat caagaacacg cctgtacctg cggatcctcc 1980

gaccaccttc aaccagtcaa agctgaactc tttcatcacc cagtattcta ctggccaagt 2040

cagcgtggag atcgagtggg agctgcagaa ggaaaacagc aagcgctgga accccgagat 2100

ccagtacacc tccaactact acaaatctac aagtgtggac tttgctgtta atacagaagg 2160

cgtgtactct gaaccccgcc ccattggcac ccgttacctc acccgtaatc tgtaa 2215

<210> 166
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 166
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Lys Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

```
Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 167
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 167

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270
```

```
Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Lys Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480
```

```
Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Gln Gly Asn Thr Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685
```

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 168
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 168
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460


Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480


Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
                485                 490                 495


Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510
```

```
Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Gln Gly Asn Thr Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720
```

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 169
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 169
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
```

```
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
```

545 550 555 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
565 570 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
580 585 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
595 600 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
610 615 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625 630 635 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
645 650 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
660 665 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
675 680 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
690 695 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705 710 715 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 170
<211> 3075
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 170
tgagaacttt cctttcaacg attgcgtcgg acaagatggt gatctggtgg gaggagggga 60

agatgaccgc caaggtcgtg gagtcggcca aagccattct tggaggaagc aaggtgcgtg 120

tggaccagaa atgcaagtcc tcggcccaga tagacccgac tcccgtgatc gtcacctcca 180

acaccaacat gtgcgccgtg attgacggga actcaacgac cttcgagcac cagcagccgt 240

tgcaagaccg gatgttcaaa tttgaactta cccgccgtct ggatcatgac tttggaaagg 300

tcaccaagca ggaagtgaaa gacttttttcc ggtgggcaaa ggatcacgtg gttgaggtgg 360

agcatgaatt ctacgtcaaa aagggtggag ctaagaaaag acccgccccc agtgacgcag 420

atataagtga gcccaaacgg gcgcgcgagt cagttgcgca gccatcaacg tcagacgcgg 480

aagcttcgat caactacgcg gacaggtacc aaaaacaaat gttctcgtca cgtgggcatg 540

aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 600

ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaacccgtt 660

tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg 720

ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctctgaa 780

caataaatga tttaaatcag gtatggctgc cgatggttat cctccagatt ggctcgagga 840

cactctctct gaagggataa gacagtggtg gaagctcaaa cctggcccac caccaccaaa 900

gcccgcagag cggcataagg acgacagcag gggtcttgtg cttcctgggt acaagtacct 960

cggacccttc aacggactcg acaaggggga gccggtcaac gaggcagacg ccgcggccct 1020

cgagcacgac aaggcctacg accggcagct cgacagcgga gacaacccgt acctcaagta 1080

caaccacgcc gacgcagagt ttcaggagcg ccttaaagaa gatacgtctt ttgggggcaa 1140

cctcggacga gcagtcttcc aggcgaaaaa gagggttctt gaacctctgg gcctggttga 1200

ggaacctgtt aagacggctc cgggaaaaaa gaggccggta gagcactctc ctgtggagcc 1260

agactcctcc tcgggaaccg gaaaagcggg ccagcggcct gcaagaaaaa gattaaattt 1320

tggtcagact ggagacgcag actccgtacc tgacccccag cctctcggac agccaccagc 1380

agccccctct ggtctgggat ctactacaat ggctacaggc agtggcgcac caatggcaga 1440

caataacgag ggtgccgatg gagtgggtaa ttcctcagga aattggcatt gcgattccca 1500

atggctgggc gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacatacaa 1560

caaccacctc tacaagcaaa tctccagcca atcaggagcc agcaacgaca accactactt 1620

tggctacagc acccccctggg ggtattttga cttcaacaga ttccactgcc acttttcacc 1680

acgtgactgg caaagactca tcaacaacaa ctggggattc cggcccaaaa gactcaactt 1740

caagctcttt aatattcaag tcaaagaggt cacgcagaat gacggtacga cgacgattgc 1800

caataacctt accagcacgg ttcaggtgtt tactgactcg gagtaccagc tcccgtacgt 1860

cctgggctcg gcgcatcaag gatgcctccc gccgtttcca gcggacgtct tcatggtccc 1920

acagtatgga tacctcaccc tgaacaacgg gagtcaggcg gtaggacgct cttcctttta 1980

ctgcctggag tactttcctt ctcagatgct gcgtactgga aacaactttc agttcagcta 2040

cacttttgaa gacgtgcctt tccacagcag ctacgctcac agccagagtc tggatcggct 2100

gatgaatcct ctgatcgacc agtacctgta ttatctgaac aagacacaaa caaatagtgg 2160

aactcttcag cagtctcggc tactgtttag ccaagctgga ccaaccaaca tgtctcttca 2220

agctaaaaac tggctgcctg gaccttgcta cagacagcag cgtctgtcaa aacaggcaaa 2280

cgacaacaac aacagcaact ttccctggac tgcagctaca aagtatcatc taaatggccg 2340

ggactcgttg gttaatccag gaccagctat ggccagtcac aaggatgacg aagaaaagtt 2400

tttccccatg catggaaccc tgatatttgg taaacaagga acaaatgcca acgacgcgga 2460

tttggaaaat gtcatgatta cagatgaaga agaaatcagg gccaccaatc ccgtggctac 2520

ggagcagtac gggactgtgt caaataattt gcaaaactca aacactggtc caactactgg 2580

aactgtcaat cgccaaggag cgttacctgg tatggtgtgg caggatcgag acgtgtacct 2640

gcagggaccc atttgggcca agattcctca caccgatgga cactttcatc cttctccact 2700

gatgggaggt tttggactca aacacccgcc tcctcagatc atgatcaaaa acactcccgt 2760

tccagccaat cctcccacaa acttcagttc tgccaagttt gcttctttca tcacacagta 2820

ttccacggga caggtcagcg tggagatcga gtgggagctg cagaaggaga acagcaaacg 2880

ctggaatccc gaaattcagt acacttccaa ctacaacaag tctgttaatg tggactttac 2940

tgtggacact aatggtgtgt attcagagcc tcgccccatt ggcaccagat acctgactcg 3000

taatctgtaa ttgcttgtta atcaataaac cgtttaattc gtttcagttg aactttggtc 3060

tctgcgaagg gcgaa 3075

<210> 171
<211> 3142
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 171
aaaacgacgg gccagtgatt gtaatacgac tcactatagg gcgaaattga aattagcggc 60

cgcgaattcg cctttcgcag agaccaaagt tcaactgaaa cgaattaaac ggtttattga 120

ttaacaagca attacagatt acgagtcagg tatctggtgc caatggggcg aggctctgaa 180

tacacaccat tagtgtccac agtaaagtcc acattaacag acttgttgta gttggaagtg 240

tactgaattt cgggattcca gcgtttgctg ttctccttct gcagctccca ctcgatctcc 300

acgctgacct gtcccgtgga atactgtgtg atgaaagaag caaacttggc agaactgaag 360

tttgtgggag gattggctgg aacgggagtg tttttgatca tgatctgagg aggcgggtgt 420

ttgagtccaa aacctcccat cagtggagaa ggatgaaagt gtccatcggt gtgaggaatc 480

ttggcccaaa tgggtccctg caggtacacg tctcgatcct gccacaccat accaggtaac 540

gctccttggt gattgacagt tccagtagtt ggaccagtgt ttgagttttg caaattattt 600

gacacagtcc cgtactgctc cgtagccacg ggattggtgg ccctgatttc ttcttcatct 660

gtaatcatga cattttccaa atccgcgtcg ttggcatttg ttccttgttt accaaatatc 720

agggttccat gcatggggaa aaacttttct tcgtcatcct tgtgactggc catagctggt 780

cctggattaa ccaacgagtc ccggccattt agatgatact ttgtagctgc agtccaggga 840

aagttgctgt tgttgttgtc gtttgcctgt tttgacagac gctgctgtct gtagcaaggt 900

ccaggcagcc agtttttagc ttgaagagac atgttggttg gtccagcttg gctaaacagt 960

agccgagact gctgaagagt tccactattt gtttgtgtct tgttcagata atacaggtac 1020

tggtcgatca gaggattcat cagccgatcc agactctggc tgtgagcgta gctgctgtgg 1080

aaaggcacgt cttcaaaagt gtagctgaac tgaaagttgt ttccagtacg cagcatctga 1140

gaaggaaagt actccaggca gtaaaaggaa gagcgtccta ccgcctgact cccgttgttc 1200

agggtgaggt atccatactg tgggaccatg aagacgtccg ctggaaacgg cgggaggcat 1260

ccttgatgcg ccgagcccag gacgtacggg agctggtact ccgagtcagt aaacacctga 1320

accgtgctgg taaggttatt ggcaatcgtc gtcgtaccgt cattctgcgt gacctctttg 1380

acttgaatat taaagagctt gaagttgagt cttttgggcc ggaatccccg gttgttgttg 1440

acgagtcttt gccagtcacg tggtgaaaag tggcagtgga atctgttgaa gtcaaaatac 1500

ccccaggggg tgctgtagcc aaagtagtgg ttgtcgttgc tggctcctga ttggctggag 1560

atttgcttgt agaggtggtt gttgtatgtg ggcagggccc aggttcgggt gctggtggtg 1620

atgactctgt cgcccagcca ttgggaatcg caatgccaat ttcctgagga attacccact 1680

ccatcggcac cctcgttatt gtctgccatt ggtgcgccac tgcctgtagc cattgtagta 1740

gatcccagac cagaggggggc tgctggtggc tgtccgagag gctgggggtc aggtacggag 1800

tctgcgtctc cagtctgacc aaaatttaat ctttttcttg caggctgctg gcccgctttt 1860

ccggttcccg aggaggagtc tggctccaca ggagagtgct ctaccggcct ctttttccc 1920

ggagccgtct taacaggctc ctcaaccagg cccagaggtt caagaaccct ctttttcgcc 1980

tggaagactg ctcgtccgag gttgccccca aaagacgtat cttctttaag gcgctcctga 2040

aactctgcgt cggcgtggtt gtacttgagg tacgggttgt ctccgctgtc gagctgccgg 2100

tcgtaggcct tgtcgtgctc gagggccgcg gcgtctgcct cgttgaccgg ctcccccttg 2160

tcgagtccgt tgaagggtcc gaggtacttg tacccaggaa gcacaagacc cctgctgtcg 2220

tccttatgcc gctctgcggg ctttggtggt ggtgggccag gtttgagctt ccaccactgt 2280

cttattcctt cagagagagt gtcctcgagc caatctggaa gataaccatc ggcagccata 2340

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cgcgtagttg atcgaagctt ccgcgtctga cgtcgatggc tgcgcaactg actcgcgcgc 2700

ccgtttgggc tcacttatat ctgcgtcact gggggcgggt cttttcttag ctccaccctt 2760

tttgacgtag aattcatgct ccacctcaac cacgtgatcc tttgcccacc ggaaaaagtc 2820

tttcacttcc tgcttggtga cctttccaaa gtcatgatcc agacggcggg taagttcaaa 2880

tttgaacatc cggtcttgca acggctgctg gtgctcgaag gtcgttgagt tcccgtcaat 2940

cacggcgcac atgttggtgt tggaggtgac gatcacggga gtcgggtcta tctgggccga 3000

ggacttgcat ttctggtcca cacgcacctt gcttcctcca agaatggctt tggccgactc 3060

cacgaccttg gcggtcatct tcccctcctc ccaccagatc accatcttgt cgacgcaatg 3120

gtaaaaggaa agttctcatt gg 3142

<210> 172
<211> 735
<212> PRT
<213> Adeno-associated virus-2

<400> 172
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

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            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

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305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asp Lys Ala Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
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        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
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725 730 735

<210> 173
<211> 740
<212> PRT
<213> Adeno-associated virus-2

<400> 173
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

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Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590
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Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
                725                 730                 735


Leu Ala Ala Ala
            740


<210> 174
<211> 734
<212> PRT
<213> Adeno-associated virus-2

<400> 174
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
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            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr

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        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Met Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
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645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Ile Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730

<210> 175
<211> 734
<212> PRT
<213> Adeno-associated virus-2

<400> 175
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Glu Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730

<210> 176
<211> 739
<212> PRT
<213> Adeno-associated virus-2

<400> 176
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
```

```
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
```

580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
725 730 735

Leu Ala Ala

<210> 177
<211> 725
<212> PRT
<213> Adeno-associated virus-2

<400> 177
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro
725

<210> 178
<211> 707
<212> PRT
<213> Adeno-associated virus-2

<400> 178
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
```

```
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
```

```
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Cys Ile Tyr Gln Pro Pro Glu Arg Gln Gln Thr Ser Ser Tyr
            580                 585                 590

Arg Arg Cys Gln His Thr Arg Arg Ser Ser Arg His Gly Leu Ala Gly
        595                 600                 605

Gln Arg Cys Val Pro Ser Gly Ala His Leu Gly Lys Asp Ser Thr His
    610                 615                 620

Gly Arg Thr Phe Ser Pro Leu Ser Pro His Gly Trp Ile Arg Thr Thr
625                 630                 635                 640

Pro Ser Ser Thr Asp Ser His Gln Glu His Pro Gly Thr Cys Glu Ser
                645                 650                 655

Phe Asp His Leu Gln Cys Gly Lys Val Cys Phe Leu His His Thr Val
            660                 665                 670

Leu His Gly Thr Gly Gln Arg Gly Asp Arg Val Arg Ala Ala Glu Gly
        675                 680                 685

Lys Gln Gln Thr Leu Glu Ser Arg Asn Ser Val His Phe Gln Leu Gln
    690                 695                 700

Gln Val Cys
```

705

<210> 179
<211> 739
<212> PRT
<213> Adeno-associated virus-2

<400> 179
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590
```

```
Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
                725                 730                 735


Leu Ala Ala



<210> 180
<211> 737
<212> PRT
<213> Adeno-associated virus-2

<400> 180
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
```

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg

```
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala
            580                 585                 590

Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His His Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

Leu

<210> 181
<211> 741
<212> PRT
<213> Adeno-associated virus-2

<400> 181
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Leu Ala Asn His Asn
            580                 585                 590

Asn Thr Thr Asn Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
        595                 600                 605

Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
    610                 615                 620

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro
625                 630                 635                 640

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
                645                 650                 655

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser
            660                 665                 670

Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
        675                 680                 685

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
    690                 695                 700
```

```
Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Ile Asn Val
705                 710                 715                 720


Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile
                725                 730                 735


Gly Thr Arg Tyr Leu
            740


<210> 182
<211> 730
<212> PRT
<213> Adeno-associated virus-2

<400> 182
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
```

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
```

```
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
```

545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg
725 730

<210> 183
<211> 735
<212> PRT
<213> Adeno-associated virus-2

<220>
<221> MOD_RES
<222> (239)..(239)
<223> Any naturally occurring amino acid

<400> 183
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

<210> 184
<211> 733
<212> PRT
<213> Adeno-associated virus-2

<400> 184
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Leu Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr
                725                 730


<210> 185
<211> 734
<212> PRT
<213> Adeno-associated virus-2

<400> 185
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
```

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
```

```
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Asn Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Asn Gln Ser Gly Ser Ala Gln Asn Asn Asp Leu Leu Phe Ser Arg
    450                 455                 460

Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly
            500                 505                 510

Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys
```

```
    530                 535                 540

Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg Phe
                565                 570                 575

Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala Thr
            580                 585                 590

Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr
705                 710                 715                 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730
```

<210> 186

<211> 734
<212> PRT
<213> Adeno-associated virus-2

<400> 186

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Ser Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Ile Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730
```

<210> 187
<211> 738
<212> PRT
<213> Adeno-associated virus-2

<400> 187

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
```

```
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
```

```
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Gly Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
```

```
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
```

675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu Leu
725 730 735

Arg Pro

<210> 188
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 188
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatgg cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg gcaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga cgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 189
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 189
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

```
Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Gly Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
```

```
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Gly Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

```
Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Thr Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 190
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 190
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc tcgcagagcg gcatcaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc acggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tcctttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caaccttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

tacagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgcg gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 191
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 191
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Leu Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Thr Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Leu Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Tyr Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Arg Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
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Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 192
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 192
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcgtcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 193
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 193
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180   185   190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195   200   205

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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

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Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr Arg Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 194
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 194
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatcaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc gaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgccct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccggctga tgaatcctct gatcgaccag 1320

tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tgggaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 195
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 195
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
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325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Pro Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
450 455 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
485 490 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys

```
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 196

<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 196
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacttg ggccctgccc acctacaaca accatctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctgc agggcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

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caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

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acttccaact acaacaaatc tgttaatgtg gactttactg ttgacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 197
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 197
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
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Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Gly Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
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Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
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Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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aaggtcatgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa 180

tgtaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccaacatg 240

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gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420

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cagaaggact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

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<211> 3162
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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tggggcgagg ctctgaatac acgccattag tgtccacagt aaagtccaca ttaacagact 180

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<211> 3164
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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tttttcccca tgcatggaac cctaatattt ggtaaagaag gaacaaatgc taccaacgcg 2520

gaattggaaa atgtcatgat tacagatgaa gaggaaatca ggaccaccaa tcccgtggct 2580

acagagcagt acggatatgt gtcaaataat ttgcaaaact caaatactgc tgcaagtact 2640

gaaactgtga atcaccaagg agcattacct ggtatggtgt ggcaggatcg agacgtgtac 2700

ctgcagggac ccatttgggc caagattcct cacaccgatg gacactttca tccttctcca 2760

ctgatgggag gttttggact caaacacccg cctcctcaga ttatgatcaa aaacactccc 2820

gttccagcca atcctcccac aaacttcagt tctgccaagt ttgcttcctt catcacacag 2880

tattccacgg gacaggtcag cgtggagatc gagtgggagc tgcagaagga gaacagcaaa 2940

cgctggaatc ccgaaattca gtacacttcc aactacaaca aatctgttaa tgtggacttt 3000

actgtggaca ctaatggtgt gtattcagag cctcgcccca ttggcaccag atacctgact 3060

cgtaatctgt aattgcttgt taatcaataa accgtttaat tcgtttcagt tgaactttgg 3120

tctctgcgaa gggcgaattc gcggccgcta aattcaattc gcc 3163

<210> 202
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 202
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
50 55 60

Val Asp Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

```
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
```

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        275                 280                 285

Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Leu Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
```

```
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asp Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
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690 695 700

Asn Lys Pro Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 203
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 203
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactctac 180

aagggagagc cggtcgacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga gggttcttga acctctgggc ttggttgggg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggca accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaata accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgaccggca aagactcatc 900

aacaacaact ggggattccg accaaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggcttggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactta tgggaggttt tggactcaaa 1920

cacccacctc ctcagatcat gattaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca agtcagcgtg 2040

gagatcgagt gggagctgca gaaggaggac agcaaacgct ggaaccccga gatccagtac 2100

acttccaact ataacaaacc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 204
<211> 3161
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 204
cgaattgatt tagcggccgc gaattcgccc ttcgcagaga ccaaagttca actgaaacga 60

attaaacggt ttattgatta acaagcaatt acagattacg agtcaggtat ctggtgccaa 120

tggggcgagg ctctgaatac acaccattag tgtccacagt aaagtccaca ttaacagatt 180

tgttgtagtt ggaagtgtac tggatctcgg gattccagcg tttgctgttc tccttctgta 240

gctcccactc gatctccacg ctgacccgcc ccgtggaata ctgtgtgatg aaggaagcaa 300

actttgccgc actgaaggtg gtcgaaggat tcgcaggtac cggggtgttt ttgatgagaa 360

tctgtggagg agggtgttta agtccgaatc cgcccatgag gggagagggg tgaaaatgtc 420

cgtccgtgtg cggaatcttt gcccagatag gcccctgcag gtacacgtct ctgtcctgcc 480

agaccatgcc tggaagaacg ccttgtgtgt tgacatctgc agtagatgct tgtgtgttgc 540

cgctctggag gttggtagat acagaaccat actgctccgt ggccacggga ttggtggttc 600

tgatttcctc ttcgtctgta atcatgacct tttcaatgtc cacatttgtt ttctctgatc 660

cttgttttcc aaagatgaga accccgctct gaggaaaaaa cttttcttca tcgtccttgt 720

ggctggccat tgccgggccc ggattcacca gagagtctct gccattgagg tggtacttgg 780

tagctccaat ccacgagtat tcactgttgt tgttgtccgc agatgtcttt gatactcgct 840

gctggcggta acagggtcca ggaagccagt tcctagactg atcccgaatg tcactcgctc 900

cggcctgaga aaactgaagc ctggactgcg tggtggttcc gcttggagtg tttgttctgc 960

tcaagtaata caggtactgg tcgatgagag gattcatgag acggtccaaa ctctggctgt 1020

gagcgtagct gctgtggaaa ggaacatcct caaaggtgta gctgaaggta aagttgtttc 1080

cggtacgcag catctgagaa gggaagtact ccaggcagta aaatgaagag cgtcctactg 1140

cctgactccc gttgttcagg gtgaggtatc catactgtgg caccatgaag acgtctgctg 1200

ggaacggcgg gaggcatcct tgatgcgccg agccgaggac gtacgggagc tggtactccg 1260

agtcagtaaa cacctgaacc gtgctggtaa ggttattggc aatcgtcgtc gtaccatcat 1320

tctgcgtgac ctctctgact tgaatgttaa agagcttgaa gttgagtctc ttgggccgga 1380

atccccagtt gttgttgatg agtctttgcc agtcacgtgg tgaaaagtgg cagtggaatc 1440

tgttgaagtc aaaatacccc caaggggtgc tgtagccaaa gtagtggttg tcgttgctgg 1500

ctcctgattg gctggaaatc tgcttgtaca gatggttgtt gtaggtgggc agagcccagg 1560

ttcgggtgct ggtggtgatg actctgtcgc ccatccatgt ggaatcgcaa tgccaatttc 1620

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gctggttgcc cgcttttccg gttcccgagg aggagtctgg ctccacagga gagtgctcta 1860

ccggcctctt ttttcccgga gccgtcttaa caggctcctc aaccaggccc agaggttcaa 1920

gaaccctctt ttttgcctgg aagactgctc gtccgaggtt gcccccaaaa gacgtatctt 1980

ctttaaggcg ctcctgaaac tccgcgtcgg cgtggtcgta cttgaggtac gggttgtctc 2040

cgctgtcgag ctgccggtcg taggccttgt cgtgctcgag ggccgcggcg tctgcctcgt 2100

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caagacccct gctgtcgtcc ttatgccgct ctgcgggctt tggtggtggt gggccaggtt 2220

tgagcttcca ccactgtctt attccttcag agagagtgtc ctcgagccaa tctggaagat 2280

aaccatcggc agccatacct gatttaaatc atttattgtt cagagatgca gtcatccaaa 2340

tccacattga ccagatcgca ggcagtgcaa gcgtctggca cctttcccat gatatgatga 2400

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ggaaagcact ctaaacagtc tttctgtccg tgagtgaagc agatatttga attctgattc 2520

attctctcgc attgtctgca gggaaacagc atcagattca tgcccacgtg acgagaacat 2580

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ttcttggctc cacccttttt gacgtagaat tcatgctcca cctcaaccac gtgatccttt 2760

gcccaccgga aaaagtcttt cacttcctgc ttggtgacct tcccaaagtc atgatccaga 2820

cggcgggtta gttcaaattt gaacatccgg tcttgcaacg gctgctggtg ttcgaaggtc 2880

gttgagttcc cgtcaatcac ggcgcacatg ttggtgttgg aggtggcgat cacgggagtc 2940

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atcttgtcga cacagtcgtt gaagggaaag ttctcattgg tccagttgac gcagcaaggg 3120

cgaattcgtt taaacctgca ggaactagtc ccttagtgag g 3161

<210> 205
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 205
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Tyr Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
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Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560
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Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asp Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 206
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 206
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccgccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactctac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccgg cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga gggttcttga acctctgggc ttggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggca accagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg accaaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaatca aatagtggaa cccttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aagactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactta tgggaggttt tggactcaaa 1920

cacccacctc ctcagatcat gattaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca agtcagcgta 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtac 2100

acttccaact ataacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 207
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 207
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Cys Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

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    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
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            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
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465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
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675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 208
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 208
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctgc aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagacag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

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caccagggct gcccgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaacggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgcggag aacgggcaac aactttgagt tcagctacca gtttgaggac 1260

gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaaccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aataacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttga tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aatcaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcatcctt cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta taacaaatct gttaatgtgg actttactgt ggacactaat 2160

ggtgtgtatt cagagcctcg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 209
<211> 3167
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 209
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gggcgaggct ctgaatacac accattagtg tccacagtaa agtccacatt aacagatttg 180

ttgtagttgg aagtgtactg aatctcggga ttccagcgtt tgctgttctc cttctgcagc 240

tcccactcga tctccacgct gacctgcccc gtggagtact gtgtaatgaa ggaagcaaac 300

tttgccgcac tgaaggtagt cgaaggattc gcaggtaccg gggtgttctt gatgagaatc 360

tgcgggggag ggtgtttaag tccgaatccg cccatgaggg gagaggggtg aaaatgtccg 420

tccgtgtgtg gaatctttgc ccagatgggc ccctgcaggt acacgtctct gtcctgccac 480

accatgcctg gaagaacgcc ttgtgtgttg acatctgagg tagctgcttg tgtgttgccg 540

ctctggaggt tggtagatac agaaccatac tgctccgtag ccacgggatt ggtggtcctg 600

atttcctctt cgtctgtaat catgaccttt tcaatgtcca cattagtttt tcccgagtct 660

tgttttccaa agatgagaac cccgctctga ggaaaaaact tttcttcatc gtccttgtgg 720

ctggccatgg ccgggcccgg attcaccaga gagtctcttc cattaaggtg gtacttggta 780

gctccagtcc acgagtattc actgttgttg ttatccgcag atgtctttga tactcgctgc 840

tggcggtaac agggtccagg aagccagttc ctagactggt cccgaatgtc acttgctccg 900

gcctgagaaa actgaagcct tgactgcgtg gtggttccgc ttggagtgtt tgttctgctc 960

aagtaataca ggtactggtc gatgagagga ttcatgagac ggtccaaact ctggctgtgg 1020

gcgtagctgc tgtggaaagg aacgtcctca aaggtgtagc tgaaggtaaa gttgtttccg 1080

gtacgcagca tctgagaagg aaagtactcc aggcagtaaa atgaagagcg tcctactgcc 1140

tgactcccgt tgttcagggt gaggtatcca tactgtggca ccatgaagac gtctgctggg 1200

aacggcggga ggcatccttg atgcgccgag ccgaggacgt acgggagctg gtactccgag 1260

tcagtaaaca cctgaaccgt gctggtaagg ttattggcaa tcgtcgtcgt accgtcattc 1320

tgcgtgacct ccttgacttg aatgttaaag agcttgaagt tgagtctttt gggccggaat 1380

ccccaattgt tgttgatgag tctttgccag tcacgtggcg aaaagtggca gtggaatctg 1440

ttgaagtcaa aataccccca aggggtgctg tagccaaagt agtggttgtc gtttgaggct 1500

cctgattggc tggaaatctg cttgtagagg tggttgttgt aggtgggcag agcccaggtg 1560

cgggtgctgg tggtgatgac tctgtcgccc atccatgtgg aatcgcaatg ccaatttccc 1620

gaggaattac ccactccgtc ggcgccctcg ttattgtctg ccattggtgc gccactgcct 1680

gtagccatcg tattagttcc cagaccagag ggggctgctg gtggctgtcc gagaggctgg 1740

gggtcaggta cggagtctgc gtctccagtc tgaccgaaat tcaatctctt tcttgcaggc 1800

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gcgggtgagt tcaaatttga acatccggtc ttgcaacggc tgctggtgtt cgaaggtcgt 2880

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gtctatctgg gccgaggact tgcatttctg gtccacgcgc accttgcttc ctccgagaat 3000

ggctttggcc gactccacga ccttggcggt catcttcccc tcctcccacc agatcaccat 3060

cttgtcgacg caatcattga aaggaaagtt ctcattggtc cagttgacgc agccgtagaa 3120

agggcgaatt cgtttaaacc tgcaggacta gtccctttag tgagggt 3167

<210> 210
<211> 3161
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 210
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ttaaacggtt tattgattaa caagcaatta cagattacga gtcaggtatc tggtgccaat 120

ggggcgaggc tctgaataca caccattagt gtccacagta aagtccacat taacagattt 180

gttgtagttg gaagtgtact gaatctcggg attccagcgt ttgctgttct ccttctgcag 240

ctcccactcg atctccacgc tgacctgccc cgtggagtac tgtgtaatga aggaagcaaa 300

ctttgccgca ctgaaggtag tcgaaggatt cgcaggtacc ggggtgttct tgatgagaat 360

ctgcgggggа gggtgtttaa gtccgaatcc gcccatgagg ggagaggggt gaaaatgtcc 420

gtccgtgtgt ggaatctttg cccagatggg cccctgcagg tacacgtctc tgtcctgcca 480

caccatgcct ggaagaacgc cttgtgtgtt gacatctgag gtagctgctt gtgtgttgcc 540

gctctggagg ttggtagata cagaaccata ctgctccgta gccacgggat tggtggtcct 600

gatttcctct tcgtctgtaa tcatgacctt ttcaatgtcc acattagttt ttcccgagtc 660

ttgttttcca aagatgagaa ccccgctctg aggaaaaaac ttttcttcat cgtccttgtg 720

gctggccatg gccgggcccg gattcaccag agagtctctt ccattaaggt ggtacttggt 780

agctccagtc cacgagtatt cactgttgtt gttatccgca gatgtctttg atactcgctg 840

ctggcggtaa cagggtccag gaagccagtt cctagactgg tcccgaatgt cacttgctcc 900

ggcctgagaa aactgaagcc ttgactgcgt ggtggttccg cttggagtgt ttgttctgct 960

caagtaatac aggtactggt cgacgagagg attcatgaga cggtccaaac tctggctgtg 1020

ggcgtagctg ctgtggaaag gaacgtcctc aaaggtgtag ctgaaggtaa agttgtttcc 1080

ggtacgcagc atctgagaag gaaagtactc caggcagtaa aatgaagagc gtcctactgc 1140

ctgactcccg ttgttcaggg tgaggtatcc atactgtggc accatgaaga cgtctgctgg 1200

gaacggcggg aggcatcctt gatgcgccga gccgaggacg tacgggagct ggtactccga 1260

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tccccaattg ttgttgatga gtctttgcca gtcacgtggc gaaaagtggc agtggaatct 1440

gttgaagtca aaataccccc aaggggtgct gtagccaaag tagtggttgt cgtttgaggc 1500

tcctgattgg ctggaaatct gcctgtagag gtggttgttg taggtgggca gagcccaggt 1560

gcgggtgctg gtggtgatga ctctgtcgcc catccatgtg gaatcgcaat gccaatttcc 1620

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gaattcgttt aaacctgcag gactagtccc tttagtgagg g 3161

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<211> 3172
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 211
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cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgaccgcc 120

aaggtcgtgg agtccgccaa ggccattctg ggtggaagca aggtgcgcgt ggaccaaaag 180

tgcaagtcat cggcccagat cgaccccacg cccgtgatcg tcacctccaa caccaacatg 240

tgcgccgtga tcgacgggaa cagcaccacc ttcgagcacc agcagcccct gcaggaccgc 300

atgttcaagt tcgagctcac ccgccgtctg gagcacgact ttggcaaggt gaccaagcag 360

gaagtcaaag agttcttccg ctgggctcag gatcacgtga ctgaggtggc gcatgagttc 420

tacgtcagaa agggcggagc caccaaaaga cccgccccca gtgacgcgga tataagcgag 480

cccaagcggg cctgcccctc agttgcggag ccatcgacgt cagacgcgga agcaccggtg 540

gactttgcgg acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg 600

tttccctgca agacatgcga gagaatgaat cagaatttca acgtctgctt cacgcacggg 660

gtcagagact gctcagagtg cttccccggc gcgtcggaat ctcaacccgt cgtcagaaaa 720

aagacgtatc agaaactgtg cgcgattcat catctgctgg ggcgggcacc cgagattgcg 780

tgttcggcct gcgatctcgt caacgtggac ttggatgact gtgtttctga gcaataaatg 840

acttaaacca ggtatggctg ctgacggtta tcttccagat tggctcgagg acaacctctc 900

tgagggcatt cgcgagtggt gggacctgaa acctggagcc cccaagccca aggccaacca 960

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ctctggtctg ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa 1500

cgaaggcgcc gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct 1560

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cctctacaag caaatatcca atgggacatc gggaggaagc accaacgaca acacctactt 1680

cggctacagc acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc 1740

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caagctcttc aacatccagg tcaaggaggt cacgcagaat gaaggcaccg agaccatcgc 1860

caataacctt accagcacga ttcaggtatt tacggactcg gaataccagc tgccgtacgt 1920

cctcggctcc gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc 1980

ccagtacggc taccttacac tgaacaatgg aagtcaagcc gtaggccgtt cctccttcta 2040

ctgcctggaa tattttccat ctcaaatgct gcgaactgga aacaattttg aattcagcta 2100

caccttcgag gacgtgcctt tccacagcag ctgcgcacac agccagagct cggaccgact 2160

gatgaatcct ctcatcgacc agtacctgta ctacttatcc agaactcggt ccacaggagg 2220

aactcaaggt acccagcaat tgttattttc tcaagctggg cctgcaaaca tgtcggctca 2280

ggctaagaac tggctacctg gaccttgcta ccggcagcag cgagtctcta cgacactgtc 2340

gcaaaacaac aacagcaact ttgcttggac tggtgccacc aaatatcacc tgaacggaag 2400

agactctttg gtaaatcccg gtgtcgccat ggcaacccac aaggacgacg aggaacgctt 2460

cttcccgtcg agtggagtcc tgatgtttgg aaaacagggt gctggaagag acaatgtgga 2520

ctacagcagc gttatgctaa ccagcgaaga agaaattaaa accactaacc ctgtagccac 2580

agaacaatac ggtgtggtgg ctgacaactt gcagcaaacc aatacagggc ctattgtggg 2640

aaatgtcaac agccaaggag ccttacctgg catggtctgg cagaaccgag acgtgtacct 2700

gcagggtccc atctgggcca agattcctca cacggacggc aacttccacc cttcaccgct 2760

aatgggagga tttggactga agcacccacc tcctcagatc ctgatcaaga acacgccggt 2820

acctgcggat cctccaacaa cgttcagcca ggcgaaattg gcttccttca ttacgcagta 2880

cagcaccgga caggtcagcg tggaaatcga gtgggagctg cagaaggaga acagcaaacg 2940

ctggaaccca gagattcagt acacttcaaa ctactacaaa tctacaaatg tggactttgc 3000

tgtcaataca gagggaactt attctgagcc tcgccccatt ggtactcgtt acctcacccg 3060

taatctgtaa ttgctggtta atcaataaac cgtttgattc gtttcagttg aactttggtc 3120

tctgcgaagg gcgaattcgt ttaaacctgc aggactagtc cctttagtga gg 3172

<210> 212
<211> 3172
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 212
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cccttcaacg attgcgtcga caagatggtg atctggtggg aggagggcaa gatgaccgcc 120

aaggtcgtgg agtccgccaa ggccattctg ggtggaagca aggtgcgcgt ggaccaaaag 180

tgcaagtcat cggcccagat cgaccccacg cccgtgatcg tcacctccaa caccaacatg 240

tgcgccgtga tcggcgggaa cagcaccacc ttcgagcacc agcagcccct gcaggaccgc 300

atgttcaagt tcgagctcac ccgccgtctg gagcacgact ttggcaaggt gaccaagcag 360

gaagtcaaag agttcttccg ctgggctcag gatcacgtga ctgaggtggc gcatgagttc 420

tacgtcagaa agggcggagc caccaaaaga cccgccccca gtgacgcgga tataagcgag 480

cccaagcggg cctgcccctc agttgcggag ccatcgacgt cagacgcgga agcaccggtg 540

gactttgcgg acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg 600

tttccctgca agacatgcga gagaatgaat cagaatttca acgtctgctt cacgcacggg 660

gtcagagact gctcagagtg cctccccggc gcgtcagaat ctcaacccgt cgtcagaaaa 720

aagacgtatc agaaactgtg cgcgattcat catctgctgg ggcgggcacc cgagattgcg 780

tgttcggcct gcgatctcgt caacgtggac ttggatgact gtgtttctga gcaataaatg 840

acttaaacca ggtatggctg ctgacggtta tcttccagat tggctcgagg acaacctctc 900

tgagggcatt cgcgagtggt gggacctgaa acctggagcc cccaagccca aggccaacca 960

gcagaagcag gacgacggcc ggggtctggt gcttcttggc tacaagtacc tcggaccctt 1020

caacggactc gacaaggggg agcccgtcaa tgcggcggac gcagcggccc tcgagcacga 1080

caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 1140

cgacgccgag tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg 1200

agcagtcttc caggccaaga agcgggttct cgaacctctc ggtctggttg aggaagctgc 1260

taagacggct cctggaaaga agagaccggt agaaccgtca cctcagcgtt cccccgactc 1320

ctccacgggc atcggcaaga aaggccagca gcccgctaaa aagagactga actttggtca 1380

gactggcgac tcagagtcag tccccgaccc tcaaccaatc ggagaaccac cagcaggccc 1440

ctctggtctg ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa 1500

cgaaggcgcc gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct 1560

gggcgacaga gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaacca 1620

cctctacaag caaatatcca atgggacatc gggaggaagc accaacgaca acacctactt 1680

cggctacagc acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc 1740

acgtgactgg cagcgactca tcaacaacaa ctggggattc cggccaaaaa gactcagctt 1800

caagctcttc aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc 1860

caataacctt accagcacga ttcaggtatt tacggactcg gaataccagc tgccgtacgt 1920

cctcggctcc gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc 1980

ccagtacggc taccttacac tgaacaatgg aagtcaagcc gtaggccgtt cctccttcta 2040

ctgcctggaa tattttccat ctcaaatgct gcgaactgga aacaattttg aattcagcta 2100

caccttcgag gacgtgcctt tccacagcgg ctacgcacac agccagagct tggaccgact 2160

gatgaatcct ctcatcgacc agtacctgta ctacttatcc agaactcagt ccacaggagg 2220

aactcaaggt acccagcaat tgttattttc tcaagctggg cctgcaaaca tgtcggctca 2280

ggctaagaac tggctacctg gaccttgcta ccggcagcag cgagtctcta cgacactgtc 2340

gcaaaacaac aacagcaact ttgcttggac tggtgccacc aaatatcacc tgaacggaag 2400

agactctttg gtaaatcccg gtgtcgccat ggcaacccac aaggacgacg aggaacgctt 2460

cttcccgtcg agtggagtcc tgatgtttgg aaaacagggt gctggaagag acaatgtgga 2520

ctacagcagc gttatgctaa ccagcgaaga agaaattaaa accactaacc ctgtagccac 2580

agaacaatac ggtgtggtgg ctgacaactt gcagcaaacc aatacagggc ctattgtggg 2640

aaatgtcaac agccaaggag ccttacctgg catggtctgg cagaaccgag acgtgtacct 2700

gcagggtccc atctgggcca agattcctca cacggacggc aacttccacc cttcaccgct 2760

aatgggagga tttggactga agcacccacc tcctcagatc ctgatcaaga acacgccggt 2820

acctgcggat cctccaacga cgttcagcca ggcgaaattg gcttccttca ttacgcagta 2880

cagcaccgga caggtcagcg tggaaatcga gtgggagctg cagaaggaga acagcaaacg 2940

ctggaaccca gagattcagt acacttcaaa ctactacaaa tctacaaatg tggactttgc 3000

tgtcaataca gagggaactt attctgagcc tcgccccatt ggtactcgtt acctcacccg 3060

taatctgtaa ttgctggtta atcaataaac cgtttgattc gtttcagttg aactttggtc 3120

tctgcgaagg gcgaattcgt ttaaacctgc aggactagtc cctttagtga gg 3172

<210> 213
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 213
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg aaagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc gagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg cttcaggcag tggcgcacca gtggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacagct ggggattccg acccaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caagtgttta ccgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttt atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tcctttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcccttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctgc tgaatcctct gatcgaccag 1320

tacctatatt atctgaacaa gacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca cggacgggca ctttcatcct tctccactaa tgggaggttt tgggctcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcctacaaac 1980

ttcagttctt ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ccgactcgta atctgtaa 2208

<210> 214
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 214
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Glu Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Leu Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
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His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ser Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg Asn Leu
                725                 730                 735


<210> 215
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 215
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga      480
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aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gccagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggtattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

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caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 216
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 216
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Glu Lys Arg

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    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp Tyr Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
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            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
```

545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
580 585 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 217
<211> 2209
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 217
atggctgccg atggttatcc tccagattgg ctcgaggaca ctctctctga agggataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcggcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatcg ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaat 2209

<210> 218
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 218
Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Arg Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460
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Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495


Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540


Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590


Gly Thr Val Asn Arg Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 219
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 219
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aggtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgtcga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa ggcggctccg 420

ggagaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

cattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccccca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg cgccagatac ctgactcgta atctgtaa 2208

<210> 220
<211> 735

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 220
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Val
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Ala Ala Pro Gly Glu Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly His Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
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Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590
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Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Pro Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Ala Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 221
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 221
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga taacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccggcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 222
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 222
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
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Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 223
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 223
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagacgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 224
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 224
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
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    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Thr Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
```

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            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
```

625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 225
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 225
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctgcaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ttttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

acctacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc gggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 226
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 226
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Cys Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
```

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Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
```

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Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Tyr Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 227
<211> 2208
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 227
atggctgccg atggttatct tccagattgg ctcgaggaca ccctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga taacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccggcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 228
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 228
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 229
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 229
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

ggcagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctca acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa aacggctccg 420

ggaaaaaaga gaccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accacaagca ctcgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactattttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct ccctttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagat gtgtaccttc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagattat gatcaaaaac actcccgttc cagccaatcc tcctacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacaataa tggcgtgtac 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 230

<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 230
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Gly Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asn Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Pro Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590
```

```
Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Asn Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 231
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 231
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacag ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 232
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 232
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
```

```
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
```

```
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
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705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 233
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 233
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accatctgta caagcaaatc 780

tccagccagt ctggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tatttcgact tcaacagatt ccactgccac ttctccccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgccttccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggca gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgaaga cgttcctttc 1260

catagcagct acgctcacgg ccaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgat gtccaggctt 1380

cagttttctc aggccggagc aagtgacgtt cgggaccagt ctagaaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggaagag actctctggt gaatccgggc 1560

ccagctatgg ccagccacaa ggacgatgaa gaaaaatatt ttcctcagag cggggttctc 1620

gtctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac caccaatccc gcggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacaaattct catcaagaac accccggtac ctgcgaatcc ttcgaccact 1980

ttcagtgcgg caaagtttgt ttccttcatc acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 234
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 234

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205
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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Gly Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Val Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Val Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Ala Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Val Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 235
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 235
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga aactcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgagc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctccc gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctagagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt caggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cggggttctt 1620

atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtcgggca agacagagac gtgtacctgc aggggcctac ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 236
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 236
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Ser Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
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```
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Gln Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
```

```
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Gly Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Thr Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 237
<211> 2208
<212> DNA
```

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 237
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctagggta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa agacgatgaa gaaaagtttt ttcctcagag cggggttctt 1620

atctttggga agcaaggccc agagaaaaca aatgtggata ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 238
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 238
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Gly Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

```
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 239
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 239
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 240
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 240
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Pro Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
```

```
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590


Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 241
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polynucleotide"

<400> 241

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgcgg cctggtttga ggaaacctgt taagacggct 420

ccgggaaaaa agaggccggt agagcactct cctgtggagc cagactcctc ctcgggaacc 480

ggaaaagcgg gccagcagcc tgcaagaaaa agattaaatt ttggtcagac tggagacgca 540

gactccgtac ctgaccccca gcctctcgga cagccaccag cagccccctc tggtctggga 600

tctactacaa tggctacagg cagtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctgga cgacagagtc 720

atcgccacca gcacccgaac ctgggccctg cccacataca acaaccacct ctacaagcaa 780

atctccagcc aatcaggagc ctgcaacgac aaccactact ttggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacagca actggggatt ccggcccaaa agactcaact tcaagctctt taatattcaa 960

gtcaaagagg tcacgcagaa tgacggtacg acgacgattg ccaataacct taccagcacg 1020

gttcaggtgt ttactgactc ggagtaccag ctcccgtacg tcccgggctc ggcgcatcaa 1080

ggatgcctcc cgccgtttcc agcggacgtc ttcatggtcc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtactgg aaacaacttt cagttcagct acacttttga agacgtgcct 1260

ttccacagca gctacgctca ctgccagagt ctggatcggc tgatgaatcc tctgatcgac 1320

cagtacctgt attatctgaa caagacacaa acaaatagtg gaactcttca gcagtctcgg 1380

ctactgttta gccaagctgg accaaccaac atgtctcttc aagctaaaaa ctggctgcct 1440

ggaccttgct acagacagca gcgtctgtca aaacaggcaa acgacaataa caactgcaac 1500

tttccctgga ctgcagctac aaagtatcat ctaaatggcc gggactcgtt ggttaatcca 1560

ggaccagcta tggccagtca caaggatgac gaagaaaagt ttttccccat gcatggaacc 1620

ctgatatttg gtaaacaagg aacaaatgcc aacgacgcgg atttggaaaa tgtcatgatt 1680

acagatgaag aagaaatcag gcccaccaat cccgtggcta cggagcagta cgggactgtg 1740

tcaaataatt tgcaaaactc aaacactggt ccaactacag gaactgtcaa tcaccaagga 1800

gcgttacctg gtatggtgtg gcaggatcga gacgtgtacc tgcagggacc catttgggcc 1860

aagattcctc acaccgatgg acactttcat ccttctccac tgatgggagg ttttggactc 1920

aaacacccgc ctcctcagat catgatcaaa agcactcccg ttccagccaa tcctcccaca 1980

aacttcagtt ctgccaagtt tgcttcttcc atcacacagt attccacggg acaggtcagc 2040

gtggagatcg agtgggagct gcagaaggag aacagcaaac gctggaatcc cgaaattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtggacac taatggtgtg 2160

tattcagagc ctcgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 242
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 242
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Arg Pro Gly Leu Arg Lys Pro Val Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr
145                 150                 155                 160

Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Asp Asp Arg Val
225                 230                 235                 240

Ile Ala Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Cys Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Cys Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys
        435                 440                 445

Thr Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn
                485                 490                 495

Asn Asn Cys Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Ser Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Ser Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 243
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 243
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagagga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcaaaaaaga gggttctgga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcagagccag attcctcctc cggaactgga 480

aagtcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agactcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accatctgta caagcaaata 780

tccagccagt ctggagccag caacgacaat cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctagagta ctttccttct 1200

cagatgctgc gtaccggaaa cagctttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gtcagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa agacgatgaa gaaaagttct ttcctcagag cggggttctt 1620

atctttggga agcaaggctc agagaaaaca aatgtggata ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca agacagagac gtgtacctgc aggggcctat ttgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 244
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 244

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Ser Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 245
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 245
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240
```

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 246
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 246
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile

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305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

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        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 247
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 247
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtt cacagcccgc taaaaagaaa ctcaatttcg gtcagactgg cgacacagag 540

tcagtccccg accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atgggagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gcgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

ggacccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa 1500

tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct 1620

ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc taatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gctttcaata aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagattg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 248
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 248
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
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```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 249
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 249
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cggcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 250
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 250
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Gly Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350
```

```
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560
```

```
Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 251
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 251
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtccttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

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cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 252
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 252
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Glu Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

```
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 253
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 253

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cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggtacttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac      540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga      660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc      720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt      780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg      840
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tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtaccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 254
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 254
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
```

385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp

595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 255
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 255
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagcggtgga agctcaaacc tggcccacca ccaccagagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggtactcga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagc aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg ggccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc cgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 256
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 256
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Arg Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Glu Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Ala Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Gly Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 257
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 257
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile

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145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
```

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        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
```

565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
580 585 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 258
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 258
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgttcggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccccg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 259
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 259
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
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Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Cys His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 260
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 260
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Arg
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Leu Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
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    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Ala Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Pro Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Arg Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
```

```
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Thr Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Ala Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Ala Asp Phe Ala Val Asn Thr Glu
```

705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 261
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 261
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcggac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtt 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt atcttgactt taacagattc actgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcgcc 1020

agcaccatcc aggtgtttac ggactcggaa taccagccgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctcg ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ctgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatcg cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgcgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 262
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 262
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcgtc 900

aacaacaacc ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 263
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 263
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Val Asn Asn Asn Arg
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480
```

```
Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

```
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 264
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 264

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Ser Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 265
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 265
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgagct ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattctgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 266
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 266
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Pro Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Val Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 267
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 267
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ccggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgccacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccgtcgccaa taaccttacc 1020

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caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

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agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgttg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 268
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 268
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
```

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                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Ser Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
```

```
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Leu
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 269
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 269
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aagcaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggactt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 270
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 270
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Pro Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
```

```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270


His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Val Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640
```

```
Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720


Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735


Leu



<210> 271
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 271
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
```

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    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
```

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            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Leu His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
```

```
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
```

675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Ser Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 272
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 272
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgcctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacaacca tcgctaataa ccttaccagc 1020

acggttcaag tcttctcgga ctcggagtac cagcttccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctctccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa tcctctcatc 1320

gtccaatacc tgtattacct gaacagaact caaaatcagt ccggaagtgc ccaaaacaag 1380

gacttgctgt tcagccgtgg gtctccagct ggcatgtctg ttcagcccaa aaactggcta 1440

cctggaccct gttatcggca gcagcgcgtt tctaaaacaa aaacagacaa caacaacagc 1500

aattttacct ggactggtgc ttcaaaatat aacctcaatg ggcgtgaatc catcatcaac 1560

cctggcactg ctatggcctc acacaaagac gacgaagaca agttctttcc catgagcggt 1620

gtcatgattt ttggaaaaga gagcgccgga gcttcaaaca ctgcattgga caatgtcatg 1680

attacagacg aagaggaaat taaagccact aaccctgtgg ccaccgaaag atttgggacc 1740

gtggcagtca atttccagag cagcagcaca gaccctgcga ccggagatgt gcatgctatg 1800

ggagcattac ctggcatggt gtggcaagat agagacgtgt acctgcaggg tcccatttgg 1860

gccaaaattc ctcacacaga tggacacttt cacccgtctc ctcttatggg cggctttgga 1920

ctcaagaacc cgcctcctca gatcctcatc aaaaacacgc ctgttcctgc gaatcctccg 1980

gcggagtttt cagctacaaa gtttgcttca ttcatcaccc aatactccac aggacaagtg 2040

agtgtggaaa ttgaatggga gctgcagaaa gaaaacagca agcgctggaa tcccgaagtg 2100

cagtacacat ccaattatgc aaaatctgcc agcgttgatt ttactgtgga caacaatgga 2160

ctttatactg agcctcgccc cattggcacc cgttacctta cccgtcccct gtaa 2214

<210> 273
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 273
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
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Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 274
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 274
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60
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cagtggtgga agctcagacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctga gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagggccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacccgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaaggtaga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 275
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 275
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Pro Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 276
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 276
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 277
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 277
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Arg Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Gly Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 278
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 278
atggctgccg atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatagggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcggg gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata ccccaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccgtgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 279
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 279
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Gly Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Pro Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Val Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 280
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 280
atggctgccg acggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgggc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actccccctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcactgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggccgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctctt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ctccacagca gctgcgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacagggac 1380

ttgctgttca gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccgcagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 281
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 281
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Pro Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Arg Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Ser Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Ala Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 282
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 282
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Leu His Ser Ser Cys Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Arg Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 283
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 283
atggctgccg atggctatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcatagggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacagt cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctc 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 284
<211> 735
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 284

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Arg Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Ser His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
```

```
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
```

```
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 285
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 285
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                   10                  15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
            20                  25                  30
```

```
Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
        35                  40                  45

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
    50                  55                  60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
        115                 120                 125

Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445
```

```
Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

```
Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720


Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735


Leu
```

<210> 286
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 286

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Gly Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
```

```
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
```

690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 287
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 287
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gccagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtactt caacgggggc cagcaacgac aaccactact tcggctacgg caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcgaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaacacaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcaccgctg tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaagcactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 288
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 288
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1 5 10 15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
20 25 30

Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
35 40 45

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
50 55 60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65 70 75 80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
85 90 95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
100 105 110

Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
115 120 125

Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
130 135 140

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

```
Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Glu Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605
```

```
Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705                 710                 715                 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 289
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 289

```
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1               5                   10                  15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
```

```
            20                  25                  30

Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
        35                  40                  45

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
    50                  55                  60

Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
        115                 120                 125

Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

```
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
```

```
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
```

645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 290
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 290
Arg Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu
1 5 10 15

Ser Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys
20 25 30

Pro Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu
35 40 45

Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu
50 55 60

```
Pro Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr
65                  70                  75                  80

Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His
                85                  90                  95

Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly
            100                 105                 110

Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu
        115                 120                 125

Pro Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys
    130                 135                 140

Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270
```

```
His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480
```

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Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Asn Ser Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685
```

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 291
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 291
atggctgccg atggttatct tccagattgg ctcaaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcgggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agtacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaacagga 480

aaagcgggcc agcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaag ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggctctgccc acctacaaca accatctgta caagcagatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc ccggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgcttc gtaccggaaa caactttacc ttcagctaca cctttgagga tgttcctttc 1260

cacagcagct acgctcacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtccaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg acaacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctactgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgcacctgc aggggcctat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcaaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtatt ccacagggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 292
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 292
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Lys Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Gly Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu Tyr Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Ser Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
```

```
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
```

580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val His Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 293
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 293
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcagagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttaaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acatacaaca accacctcta caagcaaatc 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctctttaa tattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tgggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagcc aagctggacc aaccaacatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctgtcaaaa caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcgcaa ggatgacgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt catgattaca 1680

gatgaagaag aaatcagggc caccaatccc gtggctacgg agcagtacgg gactgtgtca 1740

aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 294
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 294
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
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Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser Arg Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Ala Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 295
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 295
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgtcaa gacggctcca 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcggct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtacgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 296
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 296

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 297
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 297
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360
```

gcgaaaaaga gggttcttga acctctgggc ctggttgggg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa tcggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta cagacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

agcaacggga gtcaggcagt aggacgctct tcattttact gcccggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcac aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacaatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacctaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atttgtaa 2208

<210> 298
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 298
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Gly Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Arg His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
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Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Ser Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Thr Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asn Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
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```
Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Pro Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 299
<211> 2205

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 299
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ctgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcagacag ccaccagcag cccccacaag tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accaccttta caagcaaatc 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccctggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgctgc gtactggaaa caactttcag ttcagctaca cttttgaaga cgtgcctttc 1260

cacagcagct acgctcacag ccagagtttg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctaaacag aacacaaaca gctagtggaa ctcagcagtc tcggctactg 1380

tttagccaag ctggacccac aagcatgtct cttcaagcta aaaactggct gcctggaccg 1440

tgttatcgcc agcagcgttt gtcaaagcag gcaaacgaca acaacaacag caactttccc 1500

tggactggag ctaccaagta ctacctcaat ggcagagact ctttggtgaa cccgggcccg 1560

gccatggcca gccacaagga cgatgaagaa aagtttttcc ccatgcatgg aaccctaata 1620

tttggtaaag aaggaacaaa tgctaccaac gcggaattgg aaaatgtcat gattacagat 1680

gaagaggaaa tcaggaccac caatcccgtg gctacagagc agtacggata tgtgtcaaat 1740

aatttgcaaa actcaaatac tgctgcaagt actgaaactg tgaatcacca aggagcatta 1800

cctggtatgg tgtggcagga tcgagacgtg tacctgcagg gacccatttg ggccaagatt 1860

cctcacaccg atggacactt tcatccttct ccactgatgg gaggttttgg actcaaacac 1920

ccgcctcctc agattatgat caaaaacact cccgttccag ccaatcctcc cacaaacttc 1980

agttctgcca agtttgcttc cttcatcaca cagtattcca cgggacaggt cagcgtggag 2040

atcgagtggg agctgcagaa ggagaacagc aaacgctgga atcccgaaat tcagtacact 2100

tccaactaca acaaatctgt taatgtggac tttactgtgg acactaatgg tgtgtattca 2160

gagcctcgcc ccattggcac cagatacctg actcgtaatc tgtaa 2205

<210> 300
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 300
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
```

```
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
```

660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 301
<211> 3160
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 301
acccttcact aaagggacta gtcctgcagg tttaaacgaa ttcgcccttg ctgcgtcaac 60

tggaccaatg agaactttcc cttcaacgac tgtgtcgaca agatggtgat ttggtgggag 120

gaggggaaga tgaccgccaa ggtcgtggag tcggccaaag ccattctcgg aggaagcaag 180

gtgcgcgtgg accagaaatg caagtcctcg gcccagatag atccgactcc cgtgatcgtc 240

acctccaaca ccaacatgtg cgccgtgatt gacgggaact caacgacctt cgaacaccag 300

cagccgttgc aagaccggat gttcaaattt gaactcaccc gccgtctgga tcatgacttt 360

gggaaggtca ccaagcggga agtcaaagac tttttccggt gggcaaagga tcacgtggtt 420

gaggtggagc atgaattcta cgtcaaaaag ggtggagcca agaaaagacc cgcccctagt 480

gacgcagata taagtgagcc caaacgggtg cgcgagtcag ttgcgcagcc atcgacgtca 540

gacgcggaag cttcgatcaa ctacgcggac aggtaccaaa acaaatgttc tcgtcacgtg 600

ggcatgaatc tgatgctgtt tccctgcaga caatgcgaga gaatgaatca aaattcaaat 660

atctgcttca ctcacggaca gaaagactgt ttagagtgct ttcccgtgtc agaatctcaa 720

cctgtttctg tcgtcaaaaa ggcgtatcag aaactgtgct acattcatca tatcatggga 780

aaggtgccag acgcttgcac tgcctgcgat ctggtcaatg tggatttgga tgactgcatc 840

tctgaacaat aaatgattta aatcaggtat ggctgccgat ggttatcttc cagattggct 900

cgaggacact ctctctgaag gaataagaca gtggtggaag ctcaaacctg gcccaccacc 960

accaaagccc gcagagcggc ataaggacga cagcaggggt cttgtgcttc ctgggtacaa 1020

gtacctcgga cccttcaacg gactcgacaa gggagagccg gtcaacgagg cagacgccgc 1080

ggccctcgag cacgacaagg cctacgaccg gcagctcgac agcggagaca acccgtacct 1140

caagtacaac cacgccgacg cggagtttca ggagcgtctt aaagaagata cgtcttttgg 1200

gggcaacctc ggacgagcag tcttccaggc gaaaaagagg gttcttgaac ctctgggcct 1260

ggttgaggaa cctgttaaga cggctccggg aaaaaagagg ccggtagagc actctcctgc 1320

ggagccagac tcctcctcgg gaaccggaaa agcgggccag cagcctgcaa gaaaaagact 1380

gaatttcggt cagactggag acgcagactc cgtacctgac ccccagcctc tcagacagcc 1440

accagcagcc cccacaagtt tgggatctac tacaatggct acaggcagtg gcgcaccaat 1500

ggcagacaat aacgagggtg ccgatggagt gggtaattcc tcaggaaatt ggcattgcga 1560

ttcccaatgg ctgggcgaca gagtcatcac caccagcacc cgaacctggg ccctgcccac 1620

ctacaacaac cacctttaca agcaaatctc cagccaatca ggagcctcaa acgacaacca 1680

ctactttggc tacagcaccc cctgggggta ttttgacttc aacagattcc actgccactt 1740

ttcaccacgt gactggcaaa gactcatcaa caacaactgg ggattccgac ccaagagact 1800

caacttcaag ctctttaaca ttcaagtcaa agaggtcacg cagaatgacg gtacgacgac 1860

gattgccaat aaccttacca gcacggttca ggtgtttact gactcggagt accagctccc 1920

gtacgtcctc ggctcggcgc atcaaggatg cctcccgccg tttccagcgg acgtcttcat 1980

ggtcccacag tatggatacc tcaccctgaa caacgggagt caggcggtag gacgctcttc 2040

cttttactgc ctggagtact ttccttctca gatgctgcgt actggaaaca actttcagtt 2100

cagctacact tttgaagacg tgcctttcca cagcagctac gctcacagcc agagtttgga 2160

tcggctgatg aatcctctga tcgaccagta cctgtattat ctaaacagaa cacaaacagc 2220

tagtggaact cagcagtctc ggctactgtt tagccaagct ggacccacaa gcatgtctct 2280

tcaagctaaa aactggctgc ctggaccgtg ttatcgccag cagcgtttgt caaagcaggc 2340

aaacgacaac aacaacagca actttccctg gactggagct accaagtact acctcaatgg 2400

cagagactct ttggtgaacc cgggcccggc catggccagc cacaaggacg atgaagaaaa 2460

gtttttcccc atgcatggaa ccctaatatt tggtaaagaa ggaacaaatg ctaccaacgc 2520

ggaattggaa aatgtcatga ttacagatga agaggaaatc aggaccacca atcccgtggc 2580

tacagagcag tacggatatg tgtcaaataa tttgcaaaac tcaaatactg ctgcaagtac 2640

tgaaactgtg aatcaccaag gagcattacc tggtatggtg tggcaggatc gagacgtgta 2700

cctgcaggga cccatttggg ccaagattcc tcacaccgat ggacactttc atccttctcc 2760

actgatggga ggttttggac tcaaacaccc gcctcctcag attatgatca aaaacactcc 2820

cgttccagcc aatcctccca caaacttcag ttctgccaag tttgcttcct tcatcacaca 2880

gtattccacg ggacaggtca gcgtggagat cgagtgggag ctgcagaagg agaacagcaa 2940

acgctggaat cccgaaattc agtacacttc caactacaac aaatctgtta atgtggactt 3000

tactgtggac actaatggtg tgtattcaga gcctcgcccc attggcacca gatacctgac 3060

tcgtaatctg taattgcttg ttaatcaata aaccgtttaa ttcgtttcag ttgaactttg 3120

gtctctgcga agggcgaatt cgcggccgct aaatcaatcg 3160

<210> 302
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 302
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Gly Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445
```

```
Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Gly
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Arg Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655
```

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 303
<211> 3157
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 303
ctcactaagg gactagtcct gcaggtttaa acgaattcgc ccttgctgcg tcaactggac 60

caatgagaac tttcccttca acgactgtgt cgacaagatg gtgatttggt gggaggaggg 120

gaagatgacc gccaaggtcg tggagtcggc caaagccact ctcggaggaa gcaaggtgcg 180

cgtggaccag aaacgcaagt cctcggccca gatagatccg actcccgtga tcgtcacctc 240

caacaccaac atgtgcgccg tgattgacgg gaactcaacg accttcgaac accagcagcc 300

gttgcaagac cgaatgttca aatttgaact cacccgccgt ctggatcatg acttcgggaa 360

ggtcaccaag caggaagtca aagacttttt ccggtgggca aaggatcacg tggttgaggt 420

ggagcatgaa ttctacgtca aaaagggtgg agccaagaaa agacccgccc ctagtgacgc 480

agatataagt gagcccaaac gggtgcgcga gtcagttgcg cagccatcga cgtcagacgc 540

ggaagcttcg atcaactacg cggacaggta ccaaaacaaa tgttctcgtc acgtgggcat 600

gaatctgatg ctgtttccct gcagacaatg cgagagaatg aatcaaaatt caaatatctg 660

cttcactcac ggacagaaag actgtttaga gtgctttccc gtgtcagaat ctcaacctgt 720

ttctgtcgtc aaaaaggcgt atcagaaact gtgctacatt catcatatca tgggaaaggt 780

gccagacgct tgcactgcct gcgatctggt caatgtggat ttggatgact gcatctctga 840

acaataaatg atttaaatca ggtatggctg ccgatggtta tcttccagat tggctcgagg 900

acactctctc tgaaggaata agacagtggt ggaagctcaa acctggccca ccaccaccaa 960

agcccgcaga gcggcataag gacgacagca ggggtcttgt gcttcctggg tacaagtacc 1020

tcggaccctt caacggactc gacaagggag agccggtcaa cgaggcagac gccgcggctc 1080

tcgagcacga caaggcctac gaccggcagc tcgacagcgg agacaacccg tacctcaagt 1140

acaaccacgc cgacgcggag tttcaggagc gtcttaaaga agatacgtct tttgggggca 1200

acctcggacg agcagtcttc caggcgaaaa agagggttct tgaacctctg ggcctggttg 1260

aggaacctgt taagacggct ccgggaaaaa agaggccggt agagcactct cctgcggagc 1320

cagactcctc ctcgggaacc ggaaaagcgg gccagcagcc tgcaagaaaa agactgaatt 1380

tcggtcagac tggagacgca gactccgtac ctgaccccca gcctctcgga cagccaccag 1440

cagcccccac aagtttggga tctactacaa tggctacagg cagtggcgca ccaatggcag 1500

acaataacga gggtgccgat ggagtgggta attcctcagg aaattggcat tgcgattccc 1560

aatggctggg cgacagagtc atcaccacca gcacccgaac ctgggccctg cccacctaca 1620

acaaccacct ttacaagcaa atctccagcc aatcaggagc ctcaaacgac aaccactact 1680

ttggctacag caccccctgg gggtattttg acttcaacag attccactgc cgcttttcac 1740

cacgtgactg gcaaagactc atcaacaaca actggggatt ccgacccaag agactcaact 1800

tcaagctctt taacattcaa gtcaaagagg tcacgcagaa tgacggtacg acgacgattg 1860

ccaataacct taccagcacg gttcaggtgt ttactgactc ggagtaccag ctcccgtacg 1920

tcctcggctc ggcgcatcaa ggatgcctcc cgccgtttcc agcggacgtc ttcatggtcc 1980

cacagtatgg atacctcacc ctgaacaacg ggagtcaggc ggtaggacgc tcttcctttt 2040

actgcctgga gtactttcct tctcagatgc tgcgtactgg aaacaacttt cagttcagct 2100

acacttttga agacgtgcct ttccacagca gctacgctca cagccagggt ttggatcggc 2160

tgatgaatcc tctgatcgac cagtacctgt attatctaaa cagaacacaa acagctagtg 2220

gaactcagca gtctcggcta ctgtttagcc aagctggacc cacaagcatg tctcttcaag 2280

ctaaaaactg gctgcctgga ccgtgttatc gccagcagcg tttgtcaaag caggcaaacg 2340

acaacaacaa cagcaacttt ccctggactg gagctaccaa gtaccacctc aatggcggag 2400

actctttggt gaacccgggc ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt 2460

tccccatgca tggaacccta atatttggta aagaaggaac aaatgctacc aacgcggaat 2520

tggaaaatgt catgattaca gatgaagagg aaatcaggac caccaatccc gtggctacag 2580

agcagtacgg atatgtgtca ataaatttgc aaaactcaaa tactgctgca agtactgaaa 2640

ctgtgaatca ccaaggagca ttacctggta tggtgtggca ggatcgagac gtgtacctgc 2700

ggggacccat ttgggccaag attcctcacg ccgatggaca ctttcatcct tctccactga 2760

tgggaggttt tggactcaaa cacccgcctc ctcagattat gatcaaaaac actcccgttc 2820

cagccaatcc tcccacaaac ttcagttctg ccaagtttgc ttccttcatc acacagtatt 2880

ccacgggaca ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct 2940

ggaatcccga aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg 3000

tggacactaa tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta 3060

atctgtaatt gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc 3120

tgcgaagggc gaattcgcgg ccgctaaatt caattcg 3157

<210> 304
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 304
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
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```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Cys Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445
```

```
Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655
```

```
Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685


Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690                 695                 700


Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705                 710                 715                 720


Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 305
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 305
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctggatac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag      360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg      420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga      480

aaagcgggca accagcctgc aagaaaaaga ttgaatttcg gtcagactgg agacgcagac      540

tccgtacctg acccccagcc tctcggacag ccaccagcat ccccctctgg tctgggaact      600
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aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcgtc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcagatt 780

tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcgccac gcgactggca gagactcatc 900

aacaacaact ggggattccg gcccaaaaga ctcaacttca agctgtttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgacttgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gcaccggaaa caactttacc ttcagctaca cttttgaaga cgttcctttc 1260

cacagcagct acgctcacag tcaaagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccactacgca gtccaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcaaag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcccat ctgggcaaaa 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt tggacttaaa 1920

caccctcctc cacagattct cattaagaat accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagcgcgg caaagtttgc ttccttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggggtgtat 2160

tcagagcctc gccctattgg caccagatac ctgactcgta atctgtaa 2208

<210> 306
<211> 3159
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 306
gattgattta gcggccgcga attcgccctt gctgcgtcaa ctggaccaat gagaactttc 60

ccttcaacga ttgcgtcgac aagatggtga tctggtggga ggagggaaag atgaccgcca 120

aggtcgtgga gtcggccaaa gccattctcg gaggaagcaa ggtgcgtgtg gaccaaaagt 180

gcaagtcttc ggcccagatc gacccgactc ccgtgatcgt cacctccaac accaacatgt 240

gcgccgtgat tgatggaaac tcaacgacct tcgagcacca gcagccgttg caagaccgga 300

tgttcaaatt tgaacttacc cgccgtctgg atcatgactt tggaaaggtc accaagcagg 360

aagtgaaaga ctttttccgg tgggcaaagg atcacgtggt tgaggtggag catgagttct 420

acgtcaaaaa gggtggagcc aaaaaaagac ccgcccccag tgacgcagat ataagtgagc 480

ccaaacgggc gcgcgagtca gttgcgcagc catcgacgtc agacgcggaa gcttcgatca 540

actacgcgga caggtaccaa aacaaatgtt ctcgtcacgt gggcatgaat ctgatgctgt 600

ttccctgcag acaatgcgag agaatgaatc agaattcaaa tatctgcttc actcacggac 660

agaaagactg tccatagtgc tttcccgtgt cagaatctca acccgtttct gtcgtcaaaa 720

aggcgtatca gaaactgtgc tacattcatc acatcatggg aaaggtgcca gacgcttgca 780

ctgcttgcga cctggtcaat gtggatttgg atgactgcat ctctgaacaa taaatgattt 840

aaatcaggta tggctgccga tggttatctt ccagattggc tcgaggacac tctctctgaa 900

ggaataagac agtggtggaa gctcaaacct ggcccaccac caccaaagcc cgcagagcgg 960

cataaggacg acagcagggg tcttgtgctt cctggataca agtacctcgg acccttcaac 1020

ggactcgaca agggagagcc ggtcaacgag gcagacgccg cggccctcga gcacgacaag 1080

gcctacgacc ggcagctcga cagcggagac aacccgtacc tcaagtacaa ccacgccgac 1140

gcggagtttc aggagcgcct taaagaagat acgtcttttg ggggcaacct cggacgagca 1200

gtcttccagg cgaaaaagag ggttcttgaa cctctgggcc tggttgagga acctgttaag 1260

acggctccgg gaaaaaagag gccggtagag cactctcctg tggagccaga ctcctcctcg 1320

ggaaccggaa aagcgggcaa ccagcctgca agaaaaagat tgaatttcgg tcagactgga 1380

gacgcagact ccgtacctga cccccagcct ctcggacagc caccagcatc cccctctggt 1440

ctgggaacta atacgatggc tacaggcagt ggcgcaccaa tggcagacaa taacgagggc 1500

gccgacggag tgggtaattc ctcgggaaat tggcattgcg attccacatg gatgggcgac 1560

agagtcgtca ccaccagcac ccgcacctgg gccctgccca cctacaacaa ccacctctac 1620

aagcagattt ccagccaatc aggagccagc aacgacaacc actactttgg ctacagcacc 1680

ccttgggggt attttgactt caacagattc cactgccact tttcgccacg cgactggcag 1740

agactcatca acaacaactg gggattccgg cccaaaagac tcaacttcaa gctgtttaac 1800

attcaagtca aggaggtcac gcagaatgac ggtacgacga cgattgccaa taaccttacc 1860

agcacggttc aggtgtttac tgacttggag taccagctcc cgtacgtcct cggctcggcg 1920

catcaaggat gcctcccgcc gttcccagca gacgtcttca tggtgccaca gtatggatac 1980

ctcaccctga acaacgggag tcaggcggta ggacgctctt ccttttactg cctggagtac 2040

tttccttctc agatgcttcg caccggaaac aactttacct tcagctacac ttttgaagac 2100

gttcctttcc acagcagcta cgctcacagt caaagtctgg accgtctcat gaatcctctc 2160

atcgaccagt acctgtatta cttgagcaga acaaacactc caagcggaac cactacgcag 2220

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agtgaatact cgtggactgg agctaccaag taccacctca atggcagaga ctctctggtg 2400

aatccgggcc cggccatggc cagccacaag gacgatgaag aaaagttttt tcctcaaagc 2460

ggggttctca tctttgggaa gcaaggctca gagaaaacaa atgtggacat tgaaaaggtc 2520

atgattacag acgaagagga aatcaggacc accaatcccg tggctacgga gcagtatggt 2580

tctgtatcta ccaacctcca gagcggcaac acacaagcag ctacctcaga tgtcaacaca 2640

caaggcgttc ttccaggcat ggtctggcag gacagagacg tgtacctgca ggggcccatc 2700

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ggacttaaac accctcctcc acagattctc attaagaata ccccggtacc tgcgaatcct 2820

tcgaccacct tcagcgcggc aaagtttgct tccttcatca cacagtattc cacggggcag 2880

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaatcccgaa 2940

attcagtaca cttccaacta caacaaatct gttaatgtgg actttactgt ggacactaat 3000

ggggtgtatt cagagcctcg ccctattggc accagatacc tgactcgtaa tctgtaattg 3060

cttgttaatc aataaaccgt ttaattcgtt tcagttgaac tttggtctct gcgaagggcg 3120

aattcgttta aacctgcagg actagtccct ttagtgagg 3159

<210> 307
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 307
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ser Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
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Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 308
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 308
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agcaggggtc ttgtgcttcc tggatacaag tacctcggac ccttcaacgg actcgacaag 180

ggagagccgg tcaacgaggc agacgccgcg gccctcgagc acgacaaggc ctacgaccgg 240

cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgccgacgc ggagtttcag 300

gagcgcctta aagaagatac gtcttttggg ggcaacctcg gacgagcagt cttccaggcg 360

aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac ggctccggga 420

aaaaagaggc ccgtagagca ctctcctgtg gagccagact cctcctcggg aaccggaaaa 480

gcgggcaacc agcctgcaag aaaaagattg aatttcggtc agactggaga cgcagactcc 540

gtacctgacc cccagcctct cggacagcca ccagcagccc cctctggtct gggaactaat 600

acgatggcta caggcagtgg cgcaccaatg gcagacaata acgagggcgc cgacggagtg 660

ggtaattcct cgggagattg gcattgcgat tccacatgga tgggcgacag agtcatcacc 720

accagcaccc gcacctgggc cctgcccacc tacaacaacc acctctacaa gcagatttcc 780

agccaatcag gagccagcaa tgacaaccac tactttggct acagcacccc ttgggggtat 840

tttgacttca acagattcca ctgccacttt tcgccacgcg actggcagag actcatcaac 900

aacaactggg gattccggcc caaaagactc aacctcaagc tgtttaacat tcaagtcaag 960

gaggtcacgc agaatgacgg tacgacgacg attgccaata accttaccag cacggttcag 1020

gtgtttactg acttggagta ccagctcccg tacgtcctcg gctcggcgca tcaaggatgc 1080

ctcccgccgt tcccagcaga cgtcttcatg gtgccacagt atggatacct caccctgaac 1140

aacgggagtc aggcggtagg acgctcttcc ttttactgcc tggagtactt tccttctcag 1200

atgcttcgta ccggaaacaa ctttaccttc agctacactt ttgaagacgt tcctttccac 1260

agcagctacg ctcacagtca aagtctggac cgtctcatga atcctctcat cgaccagtac 1320

ctgtattact tgagcagaac aaacactcca agcggaacca ctacgcagtc caggcttcag 1380

ttttctcagg ccggagcgag tgacattcgg gaccagtcta ggaactggct tcctggaccc 1440

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tggactggag ctaccaagta ccacctcaat ggcagagact ctctggtgaa tccgggcccg 1560

gccatggcca gccacaagga cgatgaagaa aagtttttc ctcaaagcgg ggttctcatc 1620

tttgggaagc aaggctcaga gaaaacaaat gtggacattg aaaaggtcat gattacagac 1680

gaagaggaaa tcaggaccac caatcccgtg gctacggagc agtatggttc tgtatctacc 1740

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agcgcggcaa agtttgcttc cttcatcaca cagtattcca cggggcaggt cagcgtggag 2040

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<210> 309
<211> 3156
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgtgt ggaccaaaag 180

tgcaagtctt cggcccagat cgacccgact cccgtgatcg tcacctccaa caccaacatg 240

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atgttcaaat ttgaacttac ccgccgtctg gatcatgact ttggaaaggt caccaagcag 360

gaagtgaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgagttc 420

tacgtcaaaa agggtggagc caaaaaaaga cccgccccca gtgacgcaga tataagtgag 480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gcgaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactgtg ctacattcat cacatcatgg gaaaggtgcc agacgcttgc 780

actgcttgcg acctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

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ctacgaccgg cagctcgaca gcggagacaa cccgtacctc aagtacaacc acgccgacgc 1140

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cttccaggcg aaaaagaggg ttcttgaacc tctgggcctg gttgaggaac ctgttaagac 1260

ggctccggga aaaaagaggc ccgtagagca ctctcctgtg gagccagact cctcctcggg 1320

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cgcagactcc gtacctgacc cccagcctct cggacagcca ccagcagccc cctctggtct 1440

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cgacggagtg ggtaattcct cgggagattg gcattgcgat tccacatgga tgggcgacag 1560

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tcaagtcaag gaggtcacgc agaatgacgg tacgacgacg attgccaata accttaccag 1860

cacggttcag gtgtttactg acttggagta ccagctcccg tacgtcctcg gctcggcgca 1920

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caccctgaac aacgggagtc aggcggtagg acgctcttcc ttttactgcc tggagtactt 2040

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ggtgtattca gagcctcgcc ctattggcac cagatacctg actcgtaatc tgtaattgct 3060

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ttcgtttaaa cctgcaggac tagtcccttt agtgag 3156

<210> 310
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 310

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Lys
            20                  25                  30

Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Arg
65                  70                  75                  80

Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly Lys
145                 150                 155                 160

Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
```

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                165                 170                 175

Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
            180                 185                 190

Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300

Phe Arg Pro Lys Arg Leu Asn Leu Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320

Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335

Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
```

```
    370                 375                 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400

Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Asn
        435                 440                 445

Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln Ala
    450                 455                 460

Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn Asn
                485                 490                 495

Gly Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Arg Ala Ala Thr Ser
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580 585 590

Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
690 695 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 311
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtacg accacgccga cgcggagttt 300

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gcaaaaaaga gggttcttga acctctgggc ctggttgagg agcctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggca accagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgatgg cgccgacgga 660

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tccagccaat caggagccag caacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg gcccaagaga ctcaacttca agctctttaa cattcaagtc 960

agagaggtca cgcagaatga tggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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cagttttctc aggccggagc gagtgacatt cgggatcagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg acaacaacaa cagtgaatac 1500

tcgtggattg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggcaatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaaggatc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcagaac caccaatccc gtggccacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca tctactgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagac gtgtacctgc aggggcctat ctgggcaaag 1860

attccgcaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcctc cacagattct catcaaaaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtatt ccacggggcg ggtcagcgtg 2040

gagatcgagt gggagctaca gaaggagaac agcaaacgct ggaatcccga gatccagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 312
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 312
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asp His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Asp Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
```

```
Asn Ser Glu Tyr Ser Trp Ile Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ser Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Arg Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 313
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 313
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagacag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattccg catggctggg cgacagagtc 720

atcaccacca gcacccgacc ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcccgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaacggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgcggag aacgggcaac aactttgagt tcagctacca gtttgaggac 1260

gtgccttttc acagcagcta cgcgcatagc caaagcctgg accggctgat gaaccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aataacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cttggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacgcacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttga tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aatcaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcatcctt cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc caagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt cagagcctcg ccccattggc acccgttacc tcacccgtaa cctgtaa 2217

<210> 314
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 314

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Ala Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Pro Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415
```

```
Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 315
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 315
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30
```

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445
```

```
Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 316
<211> 3158
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 316
gattgaattt agcggccgcg aattcgccct tgctgcgtca actggaccaa tgagaacttt 60

cctttcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc 120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgcgc ggaccagaaa 180

tgcaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccaacatg 240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg 300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag 360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc 420

tacgtcaaaa agggtggagc taagaaaaga cccgccccca gtgacgcaga tataagtgag 480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc 540

aactacgcgg gcaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg 600

tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga 900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg 960

gcataaggac gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa 1020

cggactcgac aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa 1080

ggcctacgac cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga 1140

cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200

agtcttccag gcaaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa 1260

aacggctccg ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc 1320

gggaaccgga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg 1380

agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg 1440

tctgggatct actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg 1500

tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga 1560

cagagtcatc accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta 1620

caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac 1680

cccctggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca 1740

aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa 1800

cattcaagtc aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac 1860

cagcacggtt caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc 1920

gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata 1980

cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta 2040

ctttccttct cagatgctgc gtaccggaaa caactttcaa ttcagctaca cttttgaaga 2100

cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct 2160

ggtcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca 2220

gtctcggcta ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaactg 2280

gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa 2340

cagcaacttt ccctggactg cagctacaaa gtatcatcta aatggccggg actcgttggt 2400

taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca 2460

tggaaccctt atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt 2520

catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg 2580

aactgtatca aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca 2640

ccaaggagcg ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat 2700

ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt 2760

tggactcaaa cacccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc 2820

tcccacaaac ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca 2880

ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga 2940

aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa 3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060

gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc 3120

gaattcgttt aaacctgcag gactagtccc tttagtga 3158

<210> 317
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 317
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Pro Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445
```

```
Gln Thr Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Asn Met Ser Leu Gln Ala Lys Asn Arg Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Val Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655
```

```
Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 318
<211> 3159
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 318
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cctttcaatg attgcgtcga caagatggtg atctggtggg aggagggaaa gatgaccgcc      120

aaggtcgtgg agtcggccaa agccattctc ggaggaagca aggtgcgcgt ggaccagaaa      180

tgcaagtcct cggcccagat agacccgact cccgtgattg tcacctccaa caccgacatg      240

tgcgccgtga ttgacgggaa ctcaacgacc ttcgaacacc agcagccgtt gcaagaccgg      300

atgttcaaat ttgaactcac ccgccgtctg gatcatgact ttgggaaggt caccaagcag      360

gaagtcaaag actttttccg gtgggcaaag gatcacgtgg ttgaggtgga gcatgaattc      420

tacgtcaaaa agggtggagc taagaaaaga cccgccccca gtgacgcaga tataagtgag      480

cccaaacggg cgcgcgagtc agttgcgcag ccatcgacgt cagacgcgga agcttcgatc      540

aactacgcgg acaggtacca aaacaaatgt tctcgtcacg tgggcatgaa tctgatgctg      600
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tttccctgca gacaatgcga gagaatgaat cagaattcaa atatctgctt cactcacgga 660

cagaaagact gtttagagtg ctttcccgtg tcagaatctc aacccgtttc tgtcgtcaaa 720

aaggcgtatc agaaactttg ctacattcat catatcatgg gaaaggtgcc agacgcttgc 780

actgcctgcg atctggtcaa tgtggatttg gatgactgca tctctgaaca ataaatgatt 840

taaatcaggt atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga 900

aggaataaga cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg 960

gcataaggac gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa 1020

cggactcgac aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa 1080

ggcctacgac cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga 1140

cgcggagttt caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc 1200

agtcttccag gcaaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa 1260

aacggctccg ggaaaaaaga ggccggtaga gcaccctcct gtggagccag actcctcctc 1320

gggaaccgga aaagcgggcc agcagcctgc aagaaaaaga ttgaatttcg gtcagactgg 1380

agacgcagac tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg 1440

tctgggatct actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg 1500

tgccgatgga gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggcga 1560

cagagtcatc accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta 1620

caagcaaatc tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac 1680

cccctggggg tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca 1740

aagactcatc aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa 1800

cattcaagtc aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac 1860

cagcacggtt caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc 1920

gcatcaagga tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata 1980

cctcaccctg aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta 2040

ctttccttct cagatgctgc gtaccggaaa caactttcag ttcagctaca cttttgaaga 2100

cgtgcctttc cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct 2160

gatcgaccag tacctgtatt atctgaacaa gacacaaaca aatagtggaa ctcttcagca 2220

gtctcggcta ctgtttagcc aagctggacc caccaacatg tctcttcaag ctaaaaaccg 2280

gctgcctgga ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa 2340

cagcaacttt ccctggaccg cagctacaaa gtatcatcta aatggccggg actcgttggt 2400

taatccagga ccagctatgg ccagtcacaa ggatgacgaa gaaaagtttt tccccatgca 2460

tggaaccctt atatttggta aacaaggaac aaatgccaac gacgcggatt tggaaaatgt 2520

catgattaca gatgaagaag aaatcaggac caccaatccc gtggctacgg agcagtacgg 2580

aactgtatca aataatttgc aaaactcaaa cactggtcca actactggaa ctgtcaatca 2640

ccaaggagcg ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat 2700

ttgggccaag attcctcaca ccgatggaca ctttcatcct tctccactgg tgggaggttt 2760

tggactcaaa cacccacctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc 2820

tcccacaaac ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca 2880

ggtcagcgtg gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga 2940

aattcagtac acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa 3000

tggtgtgtat tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaatt 3060

gcttgttaat caataaaccg tttaattcgt ttcagttgaa ctttggtctc tgcgaagggc 3120

gaattcgttt aaacctgcag gactagtccc tttagtgag 3159

<210> 319
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 319
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gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac cccaagtaca accacgccga cgcggagttc 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaagaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caagcagatt 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcgccac gtgactggca aagactcatc 900

aacaacaatt ggggattccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtgtggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

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caccctcccc cgcagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccaggtac ctgactcgta atctgtaa 2208

<210> 320
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 320
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Pro Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
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Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 321
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gacagcaggg gtcttgtgct tcctgggtac aagtaccttg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acggcggaga caacccgtac ctcaagtaca accacgccga cgcggagttc 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctctt gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaggaga ttgaatttcg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgcacctg ggctctgccc acctacaaca accacctcta caggcagatt 780

tccagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcgccac gtgactggca aagactcatc 900

aacaacaatt ggggatcccg gcccaaaaga ctcaacttca agctctttaa cattcaagtc 960

aaggaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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cagatgctgc gtaccggaaa caactttacc ttcagctaca cctttgagga cgttcctttc 1260

cacagcagct acgcccacag ccagagtttg gaccgtctca tgaatcctct cgtcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagcggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc aagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctt aatggaagag actctctggt gaatccgggc 1560

ccggccatgg ccagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggaa aacaagactc gggaaaaact aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac caccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtgtggca ggacagagac gtgtacctgc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggcggatt cggacttaaa 1920

caccctcccc cgcagattct catcaagaac accccggtac ctgcgaatcc ttcgactacc 1980

ttcagtgcgg caaagtttgc ttccttcatt acacagtact ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaaacgct ggaatcccga gattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 322
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 322
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Gly Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Leu Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Arg Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
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Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Arg Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

```
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 323
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 323
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ala Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Glu Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Cys Ala His Ser Gln Ser
            420                 425                 430

Ser Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Arg Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 324
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 324
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcttggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaatgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcggcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacgacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 325
<211> 738

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 325
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Leu
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Gly Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590
```

```
Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 326
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 326

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Pro Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

```
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 327
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 327
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
```

```
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
```

```
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
```

```
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
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675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 328
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 328
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg gacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

ctgtttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcaccta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggca tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920

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ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 329
<211> 2211
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 329
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 330
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

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tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

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cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa aacacaatca aatagtggaa ctcttcagca gtctcggcta 1380

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ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

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aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccaaggagcg 1800

ttacctggca tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920

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ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 331
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 331
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

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tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

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atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg agggagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

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cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

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gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

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aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac tgccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 332
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 332

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
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Glu Gly Thr Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190
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Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
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Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605
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Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 333
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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aacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccctccaa cggactcgac      180

aaaggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240
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cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaagcgggcc atcagcctgc gagaaagaga ttgaattttg gtcagactgg agacgcagac 540

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gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

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tattttgact tcaacagatt ccactgtcac ttctccccac gtgattggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

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tatctatatt atctgaacag gacacaatca aatagtggaa ctcttcagca gtctaggcta 1380

ctgtttagcc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctgcctgga 1440

ccttgctaca gacagcagcg tctttcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtatcatcta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagccacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggagcatgt tatgattaca 1680

gatgaagaag aaatcaggac caccaatcct gtggctacag agcagtacgg aaacgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actacagaaa atgtcaatca ccagggagcg 1800

ttacctggta tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgacggaca ctttcaccct tctccactga tgggaggttt tggactcaaa 1920

cacccgcctc ctcaaatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacgggcca ggtcagcgtg 2040

gagattgagt gggagctgca gaaggagaac agcaaacgct ggaaccccga gatccagtat 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggtgtgtat 2160

tcagagcctt gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 334
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 334
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Gln Asp Asn Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Ser Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

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            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Cys Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
```

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305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Pro Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
```

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        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Cys Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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725 730 735

<210> 335
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 335
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 336
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 336
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
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Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640
```

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 337
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 337
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 338
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 338
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
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Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 339
<211> 2211
<212> DNA
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 339
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga 60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aaggggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 340
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 340
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460
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Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 341
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 341
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc      300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct      420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc      480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca      540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga      600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat      660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc      720
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atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 342
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 342
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln

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                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
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    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
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580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 343
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 343
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc cctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtgtacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 344
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 344
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
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His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 345
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 345
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat gactggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 346
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 346

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 347
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 347
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc       60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac      120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac      180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac      240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag      360
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gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

ccttttcaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 348
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 348
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540
```

```
Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
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<210> 349
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 349
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 350
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 350
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
```

225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg

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        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
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645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 351
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 351
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctccc 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctctac gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaatttcg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aacacctact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 352
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 352
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
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Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
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Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 353
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polynucleotide"

<400> 353

atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatctg ggccaagatt 1860

cctcacacgg acggcaactt ccacccgtct ccgctgatgg gcggctttgg cctgaaacat 1920

cctccgcctc agatcctgat caagaacacg cctgtacctg cggatcctcc gaccaccttc 1980

aaccagtcaa agctgaactc tttcatcacg caatacagca ccggacaggt cagcgtggaa 2040

attgaatggg agctgcagaa ggaaaacagc aagcgctgga atcccgaagt gcagtataca 2100

tctaactatg caaaatctgc caacgttgat ttcactgtgg acaacaatgg actttatact 2160

gagcctcgcc ccattggcac ccgttacctc acccgtcccc tgtaa 2205

<210> 354
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 354
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
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Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480
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Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
                565                 570                 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
            580                 585                 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
                645                 650                 655

Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685
```

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala
690 695 700

Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730

<210> 355
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 355
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagt gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

accgacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 356
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 356
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Trp Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 357
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 357
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctcggcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtcttcatgg tgccacagta tggatacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggacttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 358
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 358
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile

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305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
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515 520 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
530 535 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545 550 555 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
565 570 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
580 585 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Asp Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn

725 730 735

Leu

<210> 359
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 359
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aactgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

accaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatctg ggccaagatt 1860

cctcacacgg acggcaactt ccacccgtct ccgctgatgg gcggctttgg cctgaaacat 1920

cctccgcctc agatcctgat caagaacacg cctgttcctg cgaatcctcc ggcggagttt 1980

tcagctacaa agtttgcttc attcatcacc cagtactcca caggacaagt gagtgtggaa 2040

attgaatggg agctgcagaa agaaaacagc aagcgctgga atcccgaagt gcagtacaca 2100

tccaattatg caaaatctgc caacgttgat tttactgtgg acaacaatgg actttatact 2160

gagcctcgcc ccattggcac ccgttacctt accaaacctc tgtaa 2205

<210> 360
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 360

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Cys Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Thr Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
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Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415
```

```
Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480

Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
                565                 570                 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
            580                 585                 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620
```

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala
690 695 700

Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Lys Pro Leu
725 730

<210> 361
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 361
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aagggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacttaca acaaccatct ctacaagcaa 780

atctccagcc aatcaggagc ttcaaacgac aaccactact ttggctacag caccccttgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacttgag cagaacaaac actccaagtg gaaccaccac gcagtcaagg 1380

cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 362
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 362
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
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Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

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Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 363
<211> 2214
<212> DNA
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 363
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatggg 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcaata cggctacctg 1140

acgctcaaca atggcagcca agccgtggga cgttcatcct tttactgcct ggaatatttc 1200

ccttctcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggaagtg 1260

cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactatta caagtctaat aatgttgaat ttgctgttaa tactgaaggt 2160

gtatatagtg aaccccgccc cattggcacc agatacctga ctcgtaatct gtaa 2214

<210> 364
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 364
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460
```

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Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670
```

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 365
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 365
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaact ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaagaggtta cggacaacaa tggagtcaag accatcgcca ataaccttac cagcacggtc 1020

caggtcttca cggactcaga ctatcagctc ccgtacgtgc tcgggtcggc tcacgagggc 1080

tgcctcccgc cgttcccagc ggacgttttc atgattcctc agtacgggta tctgacgctt 1140

aatgatggaa gccaggccgt gggtcgttcg tccttttact gcctggaata tttcccgtcg 1200

caaatgctaa gaacgggtaa caacttccag ttcagctacg agtttgagaa cgtacctttc 1260

catagcagct acgctcacag ccaaagcctg gaccgactaa tgaatccact catcgaccaa 1320

tacttgtact atctctcaaa gactattaac ggttctggac agaatcaaca aacgctaaaa 1380

ttcagtgtgg ccggacccag caacatggct gtccagggaa gaaactacat acctggaccc 1440

agctaccgac aacaacgtgt ctcaaccact gtgactcaaa acaacaacag cgaatttgct 1500

tggcctggag cttcttcttg ggctctcaat ggacgtaata gcttgatgaa tcctggacct 1560

gctatggcca gccacaaaga aggagaggac cgtttctttc ctttgtctgg atctttaatt 1620

tttggcaaac aaggaactgg aagagacaac gtggatgcgg acaaagtcat gataaccaac 1680

gaagaagaaa ttaaaactac taacccggta gcaacggagt cctatggaca agtggccaca 1740

aaccaccaga gtgcccaagc acaggcgcag accggctggg ttcaaaacca aggaatactt 1800

ccgggtatgg tttggcagga cagagatgtg tacctgcaag gacccatttg ggccaaaatt 1860

cctcacacgg acggcaactt tcacccttct ccgctgatgg gagggtttgg aatgaaacac 1920

ccgcctcctc agatcctcat caaaaacaca cctgtacctg cggatcctcc aacggccttc 1980

aacaaggaca agctgaactc tttcatcacc cagtattcta ctggccaagt cagcgtggag 2040

atcgagtggg agctgcagaa ggaaaacagc aagcgctgga accccgagat ccagtacacc 2100

tccaactact acaaatctac aagtgtggac tttgctgtta atacagaagg cgtgtactct 2160

gaaccccgcc ccattggcac ccgttacctc acccgtaatc tgtaa 2205

<210> 366
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 366
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly

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145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp
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        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu
                405                 410                 415

Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr
        435                 440                 445

Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala
    450                 455                 460

Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro
465                 470                 475                 480

Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn
                485                 490                 495

Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg
            500                 505                 510

Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly
        515                 520                 525

Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln
    530                 535                 540

Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn
545                 550                 555                 560

Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly
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565 570 575

Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly
580 585 590

Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg
595 600 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His
625 630 635 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
645 650 655

Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
675 680 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr
690 695 700

Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser
705 710 715 720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 367
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 367
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

cagggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccct ctcccctcat gggtggattc 1920

ggacttaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 368
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 368
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430


Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445


Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460


Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480
```

```
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685
```

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 369
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 369
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga 60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aaggggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caggtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 370
<211> 736

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 370

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590
```

```
Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 371
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 371
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcga       60

gagtggtggg cgctgcaacc tggagcccct aaacccaagg caaatcaaca acatcaggac      120
```

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccggcaa cggactcgac 180

aaggggggaac ccgtcaacgc agcggacgcg gcagccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 372
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 372
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 373
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 373
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 374
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 374
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
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    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
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            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 375
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 375
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca acggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaaccaccag cagcccccac aagtttggga 600

tctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa ccgcttccac tgccacttct cgccaagaga ctggcaaaga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta tggatacctc 1140

accctgaaca acggaagtca agcggtggga cgctcatcct tttactgcct ggagtacttc 1200

ccttcgcaga tgctaaggac tggaaataac ttccaattca gctatacctt cgaggatgta 1260

ccttttcaca gcagctacgc tcacagccag agtttggatc gcttgatgaa tcctcttatt 1320

gatcagtatc tgtactacct gaacagaacg caaggaacaa cctctggaac aaccaaccaa 1380

tcacggctgc tttttagcca ggctgggcct cagtctatgt ctttgcaggc cagaaattgg 1440

ctacctgggc cctgctaccg gcaacagaga ctttcaaaga ctgctaacga caacaacaac 1500

agtaactttc cttggacagc agccagcaaa tatcatctca atggccgcga ctcgctggtg 1560

aatccaggac cagctatggc cagtcacaag gacgatgaag aaaaattttt ccctatgcac 1620

ggcaatctaa tatttggcaa agaagggaca acggcaagta acgcagaatt agataatgta 1680

atgattacgg atgaagaaga gattcgtacc accaatcctg tggcaacaga gcagtatgga 1740

actgtggcaa ataacttgca gagctcaaat acagctccca cgactagaac tgtcaatgat 1800

caggggggcct tacctggcat ggtgtggcaa gatcgtgacg tgtaccttca ggggcccatc 1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc 1920

ggacttaaac accctcctcc gcagattctc atcaagaaca ccccggtacc tgcgaatcct 1980

tcgaccacct tcagtgcggc aaagtttgct tccttcatca cacagtactc cacgggacag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2100

atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa 2160

ggtgtatata gtgaaccccg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 376
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 376
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Thr Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
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Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn
                485                 490                 495

Asp Asn Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser
        515                 520                 525

His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
545                 550                 555                 560


Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
            580                 585                 590


Pro Thr Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
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<210> 377
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 377
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcagcttca agctcttcaa catccaggtc 960

aaggaggtca cgcagaatga aggcaccaag accatcgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct gattgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggactatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccg tctccgctga tgggcggctt tggcctgaaa 1920

catcctccgc ctcagatcct gatcaagaac acgcctgtac ctgcggatcc tccgaccacc 1980

ttcaaccagt caaagctgaa ctctttcatc actcagtatt ctactggcca agtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaagcgct ggaaccccga gatccagtac 2100

acctccaact actacaaatc tacaagtgtg gactttgctg ttaatacaga aggcgtgtac 2160

tctgaacccc gccccattgg cacccgttac ctcacccgta atctgtaa 2208

<210> 378
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 378
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445
```

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Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Tyr Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655
```

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Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 379
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 379
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct      420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc      480

aagacaggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac      540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact      600
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aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ttgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agtttttttcc tcagagcggg 1620

gttctcatct ttgggaagca aggctcagag aaaacaaatg tggacattga aaaggtcatg 1680

attacagacg aagaggaaat caggacaacc aatcccgtgg ctacggagca gtatggttct 1740

gtatctacca acctccagag aggcaacaga caagcagcta ccgcagatgt caacacacaa 1800

ggcgttcttc caggcatggt ctggcaggac agagatgtgt accttcaggg gcccatctgg 1860

gcaaagattc cacacacgga cggacatttt cacccctctc ccctcatggg tggattcgga 1920

cttaaacacc ctccgcctca gatcctgatc aagaacacgc ctgtacccgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcaccc agtattctac tggccaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 380
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 380
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

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Lys Thr Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
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Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Phe Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 381
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 381

atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaaccaccag cagcccccac aagtttggga 600

tctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggtgccgat 660

ggagtgggta attcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccttg cccacctaca ataaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa ccgcttccac tgccacttct cgccaagaga ctggcaaaga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta tggatacctc 1140

accctgaaca acggaagtca agcggtggga cgctcatcct tttactgcct ggagtacttc 1200

ccttcgcaga tgctaaggac tggaaataac ttccaattca gctatacctt cgaggatgta 1260

ccttttcaca gcagctacgc tcacagccag agtttggatc gcttgatgaa tcctcttatt 1320

gatcagtatc tgtactacct gaacagaacg caaggaacaa cctctggaac aaccaaccaa 1380

tcacggctgc tttttagcca ggctgggcct cagtctatgt ctttgcaggc cagaaattgg 1440

ctacctgggc cctgctaccg gcaacagaga ctttcaaaga ctgctaacga caacaacaac 1500

agtaactttc cttggacagc agccagcaaa tatcatctca atggccgcga ctcgctggtg 1560

aatccaggac cagctatggc cagtcacaag gacgatgaag aaaaattttt ccctatgcac 1620

ggcaatctaa tatttggcaa agaagggaca acggcaagta acgcagaatt agataatgta 1680

atgattacgg atgaagaaga gattcgtacc accaatcctg tggcaacaga gcagtatgga 1740

actgtggcaa ataacttgca gagctcaaat acagctccca cgactagaac tgtcaatgat 1800

caggggggcct tacctggcat ggtgtggcaa gatcgtgacg tgtaccttca ggggcccatc 1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc 1920

ggacttaaac accctcctcc gcagattctc atcaagaaca ccccggtacc tgcgaatcct 1980

tcgaccacct tcagtgcggc aaagtttgct tccttcatca cacagtactc cacgggacag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2100

atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa 2160

ggtgtatata gtgaaccccg ccccattggc accagatacc tgactcgtaa tctgtaa 2217

<210> 382
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 382
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

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    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
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            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp
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465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn
                485                 490                 495

Asp Asn Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser
        515                 520                 525

His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile
    530                 535                 540

Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
545                 550                 555                 560

Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
            580                 585                 590

Pro Thr Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
```

675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 383
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 383
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 384
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 384
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145   150   155   160

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Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365
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Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575
```

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 385
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 385
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc caaaaagaga ctcaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacagca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac gactactttg gctacagcac cccttggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgagg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 386
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 386
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Ser Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn Asp Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
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Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Glu Asp Asn Asn
                485                 490                 495
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Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
```

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 387
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 387
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttc 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcaacttca agctctttaa catccaggtc 960

aaggaggtca cgcagaatga aggcaccaag accatcgcca ataacctcac cagcaccatc 1020

caggtgttta cggactcgga gtaccagctg ccgtacgttc tcggctctgc ccaccagggc 1080

tgcctgcctc cgttcccggc ggacgtgttc atgattcccc agtacggcta cctaacactc 1140

aacaacggta gtcaggccgt gggacgctcc tccttctact gcctggaata ctttccttcg 1200

cagatgctga gaaccggcaa caacttccag tttacttaca ccttcgagga cgtgcctttc 1260

cacagcagct acgcccacag ccagagcttg gaccggctga tgaatcctct gattgaccag 1320

tacctgtatt acttgtctcg gactcaaaca acaggaggca cgacaaatac gcagactctg 1380

ggcttcagcc aaggtgggcc taatacaatg gccaatcagg caaagaactg gctgcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt tatgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acagggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc agggtcccat ttgggccaaa 1860

attcctcaca cagatggaca ctttcacccg tcccctctta tgggcggctt tggactcaag 1920

aacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag 1980

ttttcagcta caaagtttgc ttcattcatc acccaatact ccacaggaca agtgagtgtg 2040

gaaattgaat gggagctgca gaaagaaaac agcaagcgct ggaatcccga agtgcagtac 2100

acatccaatt atgcaaaatc tgccaacgtt gattttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctcacccgta atctgtaa 2208

<210> 388
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 388
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195   200   205

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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe Glu
                405                 410                 415
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Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe Ser Gln
    450                 455                 460

Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
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Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 389
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 389
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
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gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacgac aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca gcagcgagta tcaaagacat ttgcggataa caacaacagt 1500

gaatactcgt ggactggagc taccaagtac cacctcaatg gcagagactc tctggtgaat 1560

ccgggcccgg ccatggcaag ccacaaggac gatgaagaaa agtttttttcc tcagagcggg 1620

gttctcatct ttgggaagca aggctcagag aaaacaaatg tggacattga aaaggtcatg 1680

attacagacg aagaggaaat caggacaacc aatcccgtgg ctacggagca gtatggttct 1740

gtatctacca acctccagag aggcaacaga caagcagcta ccgcagatgt caacacacaa 1800

ggcgttcttc caggcatggt ctggcaggac agagatgtgt accttcaggg gcccatctgg 1860

gcaaagattc cacacacgga cggacatttt caccctctc ccctcatggg tggattcgga 1920

cttaaacacc ctccgcctca gatcctgatc aagaacacgc ctgtacccgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcaccc agtattctac tggccaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 390
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 390
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
```

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                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Phe Ala Asp
                485                 490                 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
```

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    530                 535                 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
            580                 585                 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
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<210> 391
<211> 2196
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 391
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag 480

cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc 540

caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgct 600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca 660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgtgactggc agcgactcat caacaacaac 900

tgggggttcc ggcccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcgg agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg 1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440

cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500

gcgaccaagt accacctgaa cggccgagac tccctggtga gccccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680

atcaagacca ccaaccctgt ggccacggag cagtacggcg tggtggctga caatctgcag 1740

cagaccaact cagctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 392
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 392
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln
145                 150                 155                 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
                165                 170                 175

Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His
    210                 215                 220
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Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240


Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255


Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270


Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285


Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300


Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320


Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335


Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350


Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365


Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380


Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400


Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415


Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430
```

```
Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Ser Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640
```

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
645 650 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
660 665 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
690 695 700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 393
<211> 2196
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 393
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccggcag 480

cccgcgaaaa agagactgaa ttttgggcag actggcgact cagagtcagt gcctgacccc 540

caacctctct cagaaccacc cgcaggtccc tctggtctgg gatctggtac aatggctgca 600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgcctca 660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgtgactggc agcgactcat caacaacaac 900

tggggattcc ggcccaagag gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccatcgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcga agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg 1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440

cagcagcgcg tctctacgac agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500

gcgaccaagt accacctgaa cggccgagac tccctggtga accccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680

atcaagacca ccaaccctgt ggccacggag cagtacggtg tggtggctga caatctgcag 1740

cagaccaact cggctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag tgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 394
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 394
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Arg Gln
145                 150                 155                 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
                165                 170                 175

Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Lys Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350
```

```
Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560
```

```
Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575


Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590


Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605


Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620


His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640


Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655


Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670


Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685


Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
    690                 695                 700


Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705                 710                 715                 720


Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730


<210> 395
<211> 2196
<212> DNA
<213> Artificial Sequence

<220>
<221> source
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 395
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg caacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacga ggcggacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtccttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggtactcga gcctctgggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaagc ggccagtaga accggactcc agctcgggca tcggcaagtc aggccagcag 480

cccgcgaaaa agagactgaa ttttgggccg actggcgact cagagtcagt gcctgacccc 540

caacctctct cagaaccacc tgcaggtccc tctggtctgg gatctggtac aatggctgca 600

ggcggtggcg ctccaatggc agacaataac gaaggcgccg acggagtggg taatgtctca 660

ggaaattggc attgcgattc cacatggctg ggcgaccgag tcatcaccac cagcactcgg 720

acctgggccc tccccaccta caacaaccac ctctacaagc aaatctccaa cgggacctcg 780

ggaggcagca gcaacgacaa cacctacttt ggctacagca ccccctgggg gtattttgac 840

tttaacagat tccactgcca cttttcacca cgcgactggc agcgactcat caacaacaac 900

tggggattcc ggcccaagaa gctcaacttc aagctcttca acatccaggt caaggaggtc 960

acccagaatg aaggcaccaa gaccaccgcc aataacctca ccagcacggt gcaggtcttt 1020

acggactcgg agtaccagct cccgtacgtg ctcggctctg cccaccaggg ctgcctgcct 1080

ccgttcccgg cggacgtgtt catgattccg cagtacgggt acctgacgct gaacaacggg 1140

agccaggccg tggggcgatc ctccttctac tgcctggagt actttccctc gcagatgctg 1200

agaacgggca acaactttac cttcagctac accttcgagg acgtgccctt ccacagcagc 1260

tacgcgcaca gccagagcct ggaccggctg atgaacccgc tgattgacca gtacctgtac 1320

tacctgtctc ggactcagac caacgggacc aatgccacgc agactctgtt gtttgctcag 1380

gccgggcctc agaacatgtc ggctcaggcc aagaactggc tgcctggtcc ttgctatcgg 1440

cagcagcgcg tctctacggc agtgtcgcaa aacaacaaca gcaactttac ctggaccggg 1500

gcgaccaagt accacctgaa cggccgagac tccctggtga accccggtgt cgccatggca 1560

acgcacaagg acgacgagga gcgcttcttc ccgagcagcg gggtcctgat gtttggcaag 1620

cagggcgctg gaaaggacaa tgtcgagtac accaacgtga tgctcaccag cgaggaggag 1680

atcaagacca ccaaccctgt ggccacggag cagtacggtg tggtggctga caatctgcag 1740

cagaccaact cggctcccat tgtgggggca gtcaacagcc agggggcctt acccggtatg 1800

gtctggcaga accgggacgt gtacctgcag ggtcccatct gggccaagat cccgcatacg 1860

gacggcaact ttcacccgtc tcctctcatg ggcggctttg gactgaaaca cccgcctccc 1920

cagatcctga tcaaaaacac gccggtacct gcggatcccc cggtgaactt tacggacgct 1980

aagctggcga gtttcatcac gcagtacagc accgggcagg tcagcgtgga gattgagtgg 2040

gagctgcaga aggagaacag caagcgctgg aatcccgaga ttcagtacac ttccaattat 2100

tataaatcag ctaatgtgga ctttgccgtc aatgcagatg gtgtatatag cgaaccccgc 2160

cccattggca ctcgttacct cacccgtaat ctgtaa 2196

<210> 396
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 396
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

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Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Ser Gly Gln Gln
145                 150                 155                 160

Pro Ala Lys Lys Arg Leu Asn Phe Gly Pro Thr Gly Asp Ser Glu Ser
                165                 170                 175

Val Pro Asp Pro Gln Pro Leu Ser Glu Pro Pro Ala Gly Pro Ser Gly
            180                 185                 190

Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala Asp
        195                 200                 205

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Val Ser Gly Asn Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                245                 250                 255

Asn Gly Thr Ser Gly Gly Ser Ser Asn Asp Asn Thr Tyr Phe Gly Tyr
            260                 265                 270
```

```
Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Gln Asn Glu Gly Thr Lys Thr Thr Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Asn
        435                 440                 445

Gly Thr Asn Ala Thr Gln Thr Leu Leu Phe Ala Gln Ala Gly Pro Gln
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480
```

```
Gln Gln Arg Val Ser Thr Ala Val Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Glu Tyr Thr Asn Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Thr Asn Ser Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Val Asn
                645                 650                 655

Phe Thr Asp Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
            660                 665                 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
        675                 680                 685
```

```
Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Ala
    690                 695                 700

Asn Val Asp Phe Ala Val Asn Ala Asp Gly Val Tyr Ser Glu Pro Arg
705                 710                 715                 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
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<210> 397
<211> 4404
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 397

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gacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac      240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt      300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaacggccag      480

ccgcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac      540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct      600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc      660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc      720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc      780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc      840
```

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

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ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

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acccgttacc tcacccgtaa cctgtaaatg gctgccgatg gttatcttcc agattggctc 2220

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atggcagaca ataacgaagg cgccgacgga gtgggtagtt cctcaggaaa ttggcattgc 2880

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aagaatacac ctgttcccgc ggatcctcca actaccttca gtcaagctaa gctggcgtcg 4200

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gaaaacagca aacgctggaa cccagagatt caatacactt ccaactacta caaatctaca 4320

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cgttacctca cccgtaatct gtaa 4404

<210> 398
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 398
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1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
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```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
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Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720
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Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 399
<211> 3129
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 399
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gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaaag tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaagtttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcagagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca cgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

aaacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaaa aagacgtatc 720

ggaaactctg tgcgattcat catctgctgg gggcgggcac ccgagattgc ttgctcggcc 780

tgcgatctgg tcaacgtgga cctagatgac tgtgtttctg agcaataaat gacttaaacc 840

aggtatggct gccgatggtt atcttccaga ttggctcgag gacaacctct ctgagggcat 900

tcgcgagtgg tgggacttga aacctggagc cccgaaaccc aaagccaacc agcaaaagca 960

ggacgacggc cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact 1020

cgacaagggg gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta 1080

cgaccagcag ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga 1140

gtttcaggag cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt 1200

ccaggccaag aagcgggttc tcgaacctct cggtctggtt gaggaaggcg ctaagacggc 1260

tcctggaaag aagagaccgg tagagccatc accccagcgt tctccagact cctctacggg 1320

catcggcaag aaaggccagc agcccgcgaa aaagagactc aactttgggc agactggcga 1380

ctcagagtca gtgcccgacc ctcaaccaat cggagaaccc cccgcaggcc cctctggtct 1440

gggatctggt acaatggctg caggcggtgg cgctccaatg gcagacaata acgaaggcgc 1500

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agtcatcacc accagcaccc gaacctgggc cctccccacc tacaacaacc acctctacaa 1620

gcaaatctcc aacgggactt cgggaggaag caccaacgac aacacctact tcggctacag 1680

caccccctgg gggtattttg actttaacag attccactgc cacttctcac cacgtgactg 1740

gcagcgactc atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt 1800

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aactcagcag ttgctatttt ctcaggccgg gcctaataac atgtcggctc aggccaaaaa 2280

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tcctccaact accttcagtc aagctaagct ggcgtcgttc atcacgcagt acagcaccgg 2880

acaggtcagc gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc 2940

agagattcaa tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac 3000

agatggcact tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta 3060

attgcttgtt aatcaataaa ccggttgatt cgtttcagtt gaactttggt ctctgcgaag 3120

ggcgaattc 3129

<210> 400
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
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Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

```
Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 401
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 401
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Arg Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320
```

```
Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
        515                 520                 525
```

```
Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
                645                 650                 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
    690                 695                 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705                 710                 715                 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730
```

<210> 402
<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 402
gaattcgccc ttggctgcgt caactggacc aatgagaact ttcccttcaa cgattgcgtc 60

gacaagatgg tgatctggtg ggaggagggc aagatgacgg ccaaggtcgt ggagtccgcc 120

aaggccattc atcatctgct ggggcgggct cccgagattg cttgctcggc ctgcgatctg 180

gtcaacgtgg acctggatga ctgtgtttct gagcaataaa tgacttaaac caggtatggc 240

tgccgatggt tatcttccag attggctcga ggacaacctc tctgagggca ttcgcgagtg 300

gtgggacttg agacctggag ccccgaaacc caaagccaac cagcaaaagc aggacgacgg 360

ccggggtctg gtgcttcctg gctacaagta cctcggaccc ttcaacggac tcgacaaggg 420

agagccggtc aacgaggcag acgccgcggc cctcgagcac gacaaggcct acgacaagca 480

gctcgagcag ggggacaacc cgtacctcaa gtacaaccac gccgacgccg agtttcagga 540

gcgtcttcaa gaagatacgt cttttggggg caacctcggg cgagcagtct tccaggccaa 600

gaagcgggtt ctcgaacctc tcggtctggt tgaggaaggc gctaagacgg ctcctggaaa 660

gaagagaccc atagaatccc ccgactcctc cacgggcatc ggcaagaaag gccagcagcc 720

cgctaaaaag agactcaact ttgggcagac tggcgactca gagtcagtgc ccgaccctca 780

accaatcgga gaacccccg caggcccctc tggtctggga tctggcacaa tggctgcagg 840

cggtggcgct ccaatggcag acaataacga aggcgccgac ggagtgggta gttcctcagg 900

aaattggcat tgcgattcca catggctggg cgacagagtc atcaccacca gcacccgaac 960

ctgggccctc cccacctaca acaaccacct ctacaagcaa atctccaacg ggacatcggg 1020

aggaagcacc aacgacaaca cctacttcgg ctacagcacc ccctgggggt attttgactt 1080

taacagattc cactgccact tctcaccacg tgactggcag cgactcatca acaacaactg 1140

gggattccgg cccaagagac tcaacttcaa gctcttcaac atccaggtca aggaggtcac 1200

gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc agcacgattc aggtctttac 1260

ggactcggaa taccagctcc cgtacgtcct cggctctgcg caccagggct gcctgcctcc 1320

gttcccggcg gacgtcttca tgattcctca gtacgggtac ctgactctga acaacggcag 1380

tcaggccgtg ggccgttcct ccttctactg cctggagtac tttccttctc aaatgctgag 1440

aacgggcaac aactttgagt tcagctacca gtttgaggac gtgcctttc acagcagcta 1500

tgcgcacagc caaagcctgg accggctgat gaacccctc atcgaccagt acctgtacta 1560

cctgtctcgg actcagtcca cgggaggtac cgcaggaact cagcagttgc tattttctca 1620

ggccgggcct aataacatgt cggctcaggc caaaaactgg ctacccgggc cctgctaccg 1680

gcagcaacgc gtctccacga cagtgtcgca aaataacaac agcaactttg cttggaccgg 1740

tgccaccaag tatcatctga atggcagaga ctctctggta aatcccggtg tcgctatggc 1800

aacgcacaag ggcgacgaag agcgattttt tccatccagc ggagtcttga tgtttgggaa 1860

acagggagct ggaaaagaca acgtagacta tagcagcgtt atgctaacca gtgaggaaga 1920

aatcaaaacc accaacccag tggccacaga acagtacggc gtggtggccg ataacctgca 1980

acagcaaaac gccgctccta ttgtaggggc cgtcaacagt caaggagcct tacctggcat 2040

ggtctggcag aaccgggacg tgtacctgca gggtcctatc tgggccaaga ttcctcacac 2100

ggacggcaac tttcatcctt cgccgctgat gggaggcttt ggactgaaac acccgcctcc 2160

tcagatcctg attaagaata cacctgttcc cgcggatcct ccaactacct tcagtcaagc 2220

caagctggcg tcgttcatca cgcagtacag caccggacag gtcagcgtgg aaattgaatg 2280

ggagctgcag aaagagaaca gcaagcgctg gaacccagag attcagtata cttccaacta 2340

ctacaaatct acaaatgtgg actttgctgt caatactgag ggtacttatt cagagcctcg 2400

ccccattggc acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg 2460

ttgattcgtt tcagttgaac tttggtctca agggcgaatt c 2501

<210> 403
<211> 2187
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 403
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcaa gaaaggccag 480

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 540

ccccaacctc tcggagaacc tcccgccgcg ccctcaggtc tgggatctgg tacaatggct 600

gcaggcggtg gcgcaccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 660

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 720

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 780

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 840

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 900

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 960

acgaacgacg gcgttacgac catcgctaat aaccttacca gcacgattca ggtcttctcg 1020

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1080

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1140

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1200

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1260

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1320

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1380

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1440

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1500

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1560

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg cgaaacgggg 1620

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1680

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1740

gccggacccc agacacagac tgtcaacagc caggggctc tgcccggcat ggtctggcag 1800

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 1860

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 1920

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 1980

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2040

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2100

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2160

acccgttacc tcacccgtaa cctgtaa 2187

<210> 404
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 404
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270
```

```
Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480
```

```
Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Glu Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685
```

```
Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725

<210> 405
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 405
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320
```

```
Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525
```

```
Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720

Thr Arg Tyr Leu Thr Arg Asn Leu
                725
```

<210> 406
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 406
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

```
Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365
```

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Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575
```

```
Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590


Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 407
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 407
Met Ala Ala Asp Gly His Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
```

```
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Ser Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
```

```
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
```

625 630 635 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
645 650 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 408
<211> 3113
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 408
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg cttccctgca 600

agacatgcga gagaatgaat cagaatttca gcatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtca tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagacccat agaatccccc gactcctcca cgggcatcgg caagaaaggc 1320

cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500

tcctcaggaa attggcattg cgattccaca tagctgggcg acagagtcat caccaccagc 1560

acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620

acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740

aacagctggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800

gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

ctgcctccgt tcccggcgga cgtcttcatg attcctcagt acgggtacct gactctgaac 1980

aacggcagtc aggccgtggg ccgttcctcc ttctactgcc tggagtactt tccttctcaa 2040

atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gccttttcac 2100

agcagctacg cgcacagcca aagcctggac cggctgatga acccccctcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca ctgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaagga cgacgaagag cgatttttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa 2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000

gagcctcgcc ccattggcac ccgttacctc acccgtaacc tgtaattgcc tgttaatcaa 3060

taaaccggtt aattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 409
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 409
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Arg Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220
```

```
His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Arg Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430
```

```
Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly
        435                 440                 445

Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn
    450                 455                 460

Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe
                485                 490                 495

Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu
            500                 505                 510

Val Asn Pro Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg
        515                 520                 525

Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly
    530                 535                 540

Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu
545                 550                 555                 560

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala
                565                 570                 575

Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala Val Asn
            580                 585                 590

Ser Gln Gly Ala Leu Pro Gly Met Ala Trp Gln Asn Arg Asp Val Tyr
        595                 600                 605

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
    610                 615                 620

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
625                 630                 635                 640
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Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr
645 650 655

Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
660 665 670

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
675 680 685

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr
690 695 700

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu Pro Arg
705 710 715 720

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 410
<211> 3106
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 410
gaattcgccc ttctacggct gcgtcaactg gaccaatgag aactttccct tcaacgattg 60

cgtcgacaag atggtgatct ggtgggagga gggcaagatg acggccaagg tcgtggagtc 120

cgccaaggcc attctcggcg gcagcaaggt gcgcgtggac caaaagtgca agtcgtccgc 180

ccagatcgac cccacccccg tgatcgtcac ctccaacacc aacatgtgcg ccgtgattga 240

cgggaacagc accaccttcg agcaccagca gccgttgcag gaccggatgt tcaaatttga 300

actcacccgc cgtctggagc atgactttgg caaggcgaca aagcaggaag tcaaagagtt 360

cttccgctgg gcgcaggatc acgtgaccga ggtggcgcat gagttctacg tcagaaaggg 420

tggagccaac aagagacccg cccccgatga cgcggataaa agcgagccca agcgggcccg 480

cccctcagtc gcggatccat cgacgtcaga cgcggaagga gctccggtgg actttgccga 540

caggtaccaa aacaaatgtt ctcgtcacgc gggcatgctt cagatgctgt ttccctgcaa 600

aacatgcgag agaatgaatc agaatttcaa catttgcttc acgcacggga ccagagactg 660

ttcagaatgt ttccccggcg tgtcagaatc tcaaccggtc gtcagaaaga ggacgtatcg 720

gaaactctgt gccattcatc atctgctggg gcgggctccc gagattgctt gctcggcctg 780

cgatctggtc aacgtggacc tggatgactg tgtttctgag caataaatga cttaaaccag 840

gtatggctgc cgatggttat cttccagatt ggctcgagga caacctctct gagggcattc 900

gcgagtggtg ggacttgaaa cctggagccc cgaaacccaa agccaaccag caaaagcagg 960

acgacggccg gggtctggtg cttcctggct acaagtacct cggacccttc aacggactcg 1020

acaagggaga gccggtcaac gaggcagacg ccgcggccct cgagcacgac aaggcctacg 1080

acaagcagct cgagcagggg gacaacccgt acctcaagta caaccacgcc gacgccgagt 1140

ttcaggagcg tcttcaagaa gatacgtctt ttgggggcaa cctcgggcga gcagtcttcc 1200

gggccaagaa gcgggttctc gaacctctcg gtctggttga ggaaggcgct aagacggctc 1260

ctggaaagaa gagacccata gaatcccccg actcctccac gggcatcggc aagaaaggcc 1320

agcagcccgc taaaaagaag ctcaactttg ggcagactgg cgactcagag tcagtgcccg 1380

acccccaacc tctcggagaa cctcccgccg cgccctcagg tctgggatct ggtacaatgg 1440

ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga gtgggtaatg 1500

cctccggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc accaccagca 1560

cccgcacctg ggccctgccc acctacaaca accacctcta caagcagata tcaagtcaga 1620

gcggggctac caacgacaac cacttcttcg gctacagcac cccctggggc tattttgact 1680

tcaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatc aacaacaacc 1740

ggggattccg gcccagaaag ctgcggttca agttgttcaa catccaggtc aaggaggtca 1800

cgacgaacga cggcgttacg accatcgcta ataaccttac cagcacgatt caggtcttct 1860

cggactcgga gtaccaactg ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 1920

cgttccctgc ggacgtgttc atgattcctc agtacggata tctgactcta aacaacggca 1980

gtcagtctgt gggacgttcc tccttctact gcctggagta ctttccttct cagatgctga 2040

gaacgggcaa taactttgaa ttcagctacc agtttgagga cgtgcccttt cacagcagct 2100

acgcgcacag ccaaagcctg gaccggctga tgaaccccct catcgaccag tacctgtact 2160

acctgtctcg gactcagtcc acgggaggta ccgcaggaac tcagcagttg ctattttctc 2220

aggccgggcc taataacatg tcggctcagg ccaaaaactg gctacccggg ccctgctacc 2280

ggcagcaacg cgtctccacg acactgtcgc aaaataacaa cagcaacttt gcttggaccg 2340

gtgccaccaa gtatcatctg aatggcagag actctctggt aaatcccggt gtcgctatgg 2400

caacgcacaa ggacgacgaa gagcgatttt ttccatccag cggagtcttg atgtttggga 2460

aacagggagc tggaaaagac aacgtggact atagcagcgt tatgctaacc agtgaggaag 2520

aaatcaaaac caccaaccca gtggccacag aacagtacgg cgtggtggcc gataacctgc 2580

aacagcaaaa cgccgctcct attgtagggg ccgtcaacag tcaaggagcc ttacctggca 2640

tggcctggca gaaccgggac gtgtacctgc agggtcctat ctgggccaag attcctcaca 2700

cggacggcaa ctttcatcct tcgccgctga tgggaggctt tggactgaaa cacccgcctc 2760

ctcagatcct gattaagaat acacctgttc ccgcggatcc tccaactacc ttcagtcaag 2820

ccaagctggc gtcgttcatc acgcagtaca gcaccggaca ggtcagcgtg gaaattgaat 2880

gggagctgca gaaagagaac agcaagcgct ggaacccaga gattcagtat acttccaact 2940

actacaaatc tacaaatgtg gactttgctg tcaatactga gggtacttat tcagagcctc 3000

gccccattgg cacccgttac ctcacccgta acctgtaatt gcctgttaat caataaaccg 3060

gttaattcgt ttcagttgaa ctttggtctc tgcgaagggc gaattc 3106

<210> 411
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 411
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
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Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 412
<211> 3197
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 412
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac 1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag 1140

tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga aggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcctgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattcgt ttaaacctgc aggactagtc cctttagtga gggttaattc tgagcttggc 3180

gtaatcatgg gtcatag 3197

<210> 413
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 413
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

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Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Arg Lys Leu Arg Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asp Asp Gly Val Thr Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
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Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Glu Leu Gln Phe His
    450                 455                 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
        515                 520                 525

Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
    530                 535                 540

Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
            580                 585                 590

Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605
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Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Asp Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Ala Lys Ser Asn Asn Val Glu Phe Ala Val Asn Asn Glu Gly Val Tyr
705 710 715 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 414
<211> 3276
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 414
gaattcgccc ttcgcagaga ccaaagttca actgaaacga attaaccggt ttattgatta 60

acaggcaatt acaggttacg ggtgaggtaa cgggtgccaa tggggcgagg ctcagtataa 120

acccccttcgt tgttgacagc aaattccaca ttattagact tggcataatt tgaggtgtac 180

tgaatctctg gattccagcg tttgctgttt tctttctgca gttcccactc gatctccacg 240

ctgacctggc cggtgctgta ctgcgtgata aatgaggcaa acttggcagg agtaaacacc 300

tctggaggat tagcaggtac cggggtgttt ttgatgagaa tttgaggagg cgggtgtttg 360

agtccaaatc cgtccatcag gggagacggg tgaaagttgc cgtccgtgtg aggaattttg 420

gcccagatgg gaccctgcag gtacacgtcc cggttctgcc agaccatgcc gggcagagcc 480

ccctggctgt tgacagtctg tgtctggggt ccggccgtag acgattgcag gttgctggag 540

accacaccgt attcttctgt agccacggga ttggtggttt tgatctcctc ctcgctggtc 600

attagcacgt tttccagcgt tgtcttgttg gcagcccccg ttttgccaaa aaccagcact 660

ccgttgatgg gaaagaactg gtcctcgtcg tccttgttgg tggccatggc tacgcccggg 720

ttggttaatg aatttctacc attcagatgg tatttagtgg ccccggtcca ggcaaagtta 780

ctgttgttgt tgctgtctat gttttttgac agtctctgct gccgataaca gggtccgggc 840

agccagttct ttgattgctc ggccatggtg ttgggcccag cctgatggaa ctgcagctcc 900

cttgtggacc ccgtagtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgagg 960

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ccgtactgag gaatcatgaa cacgtccgca gggaacggag ggaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ttggtactcc gagtccgaga agacctgaat cgtgctggta 1260

aggttattag cgatggtcgt aacgccgtcg tccgtcgtga cctccttgac ctggatgttg 1320

aacaacttga accgcagctt tctgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccaggggtg 1440

ctgtagccga agtaggtgtt gtcgttggtg cttcctcccg atgtcccgtt ggagatttgc 1500

ttgtagaggt ggttgttgta ggtggggagg gcccaggttc gggtgctggt ggtgatgact 1560

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agaccagagg ggcctgcggg gggttctccg attggttgag ggtcgggcac tgactctgag 1740

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cccgtagagg agtctggaga acgctggggt gatggctcta ccggtctctt ctttccagga 1860

gccgtcttag cgccttcctc aaccagaccg agaggttcga gaacccgctt cttggcctgg 1920

aagactgctc gcccgaggtt gcccccaaaa gacgtatctt cttgaagacg ctcctgaaac 1980

tcggcgtcgg cgtggttgta cttgaggtac gggttgtccc cctgctcgag ctgcttgtcg 2040

taggccttgt cgtgctcgag ggccgcggcg tctgcctcgt tgaccggctc tcccttgtcg 2100

agtccgttga agggtccgag gtacttgtag ccaggaagca ccagaccccg gccgtcgtcc 2160

tgcttttgct ggttggcttt gggtttcggg gctccaggtt tcaagtccca ccactcgcga 2220

atgccctcag agaggttgtc ctcgagccaa tctggaagat aaccatcggc agccatacct 2280

ggtttaagtc atttattgct cagaaacaca gtcatccagg tccacgttga ccagatcgca 2340

ggccgagcaa gcaatctcgg gagcccgccc cagcagatga tgaatggcac agagtttccg 2400

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gcactcacgt gacagctaat acaggaccac tcccctatga cgtgatttac gtcagcgcta 2700

tgcccgcgtg acgagaacat ttgttttggt acctgtcggc aaagtccacc ggagctcctt 2760

ccgcgtctga cgtcgatgga tccgcgactg aggggcaggc ccgcttgggc tcgcttttat 2820

ccgcgtcatc gggggcgggt ctcttgttgg ctccaccctt tctgacgtag aactcatgcg 2880

ccacctcggt cacgtgatcc tgcgcccagc ggaagaactc tttgacttcc tgctttgtca 2940

ccttgccaaa gtcatgctcc agacggcggg tgagttcaaa tttgaacatc cggtcctgca 3000

acggctgctg gtgctcgaag gtggtgctgt tcccgtcaat cacggcgcac atgttggtgt 3060

tggaagtgac gatcacgggg gtgggatcga tctgggcgga agacttgcac ttttggtcca 3120

cgcgcacctt gctgccgccg agaatggcct tggcggactc cacgaccttg gccgtcatct 3180

tgccctcctc ccaccagatc accatcttgt cgacgcaatc gttgaaggga aagttctcat 3240

tggtccagtt gacgcagccg tagaaagggc gaattc 3276

<210> 415
<211> 738

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 415
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
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Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590
```

```
Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Val Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 416
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 416

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415
```

```
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 417
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 417
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
```

245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu

```
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
```

660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 418
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 418
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Arg Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285
```

```
Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Asn Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495
```

```
Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575

Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700
```

Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705 710 715 720

Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 419
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 419
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtgaagt 120

ccgccaaggc cattcatcat ctgctggggc gggctcccga gattgcttgc tcggcctgcg 180

atctggtcaa cgtggacctg gatgactgtg tttctgagca ataaatgact taaaccaggt 240

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 300

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 360

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 420

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 480

aagcagctcg agcaggggga caacccgtac ctcaagtaca accacgccga cgccgagttt 540

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 600

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 660

ggaaagaaga gacccataga atcccccgac tcctccacgg gcatcggcag gaaaggccag 720

cagcccgcta aaaagaagct caactttggg cagactggcg actcagagtc agtgcccgac 780

cctcaaccaa tcggagaacc ccccgcaggc ccctctggtc tgggatctgg tacaatggct 840

gcaggcggtg gcgctccaat ggcagacaat aacgaaggcg ccgacggagt gggtaatgcc 900

tccggaaatt ggcattgcga ttccacatgg ctgggcgaca gagtcatcac caccagcacc 960

cgcacctggg ccctgcccac ctacaacaac cacctctaca agcagatatc aagtcagagc 1020

ggggctacca acgacaacca cttcttcggc tacagcaccc cctggggcta ttttgacttc 1080

aacagattcc actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg 1140

ggattccggc ccagaaagct gcggttcaag ttgttcaaca tccaggtcaa ggaggtcacg 1200

acgaacgacg gcgttacgac catcgccaat aaccttacca gcacgattca ggtcttctcg 1260

gactcggagt accaactgcc gtacgtcctc ggctctgcgc accagggctg cctccctccg 1320

ttccctgcgg acgtgttcat gattcctcag tacggatatc tgactctaaa caacggcagt 1380

cagtctgtgg gacgttcctc cttctactgc ctggagtact ttccttctca gatgctgaga 1440

acgggcaata actttgaatt cagctacacc tttgaggaag tgcctttcca cagcagctat 1500

gcgcacagcc agagcctgga ccggctgatg aatcccctca tcgaccagta cctgtactac 1560

ctggcccgga cccagagcac tacggggtcc acaagggagc tgcagttcca tcaggctggg 1620

cccaacacca tggccgagca atcaaagaac tggctgcccg gaccctgtta tcggcagcag 1680

agactgtcaa aaaacataga cagcaacaac aacagtaact ttgcctggac cggggccact 1740

aaataccatc tgaatggtag aaattcatta accaacccgg gcgtagccat ggccaccaac 1800

aaggacgacg aggaccagtt ctttcccatc aacggagtgc tggtttttgg caaaacgggg 1860

gctgccaaca agacaacgct ggaaaacgtg ctaatgacca gcgaggagga gatcaaaacc 1920

accaatcccg tggctacaga agaatacggt gtggtctcca gcaacctgca atcgtctacg 1980

gccggacccc agacacagac tgtcaacagc caggggggctc tgcccggcat ggtctggcag 2040

aaccgggacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2100

tttcacccgt ctcccctgat gggcggattt ggactcaaac acccgcctcc tcaaattctc 2160

atcaaaaaca ccccggtacc tgctaatcct ccagaggtgt ttactcctgc caagtttgcc 2220

tcatttatca cgcagtacag caccggccag gtcagcgtgg agatcgagtg ggaactgcag 2280

aaagaaaaca gcaaacgctg gaatccagag attcagtaca cctcaaatta tgccaagtct 2340

aataatgtgg aatttgctgt caacaacgaa ggggtttata ctgagcctcg ccccattggc 2400

acccgttacc tcacccgtaa cctgtaattg cctgttaatc aataaaccgg ttaattcgtt 2460

tcagttgaac tttggtcaag ggcgaattc 2489

<210> 420
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 420
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

```
Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Phe Phe Gly Tyr Ser
            260                 265                 270

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
        275                 280                 285

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
    290                 295                 300

Arg Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
305                 310                 315                 320

Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile
                325                 330                 335

Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            340                 345                 350

Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
        355                 360                 365
```

```
Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val Gly
    370                 375                 380

Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr Thr
        435                 440                 445

Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr Met
    450                 455                 460

Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Arg Gln
465                 470                 475                 480

Arg Leu Ser Lys Asp Ile Asp Ser Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe Phe
        515                 520                 525

Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn Lys
    530                 535                 540

Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys Thr
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn Leu
                565                 570                 575
```

```
Gln Ser Ser Thr Ala Gly Pro Gln Thr Gln Thr Val Asn Ser Gln Gly
            580                 585                 590


Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly
        595                 600                 605


Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
    610                 615                 620


Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
625                 630                 635                 640


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr Pro
                645                 650                 655


Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
            660                 665                 670


Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
        675                 680                 685


Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val Glu
    690                 695                 700


Phe Ala Val Asn Asn Glu Gly Val Tyr Thr Glu Pro Arg Pro Ile Gly
705                 710                 715                 720


Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 421
<211> 3098
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 421
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ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcttccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accggagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

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cagcagcccg ctaaaaagaa gctcaacttt gggcagactg gcgactcaga gtcagtgccc 1380

gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

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ttcaacagat tccactgcca cttctcacca cgtgactggc agcgactcat caacaacaac 1740

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tcggactcgg agtaccaact gccgtacgtc ctcggctctg cgcaccaggg ctgcctccct 1920

ccgttccctg cggacgtgtt catgattcct cagtacggat atctgactct aaacaacggc 1980

agtcagtctg tgggacgttc ctccttctac tgcctggagt actttccttc tcagatgctg 2040

agaacgggca ataactttga attcagctac acctttgagg aagtgccttt ccacagcagc 2100

tatgcgcaca gccagagcct ggaccggctg atgaatcccc tcatcgacca gtacctgtac 2160

tacctggccc ggacccagag cactacgggg tccacaaggg agctgcagtt ccatcaggct 2220

gggcccaaca ccatggccga gcaatcaaag aactggctgc ccggaccctg ttatcggcgg 2280

cagagactgt caaaagacat agacagcaac aacaacagta actttgcctg gaccggggcc 2340

actaaatacc atctgaatgg tagaaattca ttaaccaacc cgggcgtagc catggccacc 2400

aacaaggacg acgaggacca gttctttccc atcaacggag tgctggtttt tggcaaaacg 2460

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aactttcacc cgtctccccc gatgggcgga tttggactca aacacccgcc tcctcaaatt 2760

ctcatcaaaa acaccccggt acctgctaat cctccagagg tgtttactcc tgccaagttt 2820

gcctcattta tcacgcagta cagcaccggc caggtcagcg tggagatcga gtgggaactg 2880

cagaaagaga acagcaaacg ctggaatcca gagattcagt acacctcaaa ttatgccaag 2940

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gtttcagttg aactttggtc tctgcgaagg gcgaattc 3098

<210> 422
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 422
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1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

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Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Thr Thr Gly Ser Thr Arg Gly Leu Gln Phe His
    450                 455                 460

Gln Ala Gly Pro Asn Thr Met Ala Glu Gln Ser Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Asn Ile Asp Ser Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Thr Asn Pro Gly Val Ala Met Ala Thr Asn Lys
        515                 520                 525

Asp Asp Glu Asp Gln Phe Phe Pro Ile Asn Gly Val Leu Val Phe Gly
    530                 535                 540

Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575
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Gly Val Val Ser Ser Asn Leu Gln Ser Ser Thr Ala Gly Pro Gln Thr
580 585 590

Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Tyr Thr Ser Asn Tyr Tyr Lys
645 650 655

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
660 665 670

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
675 680 685

<210> 423
<211> 2969
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 423
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gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag cacgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

gttcagaatg tttccccggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatc 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaagggag agccggtcaa cgaggcagac gccgcggccc tcgagcacga caaggcctac 1080

gacaagcagc tcgagcaggg ggacaacccg tacctcaagt acaaccacgc cgacgccgag 1140

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cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

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caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

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tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgct gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcac agccaaagcc tggaccggct gacgaacccc 2160

ctcatcgacc agtacctgta ctacctggcc cggacccaga gcactacggg gtccacaagg 2220

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gtgctggttt ttggcaaaac gggggctgcc aacaagacaa cgctggaaaa cgtgctaatg 2520

accagcgagg aggagatcaa aaccaccaat cccgtggcta cagaagaata cggtgtggtc 2580

tccagcaacc tgcaatcgtc tacggccgga ccccagacac agactgtcaa cagccagggg 2640

gctctgcccg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 2700

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aaacacccgc ctcctcaaat tctcatcaag tatacttcca actactacaa atctacaaat 2820

gtggactttg ctgtcaatac tgagggtact tattcagagc ctcgccccat tggcacccgt 2880

tacctcaccc gtaacctgta attgcctgtt aatcaataaa ccggttaatt cgtttcagtt 2940

gaactttggt ctctgcgaag ggcgaattc 2969

<210> 424
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 424
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

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            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Glu Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Gly Pro Ser
            180                 185                 190

Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
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225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly
            260                 265                 270

Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
        275                 280                 285

Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
    290                 295                 300

Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
305                 310                 315                 320

Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser
                325                 330                 335

Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
            340                 345                 350

Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
        355                 360                 365

Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
    370                 375                 380

Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
385                 390                 395                 400

Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe Glu Asp Val
                405                 410                 415

Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
            420                 425                 430

Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser
```

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        435                 440                 445

Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Ser Gln Asn Asn Asn Ser
                485                 490                 495

Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys Gly Asp Glu
        515                 520                 525

Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly
    530                 535                 540

Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val
                565                 570                 575

Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro Ile Val Gly Ala
            580                 585                 590

Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
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645 650 655

Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
690 695 700

Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Thr Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Ser Leu
725 730

<210> 425
<211> 3113
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 425
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ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga tcccaccccc gtgatcgtca cttccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttaca agaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcacggg accagagact 660

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ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

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gaccctcaac caatcggaga acccccccgca ggcccctctg gtctgggatc tggtacaatg 1440

gctgcaggcg gtggcgctcc aatggcagac aataacgaag gcgccgacgg agtgggtagt 1500

tcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat caccaccagc 1560

acccgaacct gggccctccc cacctacaac aaccacctct acaagcaaat ctccaacggg 1620

acatcgggag gaagcaccaa cgacaacacc tacttcggct acagcacccc ctgggggtat 1680

tttgacttta acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac 1740

aacaactggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaggtcaag 1800

gaggtcacgc agaatgaagg caccaagacc atcgccaata accttaccag cacgattcag 1860

gtctttacgg actcggaata ccagctcccg tacgtcctcg gctctgcgca ccagggctgc 1920

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atgctgagaa cgggcaacaa ctttgagttc agctaccagt ttgaggacgt gccttttcac 2100

agcagctatg cgcacagcca aagcctggac cggctgatga acccctcat cgaccagtac 2160

ctgtactacc tgtctcggac tcagtccacg ggaggtaccg caggaactca gcagttgcta 2220

ttttctcagg ccgggcctaa taacatgtcg gctcaggcca aaaactggct acccgggccc 2280

tgctaccggc agcaacgcgt ctccacgaca gtgtcgcaaa ataacaacag caactttgct 2340

tggaccggtg ccaccaagta tcatctgaat ggcagagact ctctggtaaa tcccggtgtc 2400

gctatggcaa cgcacaaggg cgacgaagag cgatttttc catccagcgg agtcttgatg 2460

tttgggaaac agggagctgg aaaagacaac gtggactata gcagcgttat gctaaccagt 2520

gaggaagaaa tcaaaaccac caacccagtg gccacagaac agtacggcgt ggtggccgat 2580

aacctgcaac agcaaaacgc cgctcctatt gtaggggccg tcaacagtca aggagcctta 2640

cctggcatgg tctggcagaa ccgggacgtg tacctgcagg gtcctatctg ggccaagatt 2700

cctcacacgg acggcaactt tcatccttcg ccgctgatgg gaggctttgg actgaaacac 2760

ccgcctcctc agatcctgat taagaataca cctgttcccg cggatcctcc aactaccttc 2820

agtcaagcca agctggcgtc gttcatcacg cagtacagca ccggacaggt cagcgtggaa 2880

attgaatggg agctgcagaa agagaacagc aagcgctgga acccagagat tcagtatact 2940

tccaactact acaaatctac aaatgtggac tttgctgtca atactgaggg tacttattca 3000

gagcctcgcc ccattggcac ccgttacctc acccgtagcc tgtaattgcc tgttaatcaa 3060

taaaccggtt gattcgtttc agttgaactt tggtctctgc gaagggcgaa ttc 3113

<210> 426
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 426
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
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Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Pro Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Arg Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
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Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 427
<211> 3128
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 427
gaattcgccc tttctacggc tgcgtcaact ggaccaatga gaactttccc ttcaacgatt 60

gcgtcgacaa gatggtgatc tggtgggagg agggcaagat gacggccaag gtcgtggagt 120

ccgccaaggc cattctcggc ggcagcaagg tgcgcgtgga ccaaaagtgc aagtcgtccg 180

cccagatcga ccccaccccc gtgatcgtca cctccaacac caacatgtgc gccgtgattg 240

acgggaacag caccaccttc gagcaccagc agccgttgca ggaccggatg ttcaaatttg 300

aactcacccg ccgtctggag catgactttg gcaaggtgac aaagcaggaa gtcaaagagt 360

tcttccgctg ggcgcaggat cacgtgaccg aggtggcgca tgagttctac gtcagaaagg 420

gtggagccaa caagagaccc gcccccgatg acgcggataa aagcgagccc aagcgggcct 480

gcccctcagt cgcggatcca tcgacgtcag acgcggaagg agctccggtg gactttgccg 540

acaggtacca aaacaaatgt tctcgtcacg cgggcatgct tcagatgctg tttccctgca 600

agacatgcga gagaatgaat cagaatttca acatttgctt cacgcgcggg accagagact 660

gttcagaatg tttcccgggc gtgtcagaat ctcaaccggt cgtcagaaag aggacgtatc 720

ggaaactctg tgccattcat catctgctgg ggcgggctcc cgagattgct tgctcggcct 780

gcgatctggt caacgtggac ctggatgact gtgtttctga gcaataaatg acttaaacca 840

ggtatggctg ccgatggtta tcttccagat tggctcgagg acaacctctc tgagggcatt 900

cgcgagtggt gggacttgaa acctggagcc ccgaaaccca aagccaacca gcaaaagcag 960

gacgacggcc ggggtctggt gcttcctggc tacaagtacc tcggaccctt caacggactc 1020

gacaaggggg agcccgtcaa cgcggcggac gcagcggccc tcgagcacga caaggcctac 1080

gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc cgacgccgag 1140

tttcaggagc gtctgcaaga agatacgtct tttgggggca acctcgggcg agcagtcttc 1200

caggccaaga agcgggttct cgaacctctc ggtctggttg aggaaggcgc taagacggct 1260

cctggaaaga agagaccggt agagccatca ccccagcgtt ctccagactc ctctacgggc 1320

atcggcaaga caggccagca gcccgcgaaa aagagactca actttgggca gactggcgac 1380

tcagagtcag tgcccgaccc tcaaccaatc ggagaacccc ccgcaggccc ctctggtctg 1440

ggatctggta caatggctgc aggcggtggc gctccaatgg cagacaataa cgaaggcgcc 1500

gacggagtgg gtagttcctc aggaaattgg cattgcgatt ccacatggct gggcgacaga 1560

gtcatcacca ccagcacccg aacctgggcc ctccccacct acaacaacca cctctacaag 1620

caaatctcca acgggacatc gggaggaagc accaacgaca acacctactt cggctacagc 1680

acccccctggg ggtattttga ctttaacaga ttccactgcc acttctcacc acgtgactgg 1740

cagcgactca tcaacaacaa ctggggattc cggcccaaga gactcaactt caagctcttc 1800

aacatccagg tcaaggaggt cacgcagaat gaaggcacca agaccatcgc caataacctt 1860

accagcacga ttcaggtctt tacggactcg gaataccagc tcccgtacgt cctcggctct 1920

gcgcaccagg gctgcccgcc tccgttcccg gcggacgtct tcatgattcc tcagtacggg 1980

tacctgactc tgaacaacgg cagtcaggcc gtgggccgtt cctccttcta ctgcctggag 2040

tactttcctt ctcaaatgcg gagaacgggc aacaactttg agttcagcta ccagtttgag 2100

gacgtgcctt ttcacagcag ctacgcgcat agccaaagcc tggaccggct gatgaacccc 2160

ctcatcgacc agtacctgta ctacctgtct cggactcagt ccacgggagg taccgcagga 2220

actcagcagt tgctattttc tcaggccggg cctaataaca tgtcggctca ggccaaaaac 2280

tggctacccg ggccctgcta ccggcagcaa cgcgtctcca cgacactgtc gcaaaataac 2340

aacagcaact ttgcttggac cggtgccacc aagtatcatc tgaatggcag agactctctg 2400

gtaaatcccg gtgtcgctat ggcaacgcac aaggacgacg aagagcgatt ttttccatcc 2460

agcggagtct tgatgtttgg gaaacaggga gctggaaaag acaacgtgga ctatagcagc 2520

gttatgctaa ccagtgagga agaaatcaaa accaccaacc cagtggccac agaacagtac 2580

ggcgtggtgg ccgataacct gcaacagcaa aacgccgctc ctattgtagg ggccgtcaac 2640

agtcaaggag ccttacctgg catggtctgg cagaaccggg acgtgtacct gcagggtcct 2700

atctgggcca agattcctca cacggacggc aactttcatc cttcgccgct gatgggaggc 2760

tttggactga aacacccgcc tcctcagatc ctgattaaga atacacctgt tcccgcggat 2820

cctccaacta ccttcagtca agccaagctg gcgtcgttca tcacgcagta cagcaccgga 2880

caggtcagcg tggaaattga atgggagctg cagaaagaga acagcaagcg ctggaaccca 2940

gagattcagt atacttccaa ctactacaaa tctacaaatg tggactttgc tgtcaatact 3000

gagggtactt attcagagcc tcgccccatt ggcacccgtt acctcacccg taacctgtaa 3060

ttgcctgtta atcaataaac cggttaattc gtttcagttg aactttggtc tctgcgaagg 3120

gcgaattc 3128

<210> 428
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 428
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

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1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
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    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Pro Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
```

```
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Gly Ala
            580                 585                 590

Pro Ile Val Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
```

625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 429
<211> 1933
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> modified_base
<222> (1302)..(1302)
<223> a, c, g, or t

<400> 429
caaggcctac gaccagcagc tcaaagcggg tgacaatccg tacctgcggt ataaccacgc 60

cgacgccgag tttcaggagc gtcttcaaga agatacgtct tttgggggca acctcgggcg 120

agcagtcttc caggccaaaa agcgggttct cgaacctctt ggtctggttg agacgccagc 180

taagacggca cctggaaaga agcgaccggt agactcgcca gactccacct cgggcatcgg 240

caagaaaggc cagcagcccg cgaaaaagag actcaacttt gggcagactg gcgactcaga 300

gtcagtcccc gaccctcaac caatcggaga accaccagca ggcccctctg gtctgggatc 360

tggtacaatg gctgcaggcg gtggcgcacc aatggctgac aataacgagg gcgccgacgg 420

agtgggtaat gcctcaggaa attggcattg cgattccaca tggctgggcg acagagtcat 480

caccaccagc acccgaacct gggccctgcc cacctacaac aaccacctct acaagcaaat 540

ctccagtcag tcagcaggga gcaccaacga taacgtctat ttcggctaca gcacccccctg 600

ggggtatttt gacttcaaca gattccattg ccacttctca ccacgtgact ggcagcgact 660

tatcaacaac aactggggat tccggcccaa gaagctcaac ttcaagctct tcaacatcca 720

ggtcaaggag gtcacgacga atgacggtgt cacaaccatc gctaataacc ttaccagcac 780

ggttcaggtc ttttcggact cggaatatca actgccgtac gtcctcggct ccgcgcacca 840

gggctgcctg cctccgttcc cggcagacgt gttcatgatt ccgcagtacg gatacctgac 900

tctgaacaat ggcagccaat cggtaggccg ttcctccttc tactgcctgg agtactttcc 960

ttctcagatg ctgagaacgg gcaacaactt cacctttagc tacaccttcg aggacgtgcc 1020

tttccacagc agctacgcgc acagccagag tctggaccgg ctgatgaatc ccctcatcga 1080

ccagtacctg tactacttgg ccagaacaca gagcaacgca ggaggtactg ctggcaatcg 1140

ggaactgcag ttttatcagg gcggacctac caccatggcc gaacaagcaa agaactggct 1200

gcccggacct tgcttccggc aacagagagt atccaagacg ctggatcaaa ataacaacag 1260

caactttgcc tggactggtg ccacaaaata ccatttaaat gnaagaaatt cattggttaa 1320

tcccggtgtc gccatggcaa cccacaagga cgacgaggaa cgcttcttcc cttcgagcgg 1380

agttctaatt tttggcaaaa ctggagcagc taataaaact acattagaaa acgtgctcat 1440

gacaaatgaa gaagaaattc gtcctaccaa cccggtagct accgaggaat acgggattgt 1500

aagcagcaac ttgcaggcgg ctagcaccgc agcccagaca caagttgtta acaaccaggg 1560

agccttacct ggcatggtct ggcagaaccg ggacgtgtac ctgcaaggtc ccatttgggc 1620

caagattcct cacacggacg gcaactttca cccgtctcct ctaatgggtg gctttggact 1680

gaaacacccg cctccccaga tcctgatcaa aaacacaccg gtacctgcta atcctccaga 1740

agtgtttact cctgccaagt ttgcttcctt catcacgcag tacagcaccg ggcaagtcag 1800

cgttgagatc gagtgggagc tgcagaaaga gaacagcaag cgctggaacc cagagattca 1860

gtacacctcc aactttgaca aacagactgg agtggacttt gctgttgaca gccagggtgt 1920

ttactctgag cct 1933

<210> 430
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 430
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
```

```
Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Ser Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Gly Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala Tyr Ser Gln Ser Pro Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540
```

```
Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730

<210> 431
<211> 3105
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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 431
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acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca 120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga 180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga 240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca 300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc 360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag 420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgcccct 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt 720

gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc cgcgatctcg 780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct 840

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc ccccaagccc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tcaacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaacctct gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

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aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgtctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040

gaaatggctt acaactttgg gaaggtgccg ttccactcaa tgtatgctta cagccagagc 2100

ccggacagac tgatgaatcc cctcctggac cagtacctgt ggcacttaca gtcgaccacc 2160

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gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaagaagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatattta tcaaaaacac ccccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

gaaatcgaaa aggaacgctc caaacgctgg aatcctgaag tgcagtttac ttcaaactat 2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg 3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc 3105

<210> 432
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 432
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
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Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540
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Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730
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<210> 433
<211> 3105
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 433
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acaagatggt gatctggtgg gaggagggca agatgaccgc caaggtcgtg gagtccgcca 120

aggccattct gggcggaagc aaggtgcgcg tggaccaaaa gtgcaagtca tcggcccaga 180

tcgaccccac gcccgtgatc gtcacctcca acaccaacat gtgcgccgtg atcgacggga 240

acagcaccac cttcgagcac cagcagccgc tgcaggaccg catgttcaag ttcgagctca 300

cccgccgtct ggagcacgac tttggcaagg tgaccaagca ggaagtcaaa gagttcttcc 360

gctgggctca ggatcacgtg actgaggtgg cgcatgagtt ctacgtcaga aagggcggag 420

ccaccaaaag acccgccccc agtgacgcgg atataagcga gcccaagcgg gcctgcccct 480

cagttgcgga gccatcgacg tcagacgcgg aagcaccggt ggactttgcg gacaggtacc 540

aaaacaaatg ttctcgtcac gcgggcatgc ttcagatgct gtttccctgc aagacatgcg 600

agagaatgaa tcagaatttc aacgtctgct tcacgcacgg ggtcagagac tgctcagagt 660

gcttccccgg cgcgtcagaa tctcaacccg tcgtcagaaa aaagacgtat cagaaactgt 720

gcgcgattca tcatctgctg gggcgggcac ccgagattgc gtgttcggcc tgcgatctcg 780

tcaacgtgga cttggatgac tgtgtttctg agcaataaat gacttaaacc aggtatggct 840

gctgacggtt atcttccaga ttggctcgag gacaacctct ctgagggcat tcgcgagtgg 900

tgggacctga aacctggagc ccccaagctc aaggccaacc agcagaagca ggacgacggc 960

cggggtctgg tgcttcctgg ctacaagtac ctcggaccct tccacggact cgacaagggg 1020

gagcccgtca acgcggcgga cgcagcggcc ctcgagcacg acaaggccta cgaccagcag 1080

ctcaaagcgg gtgacaatcc gtacctgcgg tataaccacg ccgacgccga gtttcaggag 1140

cgtctgcaag aagatacgtc ttttgggggc aacctcgggc gagcagtctt ccaggccaag 1200

aagagggtac tcgaaccact gggcctggtt gaagaaggtg ctaagacggc tcctggaaag 1260

aagagaccgt tagagtcacc acaagagccc gactcctcct caggaatcgg caaaaaaggc 1320

aaacaaccag ccaaaaagag actcaacttt gaagaggaca ctggagccgg agacggaccc 1380

cctgaaggat cagataccag cgccatgtct tcagacattg aaatgcgtgc agcaccgggc 1440

ggaaatgctg tcgatgcggg acaaggttcc gatggagtgg gtaatgcctc gggtgattgg 1500

cattgcgatt ccacctggtc tgagggcaag gtcacaacaa cctcgaccag aacctgggtc 1560

ttgcccacct acaacaacca cttgtacctg cggctcggaa caacatcaaa cagcaacacc 1620

tacaacggat tctccacccc ctggggatac tttgacttta acagattcca ctgtcacttc 1680

tcaccacgtg actggcaaag actcatcaac aacaactggg gactacgacc aaaagccatg 1740

cgcgttaaaa tcttcaatat ccaagttaag gaggtcacaa cgtcgaacgg cgagactacg 1800

gtcgctaata accttaccag cacggttcag atatttgcgg actcgtcgta tgagctcccg 1860

tacgtgatgg acgctggaca agagggaagt ctgcctcctt tccccaatga cgtcttcatg 1920

gtgcctcaat atggctactg tggcattgtg actggcgaaa atcagaacca gacggacaga 1980

aatgctttct actgcctgga gtattttcct tcacaaatgc tgagaactgg caataacttt 2040

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gcaacagctg gaccttcaga tggggacttc agcaacgccc agctcatctt ccctggacca 2460

tcagtcaccg gaaacacaac aacctcagca aacaatctgt tgtttacatc agaaggagaa 2520

attgctgcca ccaacccaag agacacggac atgtttggtc agattgctga caataatcag 2580

aatgctacaa ctgctcccat aaccggcaac gtgactgcta tgggagtgct tcctggcatg 2640

gtgtggcaaa acagagacat ttactaccaa gggccaattt gggccaagat cccacacgcg 2700

gacggacatt ttcatccttc accgctaatt ggcggttttg gactgaaaca tccgcctccc 2760

cagatattta tcaaaaacac ccccgtacct gccaatcctg cgacaacctt cactgcagcc 2820

agagtggact ctttcatcac acaatacagc accggccagg tcgctgttca gattgaatgg 2880

gaaatcgaaa aggaacgctc caaacgccgg aatcctgaag tgcagtttac ttcaaactat 2940

gggaaccagt cttctatgtt gtgggctccc gatacaactg ggaagtatac agagccgcgg 3000

gttattggct ctcgttattt gactaatcat ttgtaactgc ctagttaatc aataaaccgt 3060

gtgattcgtt tcagttgaac tttggtctct gcgaagggcg aattc 3105

<210> 434
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 434
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
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Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Thr Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Gly Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540
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Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560


Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575


Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590


Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605


Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620


His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Tyr Pro Ala
                645                 650                 655


Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685


Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Cys Gly Asn
    690                 695                 700


Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720


Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730


<210> 435
<211> 3105
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 435
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actaggcagt tacaaatgat tagtcaaata acgagagcca ataacccgcg gctctgtata 120

cttcccagtt gtatcgggag cccacaacat agaagactgg ttcccacagt ttgaagtaaa 180

ctgcacttca ggattccagc gtttggagcg ttccttttcg atttcccatt caatctgaac 240

agcgacctgg ccggtgctgt attgtgtgat gaaagagtcc actctggctg cagtgaaggt 300

tgtcgcagga taggcaggta cgggggtgtt tttgataaat atctggggag gcggatgttt 360

cagtccaaaa ccgccaatta gcggtgaagg atgaaaatgt ccgtccgcgt gtgggatctt 420

ggcccaaatt ggcccttggt agtaaatgtc tctgttttgc cacaccatgc caggaagcac 480

tcccatagca gtcacgttgc cggttatggg agcagttgta gcattctgat tattgtcagc 540

aatctgacca aacatgtccg tgtctcttgg gttggtggca gcaatttctt cttctgatgt 600

aaacaacaga ttgtttgctg aggttgttgt gtttccggtg actgatggtc cagggaagat 660

gagctgggcg ttgctgaagt ccccatctga aggtccagct gttgccattg gaggtccagg 720

cgctatgttg ctccagcggt tgtttaaggt atagtgggtg tcatacttta acagagcgtt 780

gcccccgctg gcaggaatct tgtaattttg actggcagtt tttgagaatc tctgctgttt 840

aacacaaggc ccaggcagcc agttctttct gtaaaaggca aagtctccac tcctgatttt 900

tccaaatgtg gttgctgcat tgccttgatt cagagtctct ccagaggtgg tcgactgtaa 960

gtgccacagg tactggtcca ggaggggatt catcagtccg tccaggctct ggctgtgagc 1020

atacattgag tggaacggca ccttctcaaa gttgtaagcc gtttcaaagt tattgccagt 1080

tctcagcatt tgtgaaggaa aatactccag gcagtagaaa gcatttctgt ccgtctggtt 1140

ctgattttcg ccagtcacaa tgccacagta gccatattga ggcaccatga agacgtcatt 1200

ggggaaagga ggcagacttc cctcttgtcc agcgtccatc acgtacggga gctcatacga 1260

cgagtccgca aatatctgaa ccgtgctggt aaggttatta gcgaccgtag tctcgccgtt 1320

cgacgttgtg acctccttaa cttggatatt gaagatttta acgcgcatgg cttttggtcg 1380

tagtccccag ttgttgttga tgagtctttg ccagtcacgt ggtgagaagt gacagtggaa 1440

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tgctcgcccg aggttgcccc caaaagacgt atcttcttgc agacgctcct gaaactcggc 1980

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cttgtcgtgc tcgagggccg ctgcgtccgc cgcgttgacg ggctcccccct tgtcgagtcc 2100

gttgaagggt ccgaggtact cgtagccagg aagcaccaga ccccggccgt cgtcctgctt 2160

ctgctggttg gccttgggct tgggggctcc aggtttcagg tcccaccact cgcgaatgcc 2220

ctcagagagg ttgtcctcga gccaatctgg aagataaccg tcagcagcca tacctggttt 2280

aagtcattta ttgctcagaa acacagtcat ccaagtccac gttgacgaga tcgcaggccg 2340

aacacgcaat ctcgggtgcc cgccccagca gatgatgaat cgcgcacagt ttctgatacg 2400

tctttttttct gacgacgggt tgagattctg acgcgccggg gaagcactct gagcagtctc 2460

tgaccccgtg cgtgaagcag acgttgaaat tctgattcat tctctcgcat gtcttgcagg 2520

gaaacagcat ctgaagcatg cccgcgtgac gagaacattt gttttggtac ctgtccgcaa 2580

ggtccaccgg tgcttccgcg tctgacgtcg atggctccgc aactgagggg caggcccgct 2640

tgggctcgct tatatccgcg tcactggggg cgggtctttt ggtggctccg ccctttctga 2700

cgtagaactc atgcgccacc tcagtcacgt gatcctgagc ccagcggaag aactctttga 2760

cttcctgctt ggtcaccttg ccaaagtcgt gctccagacg gcgggtgagc tcgaacttga 2820

acatgcggtc ctgcagcggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg 2880

cgcacatgtt ggtgttggag gtgacgatca cgggcgtggg gtcgatctgg gccgatgact 2940

tgcacttttg gtccacgcgc accttgcttc cgcccagaat ggccttggcg gactccacga 3000

ccttggcggt catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga 3060

agggaaagtt ctcattggtc cagttgacgc agcaagggcg aattc 3105

<210> 436
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 436
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
```

```
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Gly Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
```

545 550 555 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
565 570 575

Leu Gln Pro Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
580 585 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
595 600 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
610 615 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625 630 635 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
645 650 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
660 665 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
675 680 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
690 695 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705 710 715 720

Gly Thr Arg Tyr Leu Pro Arg Asn Leu
725

<210> 437
<211> 3094
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 437
gaattcgccc ttgctgcgtc aactggacca agagaacttt cccttcaacg attgcgtcga 60

caagatggtg atctggtggg aggagggcaa gatgacggcc aaggtcgtgg agtccgccaa 120

agccattctg ggcggaagca aggtgcgcgt cgaccaaaag tgcaagtcct cggcccagat 180

cgatcccacc cccgtgatcg tcacctccaa caccaacatg tgcgccgtga tcgacgggaa 240

cagcaccacc ttcgagcacc agcagccgtt gcaggaccgg atgttcaaat ttgaactcac 300

ccgccgtctg gaacacgact ttggcaaggt gaccaagcag gaagtcaaag agttcttccg 360

ctgggctagt gatcacgtga ctgaggtgac gcatgagttc tacgtcagaa agggcggagc 420

cagcaaaaga cccgcccccg atgacgcgga tataagcgag cccaagcggg cctgtccctc 480

agtcacggac ccatcgacgt cagacgcgga aggagctccg gtggactttg ccgacaggta 540

ccaaaacaaa tgttctcgtc acgcgggcat gcttcagatg ctgtttccct gcaaaacgtg 600

cgagagaatg aatcagaatt tcaacatttg cttcacgcac ggggtcagag actgtttaga 660

atgtttcccc ggcgtgtcag aatctcaacc ggtcgtcaga aaaaagacgt atcggaagct 720

gtgtgcgatt catcatctgc tggggcgggc acccgagatt gcttgctcgg cctgcgacct 780

ggtcaacgtg gacctggacg actgtgtttc tgagcaataa atgacttaaa ccgggtatgg 840

ctgccgatgg ttatcttcca gattggctcg aggacaacct ctctgagggc attcgcgagt 900

ggtgggacct gaaacctgga gccccgaaac ccaaagccaa ccagcaaaag caggacgacg 960

gccggggtct ggtgcttcct ggctacaagt acctcggacc cttcaacgga ctcgacaagg 1020

gggagcccgt caacgcggcg gacgcagcgg ccctcgagca cgacaaggcc tacgaccagc 1080

agctcaaagc gggtgacaat ccgtacctgc ggtataacca cgccgacgcc gagtttcagg 1140

agcgtctgca agaagatacg tcatttgggg gcaacctcgg gcgagcagtc ttccaggcca 1200

agaagcgggt tctcgaacct ctcggtctgg ttgaggaagg cgctaagacg gctcctggaa 1260

agaagagacc catagactct ccagactcct ccacgggcat cggcaaaaaa ggccagcagc 1320

ccgctaaaaa gaagctcaat tttggtcaga ctggcgactc agagtcagtc cccgaccctc 1380

aacctcttgg agaacctcca gcagcgccct ctagtgtggg atctggtaca atggctgcag 1440

gcggtggcgc accaatggca gacaataacg aaggtgccga cggagtgggt aatgcctcag 1500

gaaattggca ttgcgattcc acatggctgg gcgacagagt catcaccacc agcaccagaa 1560

cctgggccct ccccacctac aacaaccacc tctacaagca aatctccagc agcagctcag 1620

gagccaccaa tgacaaccac tacttcggct acagcacccc ctgggggtat tttgacttta 1680

acagattcca ctgccacttc tcaccacgtg actggcagcg actcatcaac aacaactggg 1740

gattccggcc caagaagctg cggttcaagc tcttcaacat ccaggtcaag gaggtcacaa 1800

cgaatgacgg cgtcacgacc atcgctaata accttaccag cacggttcag gtcttctcgg 1860

actcggaata ccagctgccg tacgtcctcg gctctgcgca ccagggctgc ctgcctccgt 1920

tcccggcgga cgtcttcatg attcctcagt acggctacct gactctgaac aacggcagcc 1980

aatcggtggg ccgttcctcc ttctactgcc tggaatattt cccctctcaa atgctgagaa 2040

cgggcaacaa ctttgagttc agttacagct tcgaggacgt gcctttccac agcagctacg 2100

cgcacagcca gagcctagac cggctgatga accctctcat cgaccagtac ctgtactacc 2160

tggcccggac ccagagcacc acgggttcca ccagggaact gcaatttcat caagctgggc 2220

ccaatactat ggccgagcag tcaaagaact ggctgcctgg accctgctat aggcaacagg 2280

gactgtcaaa gaacttggac tttaacaaca acagcaattt tgcctggact gctgccacta 2340

aatatcatct gaatggcaga aactctttga ccaatcctgg cattcccatg gcaaccaaca 2400

aggatgatga ggaccagttc tttcccatca acggggtact ggtttttggc aagacgggag 2460

ctgccaacaa aactacgctg gaaaacgttc tgatgaccag cgaggaggag atcaagacca 2520

ctaaccctgt ggctacagaa gaatacggtg tggtctccag caacctgcag ccgtctacag 2580

ccgggcctca atcacagact atcaacagcc agggagcact gcctggcatg gtctggcaga 2640

accgggacgt gtatctgcag ggtcccatct gggccaaaat tcctcacacg gatggcaact 2700

ttcacccgtc tcctctgatg ggcggttttg gactcaaaca cccgcctcca cagatcctga 2760

tcaaaaacac acctgtacct gctaatcctc cggaggtgtt tactcctgcc aagtttgcct 2820

ccttcatcac gcagtacagc accggacaag tcagcgtgga aatcgagtgg gagctgcaga 2880

aagaaaacag caagcgctgg aacccagaaa ttcagtatac ttccaattat gccaagtcta 2940

ataatgttga atttgctgtg aaccctgatg gtgtttatac tgagcctcgc cccattggca 3000

ctcgttacct cccccgtaat ctgtaattgc ttgttaatca ataaaccggt tgattcgttt 3060

cagttgaact ttggtctctg cgaagggcga attc 3094

<210> 438
<211> 1458
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 438
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350
```

```
Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560
```

```
Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu Met Ala Ala Asp Gly Tyr Leu
                725                 730                 735

Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu Gly Ile Arg Glu Trp Trp
            740                 745                 750

Asp Leu Lys Pro Gly Ala Pro Lys Pro Lys Ala Asn Gln Gln Lys Gln
        755                 760                 765
```

```
Asp Asp Gly Arg Gly Leu Val Leu Pro Gly Tyr Lys Tyr Leu Gly Pro
    770                 775                 780

Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Ala Ala Asp Ala Ala
785                 790                 795                 800

Ala Leu Glu His Asp Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp
                805                 810                 815

Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg
            820                 825                 830

Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe
        835                 840                 845

Gln Ala Lys Lys Arg Val Leu Glu Pro Leu Gly Leu Val Glu Glu Gly
    850                 855                 860

Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro Ile Gly Ser Pro Asp Ser
865                 870                 875                 880

Ser Thr Gly Ile Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Lys Leu
                885                 890                 895

Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro
            900                 905                 910

Leu Gly Glu Pro Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met
        915                 920                 925

Ala Ala Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp
    930                 935                 940

Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu
945                 950                 955                 960

Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr
                965                 970                 975
```

```
Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ser Ser Ser Gly Ala
            980                 985                 990

Thr Asn Asp Asn His Tyr Phe Gly  Tyr Ser Thr Pro Trp  Gly Tyr Phe
        995                 1000                1005

Asp Phe  Asn Arg Phe His Cys  His Phe Ser Pro Arg  Asp Trp Gln
    1010                1015                1020

Arg Leu  Ile Asn Asn Asn Trp  Gly Phe Arg Pro Lys  Lys Leu Arg
    1025                1030                1035

Phe Lys  Leu Leu Asn Ile Gln  Val Lys Glu Val Thr  Thr Asn Asp
    1040                1045                1050

Gly Val  Thr Thr Ile Ala Asn  Asn Leu Thr Ser Thr  Val Gln Val
    1055                1060                1065

Phe Ser  Asp Ser Glu Tyr Gln  Leu Pro Tyr Val Leu  Gly Ser Ala
    1070                1075                1080

His Gln  Gly Cys Leu Pro Pro  Phe Pro Ala Asp Val  Phe Met Ile
    1085                1090                1095

Pro Gln  Tyr Gly Tyr Leu Thr  Leu Asp Asn Gly Ser  Gln Ser Val
    1100                1105                1110

Gly Arg  Ser Ser Phe Tyr Cys  Leu Glu Tyr Phe Pro  Ser Gln Met
    1115                1120                1125

Leu Arg  Thr Gly Asn Asn Phe  Glu Phe Ser Tyr Ser  Phe Glu Asp
    1130                1135                1140

Val Pro  Phe His Ser Ser Tyr  Ala His Ser Gln Ser  Leu Asp Arg
    1145                1150                1155

Leu Met  Asn Pro Leu Ile Asp  Gln Tyr Leu Tyr Tyr  Leu Ala Arg
    1160                1165                1170
```

```
Thr Gln  Ser Thr Thr Gly Ser  Thr Arg Glu Leu Gln  Phe His Gln
    1175                1180                1185

Ala Gly  Pro Asn Thr Met Ala  Glu Gln Ser Lys Asn  Trp Leu Pro
    1190                1195                1200

Gly Pro  Cys Tyr Arg Gln Gln  Arg Leu Ser Lys Asn  Leu Asp Phe
    1205                1210                1215

Asn Asn  Asn Ser Asn Phe Ala  Trp Thr Ala Ala Thr  Lys Tyr His
    1220                1225                1230

Leu Asn  Gly Arg Asn Ser Leu  Thr Asn Pro Gly Ile  Pro Met Ala
    1235                1240                1245

Thr Asn  Lys Asp Asp Glu Asp  Gln Phe Phe Pro Ile  Asn Gly Val
    1250                1255                1260

Leu Val  Phe Gly Lys Thr Gly  Ala Ala Asn Lys Thr  Thr Leu Glu
    1265                1270                1275

Asn Val  Leu Met Thr Ser Glu  Glu Glu Ile Lys Thr  Thr Asn Pro
    1280                1285                1290

Val Ala  Thr Glu Glu Tyr Gly  Val Val Ser Ser Asn  Leu Gln Ser
    1295                1300                1305

Ser Thr  Ala Gly Pro Gln Ser  Gln Thr Ile Asn Ser  Gln Gly Ala
    1310                1315                1320

Leu Pro  Gly Met Val Trp Gln  Asn Arg Asp Val Tyr  Leu Gln Gly
    1325                1330                1335

Pro Ile  Trp Ala Lys Ile Pro  His Thr Asp Gly Asn  Phe His Pro
    1340                1345                1350

Ser Pro  Leu Met Gly Gly Phe  Gly Leu Lys His Pro  Pro Pro Gln
    1355                1360                1365
```

```
Ile Leu  Ile Lys Asn Thr Pro  Val Pro Ala Asn Pro  Pro Glu Val
    1370                1375                1380


Phe Thr  Pro Ala Lys Phe Ala  Ser Phe Ile Thr Gln  Tyr Ser Thr
    1385                1390                1395


Gly Gln  Val Ser Val Glu Ile  Glu Trp Glu Leu Gln  Lys Glu Asn
    1400                1405                1410


Ser Lys  Arg Trp Asn Pro Glu  Ile Gln Tyr Thr Ser  Asn Tyr Ala
    1415                1420                1425


Lys Ser  Asn Asn Val Glu Phe  Ala Val Asn Pro Asp  Gly Val Tyr
    1430                1435                1440


Thr Glu  Pro Arg Pro Ile Gly  Thr Arg Tyr Leu Thr  Arg Asn Leu
    1445                1450                1455


<210> 439
<211> 3095
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 439
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta       60

acaagcaatt acagattacg ggtgaggtaa cgagtgccaa tggggcgagg ctcagtataa      120

acaccatcag ggttcacagc aaattcaaca ttattagact tggcataatt ggaagtatac      180

tgaatttctg ggttccagcg cttgctgttt tctttctgca gctcccactc gatttccacg      240

ctgacttgtc cggtgctgta ctgcgtgatg aaggaggcaa acttggcagg agtaaacacc      300

tccggaggat tagcaggtac aggtgtgttt ttgatcagga tctgtggagg cgggtgtttg      360

agtccaaaac cgcccatcag aggagacggg tgaaagttgc catccgtgtg aggaattttg      420

gcccagatgg gaccctgcag atacacgtcc cggttctgcc agaccatgcc aggcagtgct      480
```

ccctggctgt tgatagtctg tgattgaggc ccggctgtag acgactgcag gttgctggag 540

accacaccgt attcttctgt agccacaggg ttagtggtct tgatctcctc ctcgctggtc 600

atcagaacgt tttccagcgt agttttgttg gcagctcccg tcttgccaaa aaccagtacc 660

ccgttgatgg gaaagaactg gtcctcatca tccttgttgg ttgccatggg aatgccagga 720

ttggtcaaag agtttctgcc attcagatga tatttagtgg cagcagtcca ggcaaaattg 780

ctgttgttgt taaagtccaa gttctttgac agtctctgtt gcctatagca gggtccaggc 840

agccagttct ttgactgctc ggccatagta ttgggcccag cttgatgaaa ttgcagttcc 900

ctggtggaac ccgtggtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgaga 960

gggttcatca gccggtctag gctctggctg tgcgcgtagc tgctgtggaa aggcacgtcc 1020

tcgaagctgt aactgaactc aaagttgttg cccgttctca gcatttgaga ggggaaatat 1080

tccaggcagt agaaggagga acggcccacc gattggctgc cgttgtccag agtcaggtag 1140

ccgtactgag gaatcatgaa gacgtccgcc gggaacggag gcaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ctggtattcc gagtccgaga agacctgaac cgtgctggta 1260

aggttattag cgatggtcgt gacgccgtca ttcgttgtga cctccttgac ctggatgttg 1320

aggagcttga accgcagctt cttgggccgg aatccccagt tgttgttgat gagtcgctgc 1380

cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccaggggtg 1440

ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500

tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctggtggt gatgactctg 1560

tcgcccagcc atgtggaatc gcaatgccaa tttcctgagg cattacccac tccgtcggca 1620

ccttcgttat tgtctgccat tggtgcgcca ccgcctgcag ccattgtacc agatcccaca 1680

ctagagggcg ctgctggagg ttctccaaga ggttgagggt cggggactga ctctgagtcg 1740

ccagtctgac caaaattgag cttctttttа gcgggctgct ggccttttt gccgatgccc 1800

gtggaggagt ctggagagcc tatgggtctc ttctttccag gagccgtctt agcgccttcc 1860

tcaaccagac cgagaggttc gagaacccgc ttcttggcct ggaagactgc tcgcccgagg 1920

ttgcccccaa atgacgtatc ttcttgcaga cgctcctgaa actcggcgtc ggcgtggtta 1980

taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040

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ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag tcatttattg 2280

ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aagcaatctc 2340

gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct tttttctgac 2400

gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgtgcgt 2460

gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcacctg 2520

aagcatgccc gcgtgacgag aacatttgtt ttggtacctg tcggcaaagt ccaccggagc 2580

tccttccgcg tctgacgtcg atgggtccgt gactgaggga cgggcccgct tgggctcgct 2640

tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc 2700

atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt 2760

tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820

ctgcaacggt tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcacatgtt 2880

ggtgttggag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg 2940

gtccacgcgc accttgctgc cgccgagaat ggccttggcg gactccacga ccttggccgt 3000

catcttgccc tcctcccacc agatcaccat cttgtcgacg caatcgttga agggaaagtt 3060

ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> 440
<211> 3095
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 440
gaattcgccc ttcgcagaga ccaaagttca actgaaacga atcaaccggt ttattgatta 60

acaagcaatt acagattacg ggtgaggtaa cgagtgccaa tggggcgagg ctcagtataa 120

acaccatcag ggttcacagc aaattcaaca ttattagact tggcataatt ggaagtatac 180

tgaatttctg ggttccagcg cttgctgttt tctttctgca gctcccactc gatttccacg 240

ctgacttgtc cggtgctgta ctgcgtgatg aaggaggcaa acttggcagg agtaaacacc 300

tccggaggat tagcaggtac aggtgtgttt ttgatcagga tctgtggagg cgggtgttcg 360

agtccaaaac cgcccatcag aggagacggg tgaaagttgc catccgtgtg aggaattttg 420

gcccagatgg gaccctgcag atacacgtcc cggttctgcc agaccatgcc aggcagtgct 480

ccctggctgt tgatagtctg tgattgaggc ccggctgtag acgactgcag gttgctggag 540

accacaccgt attcttctgt agccacaggg ttagtggtct tgatctcctc ctcgctggtc 600

atcagaacgt tttccagcgt agttttgttg gcagctcccg tcttgccaaa aaccagtacc 660

ccgttgatgg gaaagaactg gtcctcatca tccttgttgg ttgccatggg aatgccagga 720

ttggtcaaag agtttctgcc attcagatga tatttagtgg cagcagtcca ggcaaaattg 780

ctgttgttgt taaagtccaa gttctttgac agtctctgtt gcctatagca gggtccaggc 840

agccagttct ttgactgctc ggccatagta ttgggcccag cttgatgaaa ttgcagttcc 900

ctggtggaac ccgtggtgct ctgggtccgg gccaggtagt acaggtactg gtcgatgaga 960

gggttcatca gccggtctag gctctggctg tgcgcgtagc tgctgtggaa aggcacgtcc 1020

tcgaagctgt aactgaactc aaagttgttg cccgttctca gcatttgaga ggggaaatat 1080

tccaggcagt agaaggagga acggcccacc gattggctgc cgttgttcag agtcaggtag 1140

ccgtactgag gaatcatgaa gacgtccgcc gggaacggag gcaggcagcc ctggtgcgca 1200

gagccgagga cgtacggcag ctggtattcc gagtccgaga agacctgaac cgtgctggta 1260

aggttattag cgatggtcgt gacgccgtca ttcgttgtga cctccttgac ctggatgttg 1320

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cagtcacgtg gtgagaagtg gcagtggaat ctgttaaagt caaaataccc ccaggggtg 1440

ctgtagccga agtagtggtt gtcattggtg gctcctgagc tgctgctgga gatttgcttg 1500

tagaggtggt tgttgtaggt ggggagggcc caggttctgg tgctggtggt gatgactctg 1560

tcgcccagcc atgtggaatc gcaatgccaa tttcctgagg cattacccac tccgtcggca 1620

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gtggaggagt ctggagagtc tatgggtctc ttctttccag gagccgtctt agcgccttcc 1860

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ttgcccccaa atgacgtatc ttcttgcagg cgctcctgaa actcggcgtc ggcgtggtta 1980

taccgcaggt acggattgtc acccgctttg agctgctggt cgtaggcctt gtcgtgctcg 2040

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aggtacttgt agccaggaag caccagaccc cggccgtcgt cctgcttttg ctggttggct 2160

ttgggtttcg gggctccagg tttcaggtcc caccactcgc gaatgccctc agagaggttg 2220

tcctcgagcc aatctggaag ataaccatcg gcagccatac ctggtttaag ccatttattg 2280

ctcagaaaca cagtcgtcca ggtccacgtt gaccaggtcg caggccgagc aggcaatctc 2340

gggtgcccgc cccagcagat gatgaatcgc acacagcttc cgatacgtct tttttctgac 2400

gaccggttga gattctgaca cgccggggaa acattctaaa cagtctctga ccccgtgcgt 2460

gaagcaaatg ttgaaattct gattcattct ctcgcacgtt ttgcagggaa acagcatctg 2520

aagcatgccc gcgtggcgag aacatttgtt ttggtacctg tcggcaaagt ccaccggagc 2580

tccttccgcg tctgacgtcg atgggtccgt gactgaggga caggcccgct tgggctcgct 2640

tatatccgcg tcatcggggg cgggtctttt gctggctccg ccctttctga cgtagaactc 2700

atgcgtcacc tcagtcacgt gatcactagc ccagcggaag aactctttga cttcctgctt 2760

tgtcaccttg ccaaagtcgt gttccagacg gcgggtgagt tcaaatttga acatccggtc 2820

ctgcaacggc tgctggtgct cgaaggtggt gctgttcccg tcgatcacgg cgcgcatgtt 2880

ggtgttggag gtgacgatca cgggggtggg atcgatctgg gcggacgact tgcacttttg 2940

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ctcattggtc cagttgacgc agcaagggcg aattc 3095

<210> 441
<211> 729

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 441
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

```
Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380
```

```
Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590
```

```
Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605


Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620


Ser Pro Leu Met Gly Gly Phe Gly Leu Glu His Pro Pro Pro Gln Ile
625                 630                 635                 640


Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655


Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670


Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685


Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700


Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 442
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 442
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145                 150                 155                 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
                165                 170                 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
            180                 185                 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Thr Ala
        195                 200                 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
    210                 215                 220
```

```
His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225                 230                 235                 240


Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
                245                 250                 255


Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
            260                 265                 270


Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
        275                 280                 285


Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300


Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320


Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335


Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350


Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365


Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380


Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400


Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415


Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430
```

```
Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640
```

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Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655


Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670


Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685


Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
    690                 695                 700


Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 443
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 443
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Ile Asp Ser Pro Asp Ser Ser Thr Gly Ile Gly Lys Lys Gly Gln
145 150 155 160

Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu
165 170 175

Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser
180 185 190

Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Ala Pro Met Ala
195 200 205

Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp
210 215 220

His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr
225 230 235 240

Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile
245 250 255

Ser Ser Ser Ser Ser Gly Ala Thr Asn Asp Asn His Tyr Phe Gly Tyr
260 265 270

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe

```
        275                 280                 285

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
    290                 295                 300

Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
305                 310                 315                 320

Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ser Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro
                405                 410                 415

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
            420                 425                 430

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Thr
        435                 440                 445

Thr Gly Ser Thr Arg Glu Leu Gln Phe His Gln Ala Gly Pro Asn Thr
    450                 455                 460

Met Ala Glu Gln Ser Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln
465                 470                 475                 480

Gln Arg Leu Ser Lys Asn Leu Asp Phe Asn Asn Asn Ser Asn Phe Ala
```

```
                485                 490                 495

Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Thr
            500                 505                 510

Asn Pro Gly Ile Pro Met Ala Thr Asn Lys Asp Asp Glu Asp Gln Phe
        515                 520                 525

Phe Pro Ile Asn Gly Val Leu Val Phe Gly Lys Thr Gly Ala Ala Asn
    530                 535                 540

Lys Thr Thr Leu Glu Asn Val Leu Met Thr Ser Glu Glu Glu Ile Lys
545                 550                 555                 560

Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Val Val Ser Ser Asn
                565                 570                 575

Leu Gln Ser Ser Thr Ala Gly Pro Gln Ser Gln Thr Ile Asn Ser Gln
            580                 585                 590

Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Glu Val Phe Thr
                645                 650                 655

Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Asn Asn Val
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690 695 700

Glu Phe Ala Val Asn Pro Asp Gly Val Tyr Thr Glu Pro Arg Pro Ile
705 710 715 720

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725

<210> 444
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 444
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcggcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gcccttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgcacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgctacc tcacccgtaa tctgtaa 2217

<210> 445
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 445
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Arg Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180   185   190

```
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Pro Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 446
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 446
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg ataacttgca gcaaaccaat acggggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 447
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 447
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
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Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 448
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 448
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asp Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Arg Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Ala Asn Thr Gly
            580                 585                 590


Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 449
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 449
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gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcaggatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcgggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg ttgctatggc aacgcataag gacgacgagg aacgtttctt tccatcgagc 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta tagcagcgtt 1680

atgctaacca gcgaggaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaagccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaaa ttcctcacac ggacggcaat tttcacccgt ctcctctgat gggcggcttt 1920

ggactgaagc acccacctcc ccagatcctg atcaagaata cgccggtacc tgcggatcct 1980

ccaacgacgt tcagccaggc aaaattggct tccttcatca cgcagtacag caccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgatg gaacccagaa 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caattctgag 2160

ggtacatatt cagagcctcg ccccattggt actcgttatc tgacacgtaa tctgtaa 2217

<210> 450
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 450
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gcctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttccc agtaacggga 1620

tcctgttttt ggcaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccgccccat tggcacccgt tacctcaccc gtaatctgta a 2211

<210> 451
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 451
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile

305 310 315 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
450 455 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465 470 475 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
485 490 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
500 505 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His

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        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Val Thr Gly Ser Cys Phe Trp
    530                 535                 540

Gln Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 452
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 452
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctgcgac 240

cagcggctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaagg gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaatcacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga cgaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 453
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 453
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Cys Asp
65                  70                  75                  80

Gln Arg Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
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Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640
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Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Asp Glu Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 454
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 454
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca acggtagtca ggccgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac ttttccttca gctacacttt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agtttggaca ggctgatgaa tcctctcatc 1320

gaccagtacc tgtactacct gtcaagaacc cagtctacgg gaggcacagc gggaacccag 1380

cagttgctgt tttctcaggc cgggcctagc aacatgtcga ctcaggccag aaactggctg 1440

cctggaccct gctacagaca gcagcgcgtc tccacgacac tgtcgcaaaa caacaacagc 1500

aactttgcct ggactggtgc caccaagtat catctgaacg gcagagactc tctggtgaat 1560

ccgggcgtcg ccatggcaac caacaaggac gacgaggacc gcttcttccc atccagcggc 1620

atcctcatgt ttggcaagca gggagctgga aaagacaacg tggactatag caacgtgatg 1680

ctaaccagcg aggaagaaat caagaccacc aaccccgtgg ccacagaaca gtatggcgtg 1740

gtggctgata acctacagca gcaaaacacc gctcctattg tgggggccgt caacagccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatttgg 1860

gccaagattc ctcacacaga tggcaacttt cacccgtctc ctttaatggg cggctttgga 1920

cttaaacatc cgcctcctca gatccttatc aaaaacactc ctgttcctgc ggatcctcca 1980

acagcgttca accaggccaa gctgaattct ttcatcacgc agtacagcac cggacaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgagggt 2160

gcttactctg agcctcgccc cattggcact cgttacctca cccgtaatct gtaa 2214

<210> 455
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 455
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
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Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Asn Met Ser Thr Gln Ala Arg Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr Asn
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met Phe
    530                 535                 540
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Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Ala Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 456
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 456
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaaggcc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 457
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 457
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
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Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 458
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 458
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagcacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgctga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacggttc aggtcttttc ggactcggaa taccagctgc cctacgtcct cggctccgca 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

ctgactctga acaatggcag ccaatcggtg ggtcgttcct ctttctactg cctggaatat 1200

ttcccttctc aaatgctgag aacgggcaac aacttcacct tcagctacac cttcgaggac 1260

gttcccttcc acagcagcta cgcacacagc cagagcctgg accggctgat gaatcctctt 1320

atcgaccagt acctgtatta cctggccaga acacagagca acgcaggagg cacagctggc 1380

aatcgggaac tgcagtttta tcagggcggg cctaccacca tggccgaaca agccaaaaac 1440

tggctgcctg gaccttgctt ccggcaacaa agagtctcca agacgctgga tcaaaacaac 1500

aacagcaact ttgcttggac tggtgccacc aaataccatc taaatggaag aaattcattg 1560

gttaatcccg gtgtcgccat ggcaacccac aaggacgacg aggaacgctt cttcccttcg 1620

agcggagtcc tgatttttgg aaaaactgga gcagctaata agactacact ggaaaatgtg 1680

ttaatgacaa atgaagagga aattcgtcct accaacccgg tagccaccga ggaatacggg 1740

actgttagca gcaacctgca ggcggctaac actgcagccc agacacaagt tgtcaacaac 1800

cagggagcct tacctggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac tttcacccgt ctccgctgat gggcggcttt 1920

ggactgaagc atccgcctcc tcagatcctg atcaaaaaca ctcctgttcc tgctaatccc 1980

ccggaggtgt ttacgcctgc caagtttgct tctttcatca cacagtacag caccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cctccaattt tgacaaacag actggtgtgg actttgccgt tgacagccag 2160

ggtgtttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 459
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 459
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys His Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln
```

```
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ala Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu
    450                 455                 460

Gln Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn
465                 470                 475                 480

Trp Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu
                485                 490                 495

Asp Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr
            500                 505                 510

His Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala
        515                 520                 525

Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu
    530                 535                 540

Ile Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val
```

545 550 555 560

Leu Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr
565 570 575

Glu Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala
580 585 590

Ala Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 460

<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 460
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590
```

```
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 461
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 461

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Ser
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415
```

```
Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620
```

```
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
```

<210> 462
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 462

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445
```

```
Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

```
Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 463
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 463
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
```

```
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
```

485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
530 535 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
565 570 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser

690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 464
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 464
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacaa gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca gcaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 465
<211> 2217
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 465
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgcac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acttatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggcaac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acatgggcta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacgg caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 466
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 466
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Leu Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Asn Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Met Gly Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Gly Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 467
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 467
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccggaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

gtcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gagcccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 468
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 468
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile

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145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Gly Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
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        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
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565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Ser Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 469
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 469
atggttgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcagggc 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctta aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagctt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgcg ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gccagcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagccgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 470
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 470
Met Val Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Leu Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
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Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Gln Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
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Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670
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Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Pro Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 471
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 471
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa tagcctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactccca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgtcttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacttgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 472
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 472
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

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Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Ser Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
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Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Ser Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
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Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 473
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 473
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

```
Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Val His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Ser Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Pro Thr Arg
725 730 735

Asn Leu

<210> 474
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 474
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgtgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aattcgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc ccacccgtaa tctgtaa 2217

<210> 475
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 475
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
            500                 505                 510
```

```
Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690                 695                 700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705                 710                 715                 720
```

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 476
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 476
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct cttcaacatc 960

caagtcaagg aggtcacgac gaatgacggc gtcacgacca tcgctaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggagtac cagctgccgt acgtcctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctgaaca atggcagcca atcggtggga cgttcatcct tctactgcct ggaatacttc 1200

ccttctcagg tgctgagaac gggtaacaac ttcaccttca gttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctagacc ggctgatgaa tcccctcatc 1320

gaccagtacc tgtattacct ggctagaaca cagagtaacc caggaggcac atctggcaat 1380

cgggaactgc agttttacca gggcgggcct tccaccatgg ccgaacaagc caagaactgg 1440

ttacctggac cttgcttccg gcaacaaaga gtttccaaaa cactggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcattggtg 1560

aatcctggtg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca accaacaaga ctacattgga aaacgtgtta 1680

atgacaaatg aagaagaaat tcgtcctact aatcctgtgg ccacagaaga atacgggata 1740

gtcagcagca atttacaagc ggccaatact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaaaattc ctcacacaga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 477
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 477
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
```

```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Val Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ser Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640
```

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 478
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 478
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca cacggctggg cgacagagtc 720

atcaccacca gcacccggac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacgaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 479
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 479
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
```

325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
435 440 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
450 455 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Phe Arg Gln Arg Arg Val Ser Lys Thr Leu Asp
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile

```
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
```

<210> 480
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 480
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgtc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aaagcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tccgtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tttgggatct 600

actacaatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cttcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggcccagccc acctacaaca accacctcta caagcaaatc 780

tcaagccaat caggagcctc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcgggtcggc gcatcaagga 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtcccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcggt aggacgctct tccttttact gcctggagta ctttccttct 1200

cagatgcttc gtactggaaa caactttcag ttcagctaca cctttgaaga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gatcggctga tgaatcctct gatcgaccag 1320

tacctgtatt atctgaacaa aacacaatca aatagtggag ctcttcagca gtctcggcta 1380

ctgtttagtc aagctggacc caccagcatg tctcttcaag ctaaaaactg gctacctgga 1440

ccttgctaca gacagcagcg tctgtcaaag caggcaaacg acaacaacaa cagcaacttt 1500

ccctggactg cggctacaaa gtaccaccta aatggccggg actcgttggt taatccagga 1560

ccagctatgg ccagtcacaa agacgatgaa gaaaagtttt tccccatgca tggaaccctg 1620

atatttggta aacaaggaac aaatgctaac gacgcggatt tggacaatgt catgattaca 1680

gatgaagaag aaatccgcac caccaatccc gtggctacgg agcagtacgg atatgtgtca 1740

aataatttgc aaaactcaaa tactggtcca actactggaa ctgtcaatca ccgaggagcg 1800

ttacctggca tggtgtggca ggatcgagac gtgtacctgc agggacccat ttgggccaag 1860

attcctcaca ccgatggaca ctttcatcct tctccactga tgggaggttt tgggctcaaa 1920

cacccgcctc ctcagatcat gatcaaaaac actcccgttc cagccaatcc tcccacaaac 1980

ttcagttctg ccaagtttgc ttctttcatc acacagtatt ccacggggca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaagagaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaaatc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 481
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 481
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Gln Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Lys Thr
        435                 440                 445

Gln Ser Asn Ser Gly Ala Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Gly Thr Val Asn His Arg Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

```
His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 482
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 482
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac      240

cagcagctgc aggcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt      300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct      420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc      480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca      540
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gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgcg ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

acctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgcgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 483
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 483
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Thr Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
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```
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Ala Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 484
<211> 2217
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 484
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggccgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagctgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaagca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagtgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 485
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 485
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Cys Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 486
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 486
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Ser Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 487
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 487
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacga gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccctaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

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agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 488
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 488
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

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Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Pro Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 489
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 489
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcac 60

gagtggtggg acccgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacccaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaacg tctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgtcact tctcaccacg tgaccggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cggaaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc ctcagatcct gatcaaaaac actcctgttc ctgctaatcc cccggaggtg 1980

tttacgcctg ccaagtttgc ttctttcatc acacagtaca gcaccggcca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggagaac agcaagcgct ggaacccaga gattcagtat 2100

acctccaatt ttgacaaaca gactggtgtg gactttgccg ttgacagcca gggtgtttat 2160

tctgagcctc gccccattgg tactcgttac ctcacccgta atctgtaa 2208

<210> 490
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 490
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile His Glu Trp Trp Asp Pro Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr His Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn
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    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Glu Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
```

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            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Phe
    690                 695                 700

Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val Tyr
```

705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 491
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 491
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Pro Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
```

```
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Pro Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560
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Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asp Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Val Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 492
<211> 2217

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 492
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaagg ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgacccatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctaccc tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaagac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcaggtcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 493
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 493
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttc 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggctgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gagccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggctg acaataacaa gggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gggtgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atgacagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 494
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 494
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Ala Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Lys Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
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Gln Val Lys Glu Val Thr Thr Gly Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Asp Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
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His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
```

Leu

<210> 495
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 495
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgtgtg ggagctgcag aaggagaaca gcaagcgcag gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 496
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 496
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Arg Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 497
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 497
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 498
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 498
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285
```

```
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495
```

```
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700
```

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 499
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 499
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
```

```
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
```

```
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 500
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 500
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctagac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 501
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 501
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
```

```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270


Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380


Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415


Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430
```

```
Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Arg Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640
```

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 502
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 502
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accatgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcctccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccttca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

cgggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttt cacccgtctc cgctgatggg cggctttgga 1920

ctgaagcatc cgcctcctca gatcctgatc aaaaacactc ctgttcctgc taatcccccg 1980

gaggtgttta cgcctgccaa gtttgcttct ttcatcacac agtacagcac cggccaggtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatacct ccaattttga caaacagact ggtgtggact ttgccgttga cagccagggt 2160

gtttattctg agcctcgccc cattggtact cgttacctca cccgtaatct gtaa 2214

<210> 503
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 503
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560


Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
```

<210> 504
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 504
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

```
Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575
```

```
Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590


Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
```

<210> 505
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 505

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccacccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg tgatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcttcg ccccattggc actcgttacc tcacccgtaa tctgtaa 2217

<210> 506
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 506
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270
```

```
Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480
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Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Pro Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Val Ile Glu Trp Glu
        675                 680                 685
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Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Leu Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 507
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 507
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctagaaag agactgaact ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgcc ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggctttg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc agtcagcagg tagcaccaac gacaacgtct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggccc aagaagctca acttcaagct gttcaacatc 960

caggtcaagg aggtcacaac gaatgacggc gtcacgacca tcgccaataa ccttaccagc 1020

acggttcagg tcttttcgga ctcggaatac cagctgccct acgtcctcgg ctccgcacac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctg 1140

actctgaaca atggcagcca atcggtgggt cgttcctctt tctactgcct ggaatatttc 1200

ccttctcaaa tgctgagaac gggcaacaac ttcaccatca gctacacctt cgaggacgtt 1260

cccttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcctcttatc 1320

gaccagtacc tgtattacct ggccagaaca cagagcaacg caggaggcac agctggcaat 1380

caggaactgc agttttatca gggcgggcct accaccatgg ccgaacaagc caaaaactgg 1440

ctgcctggac cttgcttccg gcaacaaaga gtctccaaga cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa taccatctaa atggaagaaa ttcattggtt 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccttcgagc 1620

ggagtcctga tttttggaaa aactggagca gctaataaga ctacactgga aaatgtgtta 1680

atgacaaatg aagaggaaat tcgtcctacc aacccggtag ccaccgagga atacgggact 1740

gttagcagca acctgcaggc ggctaacact gcagcccaga cacaagttgt caacaaccag 1800

ggagccttac ctggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacaga tggcaacttt cacccgtctc ctttaatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctcatc aaaaacactc ctgttcctgc ggatcctcca 1980

acagcgttca accaggccaa gctgaattct ttcatcacgc agtacagcac cggacaagtc 2040

agcgtggaga tcgagtggga gctgcagaag gagaacagca agcgctggaa cccagagatt 2100

cagtatactt ccaactacta caaatctaca aatgtggact ttgctgttaa tactgagggt 2160

gtttactctg agcctcgccc cattggcact cgttacctca cccgtaatct gtaa 2214

<210> 508

<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 508
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

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Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Val Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
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Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Ile Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Gln Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Thr Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590
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Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu
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<210> 509
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 509

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tagtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccgcctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gatgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aacttttcct tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc cagaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga gcggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aaccaacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacagcgt tcaaccaggc caagctgaat tcttccatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tttgtaa 2217

<210> 510
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 510
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp

65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Ala Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn

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        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
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485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Ser Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Ser
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr

690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 511
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 511
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
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Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
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Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
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<210> 512
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 512
atggctgctg acggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccc aagcccaagg ccaaccagca gaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccggtaga accgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactgaact ttggtcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atatccaatg ggacatcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg ccaaaaagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtatttac ggactcggaa taccagctgc cgtacgtcct cggctccgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcccca gtacggctac 1140

cttacactga acaatggaag tcaagccgta ggccgttcct ccttctactg cctggaatat 1200

tttccatctc aaatgctgcg aactggaaac aattttgaat tcagctacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcacacagc cagagcttgg accgactgat gaatcctctc 1320

atcgaccagt acctgtacta cttatccaga actcagtcca caggaggaac tcaaggtacc 1380

cagcaattgt tattttctca agctgggcct gcaaacatgt cggctcaggc taagaactgg 1440

ctacctggac cttgctaccg gcagcagcga gtctctacga cactgtcgca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggaagaga ctctttggta 1560

aatcccggtg tcgccatggc aacccacaag gacgacgagg aacgcttctt cccgtcgagt 1620

ggagtcctga tgtttggaaa acagggtgct ggaagagaca atgtggacta cagcagcgtt 1680

atgctaacca gcgaagaaga aattaaaacc actaaccctg tagccacaga acaatacggt 1740

gtggtggctg acaacttgca gcaaaccaat acagggccta ttgtgggaaa tgtcaacagc 1800

caaggagcct tacctggcat ggtctggcag aaccgagacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccaccctt caccgctaat gggaggattt 1920

ggactgaagc acccacctcc tcagatcctg atcaagaaca cgccggtacc tgcggatcct 1980

ccaacaacgt tcagccaggc gaaattggct tccttcatta cgcagtacag caccggacag 2040

gtcagcgtgg aaatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttcaaacta ctacaaatct acaaatgtgg actttgctgt caatacagag 2160

ggaacttatt ctgagcctcg ccccattggt actcgttacc tcacccgtaa tctgtaa 2217

<210> 513
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 513
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu

```
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Arg Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
```

645 650 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 514
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 514
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Leu Asn Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Asp Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Gly
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Lys Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

Gly Lys Lys Ser Pro His Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Glu Ala Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ser Asp Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Gln Gly Thr Asn Ala Thr Val Gln Gly Ala Lys Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Asn Met Arg Asp Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met Asn Gly Thr Leu Val Phe Gly
    530                 535                 540

Lys Asn Gly Ala Gly Asn Ser Asn Val Asp Ile Glu Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Val Val Ser Asp Asn Leu Gln Ser Ser Asn Thr Arg Pro Ile
            580                 585                 590

Thr Gly Asp Val Asp Ser Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Thr Pro Gly Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 515
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 515
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 516
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 516
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

```
Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 517
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 517
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
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            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
```

625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 518
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 518
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270
```

```
Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Arg Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 519
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 519
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525
```

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Asp Asp Glu Asp Ala Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 520
<211> 1803
<212> DNA
<213> Bovine Adeno-associated Virus

<400> 520
acggcgcctg cggcaaaaaa gaggcctcta gagcagagtc ctcaagagcc agactcctcg 60

agcggagttg gcaagaaagg caaacagcct gccagaaaga gactcaactt tgacgacgaa 120

cctggagccg gagacgggcc tcccccagaa ggaccatctt ccggagctat gtctactgag 180

actgaaatgc gtgcagcagc tggcggaaat ggtggcgatg cgggacaagg tgccgaggga 240

gtgggtaatg cctccggtga ttggcattgc gattccactt ggtcagagag ccacgtcacc 300

accacctcaa cccgcacctg ggtcctgccg acctacaaca accacctgta cctgcggctc 360

ggctcgagca acgccagcga caccttcaac ggattctcca ccccctgggg atactttgac 420

tttaaccgct tccactgcca cttctcgcca agagactggc aaaggctcat caacaaccac 480

tggggactgc gccccaaaag catgcaagtc cgcatcttca acatccaagt taaggaggtc 540

acgacgtcta acggggagac gaccgtatcc aacaacctca ccagcacggt ccagatcttt 600

gcggacagca cgtacgagct cccgtacgtg atggatgcag gtcaggaggg cagcttgcct 660

cctttcccca acgacgtgtt catggtgcct cagtacgggt actgcggact ggtaaccgga 720

ggcagctctc aaaaccagac agacagaaat gccttctact gtctggagta ctttcccagc 780

cagatgctga gaaccggaaa caactttgag atggtgtaca agtttgaaaa cgtgcccttc 840

cactccatgt acgctcacag ccagagcctg gataggctga tgaacccgct gctggaccag 900

tacctgtggg agctccagtc taccacctct ggaggaactc tcaaccaggg caattcagcc 960

accaactttg ccaagctgac caaaacaaac ttttctggct accgcaaaaa ctggctcccg 1020

gggcccatga tgaagcagca gagattctcc aagactgcca gtcaaaacta caagattccc 1080

cagggaagaa acaacagtct gctccattat gagaccagaa ctaccctcga cggaagatgg 1140

agcaattttg ccccgggaac ggccatggca accgcagcca acgacgccac cgacttctct 1200

caggcccagc tcatctttgc ggggcccaac atcaccggca acaccaccac agatgccaat 1260

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gacggagtcg gcgtgtaccc gggaatggtg tggcaggaca gagacattta ctaccaaggg 1440

cccatttggg ccaaaattcc acacacggat ggacactttc acccgtctcc tctcattggc 1500

ggatttggac tgaaaagccc gcctccacaa atattcatca aaaacactcc tgtacccgcc 1560

aatcccgcaa cgaccttctc tccggccaga atcaacagct tcatcaccca gtacagcacc 1620

ggacaggtgg ctgtcaaaat agaatgggaa atccagaagg agcggtccaa gagatggaac 1680

ccagaggtcc agttcacgtc caactacgga gcacaggact cgcttctctg ggctcccgac 1740

aacgccggag cctacaaaga gcccagggcc attggatccc gatacctcac caaccacctc 1800

tag 1803

<210> 521
<211> 1617
<212> DNA
<213> Bovine Adeno-associated Virus

<400> 521
atgcgtgcag cagctggcgg aaatggtggc gatgcgggac aaggtgccga gggagtgggt 60

aatgcctccg gtgattggca ttgcgattcc acttggtcag agagccacgt caccaccacc 120

tcaacccgca cctgggtcct gccgacctac aacaaccacc tgtacctgcg gctcggctcg 180

agcaacgcca gcgacacctt caacggattc tccacccccct ggggatactt tgactttaac 240

cgcttccact gccacttctc gccaagagac tggcaaaggc tcatcaacaa ccactgggga 300

ctgcgcccca aaagcatgca agtccgcatc ttcaacatcc aagttaagga ggtcacgacg 360

tctaacgggg agacgaccgt atccaacaac ctcaccagca cggtccagat ctttgcggac 420

agcacgtacg agctcccgta cgtgatggat gcaggtcagg agggcagctt gcctcctttc 480

cccaacgacg tgttcatggt gcctcagtac gggtactgcg gactggtaac cggaggcagc 540

tctcaaaacc agacagacag aaatgccttc tactgtctgg agtactttcc cagccagatg 600

ctgagaaccg gaaacaactt tgagatggtg tacaagtttg aaaacgtgcc cttccactcc 660

atgtacgctc acagccagag cctggatagg ctgatgaacc cgctgctgga ccagtacctg 720

tgggagctcc agtctaccac ctctggagga actctcaacc agggcaattc agccaccaac 780

tttgccaagc tgaccaaaac aaacttttct ggctaccgca aaaactggct cccggggccc 840

atgatgaagc agcagagatt ctccaagact gccagtcaaa actacaagat tccccaggga 900

agaaacaaca gtctgctcca ttatgagacc agaactaccc tcgacggaag atggagcaat 960

tttgccccgg gaacggccat ggcaaccgca gccaacgacg ccaccgactt ctctcaggcc 1020

cagctcatct ttgcggggcc caacatcacc ggcaacacca ccacagatgc caataacctg 1080

atgttcactt cagaagatga acttagggcc accaaccccc gggacactga cctgtttggc 1140

cacctggcaa ccaaccagca aaacgccacc accgttccta ccgtagacga cgtggacgga 1200

gtcggcgtgt acccgggaat ggtgtggcag gacagagaca tttactacca agggcccatt 1260

tgggccaaaa ttccacacac ggatggacac tttcacccgt ctcctctcat tggcggattt 1320

ggactgaaaa gcccgcctcc acaaatattc atcaaaaaca ctcctgtacc cgccaatccc 1380

gcaacgacct tctctccggc cagaatcaac agcttcatca cccagtacag caccggacag 1440

gtggctgtca aaatagaatg ggaaatccag aaggagcggt ccaagagatg gaacccagag 1500

gtccagttca cgtccaacta cggagcacag gactcgcttc tctgggctcc cgacaacgcc 1560

ggagcctaca aagagcccag ggccattgga tcccgatacc tcaccaacca cctctag 1617

<210> 522
<211> 1173
<212> DNA
<213> Bovine Adeno-associated Virus

<400> 522
atggcgctgg taagctggct ggtggaacat ggcatcactt ccgagaagca gtggattcag 60

gagaatcagg agagctacct gtccttcaac tccacgggaa actctcggag ccagattaaa 120

gccgcgcttg acaacgcgtc aaaaattatg agtctgacca aatctgcctc agactatctc 180

gtgggacaga ctgttccaga ggacatttct gaaaacagaa tctggcagat ttttgatctc 240

aacggctacg acccggcata cgcgggctct gttctctacg gctggtgcac tcgcgccttt 300

ggaaagagga acaccgtctg gctgtatgga cccgcgacca ccggaaagac caacatcgcg 360

gaagccatct ctcacaccgt gccctttttat ggctgtgtga actggactaa tgagaacttt 420

ccctttaatg actgtgtgga aaaaatgttg atctggtggg aggagggaaa gatgaccagc 480

aaggtggtgg aacccgccaa ggccatcttg ggggggtcta gagtacgagt ggatcaaaaa 540

tgtaaatcct ctgtacaagt agactctacc ccggtgatta tcacctccaa tactaacatg 600

tgtgtggtgg tggatgggaa ctccacgacc tttgaacacc agcagccgct ggaagaccgc 660

atgttcagat ttgaactcat gcggcggctc ccgccagatt ttggcaagat taccaagcag 720

gaagtcaaag actttttttgc ttgggcaaag gtcaaccagg tgccggtgac tcacgagttt 780

atggttccca agaaagtggc gggaactgag agggcggaga cttctagaaa acgcccactg 840

gatgacgtca ccaataccaa ctataaaagt ccggagaagc gggcccggct ctcagttgtt 900

cctgagacgc ctcgcagttc agacgtgcct gtagagcccg ctcctctgcg acctctcaac 960

tggtcttcca ggtatgaatg cagatgtgac tatcatgcta aatttgactc tgtaacgggg 1020

gaatgtgacg agtgtgaata tttgaatcgg ggcaaaaatg gctgtatctt tcataatgct 1080

acacattgtc aaatttgtca cgctgttcct ccatgggaaa aggaaaatgt gtcagatttt 1140

aatgattttg atgactgtaa taaagagcag taa 1173

<210> 523
<211> 1833
<212> DNA
<213> Bovine Adeno-associated Virus

<400> 523
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ggaatttctg acaactttgt agactgggta actggtcaaa tttgggagct gcctcccgag 120

tcagatttga atttgactct gattgagcag cctcagctga cggtggctga cagaattcgc 180

cgcgtgttcc tgtacgagtg gaacaaattt tccaagcagg agagcaaatt ctttgtgcag 240

tttgaaaagg gatctgaata ttttcatctg cacacgctcg tggagacctc cggcatctct 300

tctatggtcc ttggccgcta cgtgagtcag attcgcgccc agctggtgaa ggtggtgttc 360

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gccaataagg tggtggattc tgggtatatt cccgcctacc tgctgccgaa ggtccaacca 480

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gagcgcaaac ggctcgtcgc tcagtttcag cttgagtcct cgcagcgctc gcaagaggca 600

tcttcccaga gggacgtttc ggctgacccg gtcatcaaga gcaagacttc ccagaaatac 660

atggcgctgg taagctggct ggtggaacat ggcatcactt ccgagaagca gtggattcag 720

gagaatcagg agagctacct gtccttcaac tccacgggaa actctcggag ccagattaaa 780

gccgcgcttg acaacgcgtc aaaaattatg agtctgacca aatctgcctc agactatctc 840

gtgggacaga ctgttccaga ggacatttct gaaaacagaa tctggcagat ttttgatctc 900

aacggctacg acccggcata cgcgggctct gttctctacg gctggtgcac tcgcgccttt 960

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gaagccatct ctcacaccgt gccctttttat ggctgtgtga actggactaa tgagaacttt 1080

ccctttaatg actgtgtgga aaaaatgttg atctggtggg aggagggaaa gatgaccagc 1140

aaggtggtgg aacccgccaa ggccatcttg ggggggtcta gagtacgagt ggatcaaaaa 1200

tgtaaatcct ctgtacaagt agactctacc ccggtgatta tcacctccaa tactaacatg 1260

tgtgtggtgg tggatgggaa ctccacgacc tttgaacacc agcagccgct ggaagaccgc 1320

atgttcagat ttgaactcat gcggcggctc ccgccagatt ttggcaagat taccaagcag 1380

gaagtcaaag actttttgc ttgggcaaag gtcaaccagg tgccggtgac tcacgagttt 1440

atggttccca agaaagtggc gggaactgag agggcggaga cttctagaaa acgcccactg 1500

gatgacgtca ccaataccaa ctataaaagt ccggagaagc gggcccggct ctcagttgtt 1560

cctgagacgc ctcgcagttc agacgtgcct gtagagcccg ctcctctgcg acctctcaac 1620

tggtcttcca ggtatgaatg cagatgtgac tatcatgcta aatttgactc tgtaacgggg 1680

gaatgtgacg agtgtgaata tttgaatcgg ggcaaaaatg gctgtatctt tcataatgct 1740

acacattgtc aaatttgtca cgctgttcct ccatgggaaa aggaaaatgt gtcagatttt 1800

aatgattttg atgactgtaa taaagagcag taa 1833

<210> 524
<211> 2211
<212> DNA
<213> Bovine Adeno-associated Virus

<400> 524
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gctcgaggtc ttgtgcttcc tgggtacaag tatcttggtc ctgggaacgg ccttgataag 180

ggcgatcctg tcaattttgc tgacgaggtt gcccgagagc acgacctctc ctaccagaaa 240

cagcttgagg cgggcgataa cccttacctc aagtacaacc acgcggacgc agagtttcag 300

gagaaactcg cttctgacac ttcttttggg ggaaaccttg ggaaggctgt tttccaggct 360

aaaaagagga ttctcgaacc tcttggcctg gttgagacgc cggataaaac ggcgcctgcg 420

gcaaaaaaga ggcctctaga gcagagtcct caagagccag actcctcgag cggagttggc 480

aagaaaggca aacagcctgc cagaaagaga ctcaactttg acgacgaacc tggagccgga 540

gacgggcctc ccccagaagg accatcttcc ggagctatgt ctactgagac tgaaatgcgt 600

gcagcagctg gcggaaatgg tggcgatgcg ggacaaggtg ccgagggagt gggtaatgcc 660

tccggtgatt ggcattgcga ttccacttgg tcagagagcc acgtcaccac cacctcaacc 720

cgcacctggg tcctgccgac ctacaacaac cacctgtacc tgcggctcgg ctcgagcaac 780

gccagcgaca ccttcaacgg attctccacc ccctggggat actttgactt taaccgcttc 840

cactgccact tctcgccaag agactggcaa aggctcatca acaaccactg gggactgcgc 900

cccaaaagca tgcaagtccg catcttcaac atccaagtta aggaggtcac gacgtctaac 960

ggggagacga ccgtatccaa caacctcacc agcacggtcc agatctttgc ggacagcacg 1020

tacgagctcc cgtacgtgat ggatgcaggt caggagggca gcttgcctcc tttccccaac 1080

gacgtgttca tggtgcctca gtacgggtac tgcggactgg taaccggagg cagctctcaa 1140

aaccagacag acagaaatgc cttctactgt ctggagtact ttcccagcca gatgctgaga 1200

accggaaaca actttgagat ggtgtacaag tttgaaaacg tgcccttcca ctccatgtac 1260

gctcacagcc agagcctgga taggctgatg aacccgctgc tggaccagta cctgtgggag 1320

ctccagtcta ccacctctgg aggaactctc aaccagggca attcagccac caactttgcc 1380

aagctgacca aaacaaactt ttctggctac cgcaaaaact ggctcccggg gcccatgatg 1440

aagcagcaga gattctccaa gactgccagt caaaactaca agattcccca gggaagaaac 1500

aacagtctgc tccattatga gaccagaact accctcgacg gaagatggag caattttgcc 1560

ccgggaacgg ccatggcaac cgcagccaac gacgccaccg acttctctca ggcccagctc 1620

atctttgcgg ggcccaacat caccggcaac accaccacag atgccaataa cctgatgttc 1680

acttcagaag atgaacttag ggccaccaac ccccgggaca ctgacctgtt tggccacctg 1740

gcaaccaacc agcaaaacgc caccaccgtt cctaccgtag acgacgtgga cggagtcggc 1800

gtgtacccgg gaatggtgtg gcaggacaga gacatttact accaagggcc catttgggcc 1860

aaaattccac acacggatgg acactttcac ccgtctcctc tcattggcgg atttggactg 1920

aaaagcccgc ctccacaaat attcatcaaa aacactcctg tacccgccaa tcccgcaacg 1980

accttctctc cggccagaat caacagcttc atcacccagt acagcaccgg acaggtggct 2040

gtcaaaatag aatgggaaat ccagaaggag cggtccaaga gatggaaccc agaggtccag 2100

ttcacgtcca actacggagc acaggactcg cttctctggg ctcccgacaa cgccggagcc 2160

tacaaagagc ccagggccat tggatcccga tacctcacca accacctcta g 2211

<210> 525
<211> 4694
<212> DNA
<213> Bovine Adeno-associated Virus

<400> 525
gtggcactcc ccccccctgtc gcgttcgctc gttcgctggc tcgattgggg gggtggcagc 60

tcaaagagct gccagacgac ggccctctgg gccgtcgccc ccccaatcga gccagcgaac 120

gagcgaacgc gacaggggggg ggagtgccac actctctagc aaggggggttt tgtaggtggt 180

gatgtcattg ttgatgtcat tatagttgtc acgcgatagt taatgattaa cagtcatgtg 240

atgtgtgtta tccaatagga tgaaagcgcg cgaatgagat ctcgcgagac ttccggggta 300

taaaaggggt gagtgaacga gcccgccgcc attctctgct ctggactgct agaggaccct 360

cgctgccatg gctaccttct atgaagtcat tgttcgcgtt ccatttgatg tggaagagca 420

cctgcctgga atttctgaca actttgtaga ctgggtaact ggtcaaattt gggagctgcc 480

tcccgagtca gatttgaatt tgactctgat tgagcagcct cagctgacgg tggctgacag 540

aattcgccgc gtgttcctgt acgagtggaa caaattttcc aagcaggaga gcaaattctt 600

tgtgcagttt gaaaagggat ctgaatattt tcatctgcac acgctcgtgg agacctccgg 660

catctcttct atggtccttg gccgctacgt gagtcagatt cgcgcccagc tggtgaaggt 720

ggtgttccag aacattgagc cgcggattaa cgactgggtc gccatcacca aggtaaagaa 780

gggcggagcc aataaggtgg tggattctgg gtatattccc gcctacctgc tgccgaaggt 840

ccaaccagag cttcagtggg cgtggactaa cctcgaagag tataaattgg ccgccctcaa 900

tctggaggag cgcaaacggc tcgtcgctca gtttcagctt gagtcctcgc agcgctcgca 960

agaggcatct tcccagaggg acgtttcggc tgacccggtc atcaagagca agacttccca 1020

gaaatacatg gcgctggtaa gctggctggt ggaacatggc atcacttccg agaagcagtg 1080

gattcaggag aatcaggaga gctacctgtc cttcaactcc acgggaaact ctcggagcca 1140

gattaaagcc gcgcttgaca acgcgtcaaa aattatgagt ctgaccaaat ctgcctcaga 1200

ctatctcgtg ggacagactg ttccagagga catttctgaa aacagaatct ggcagatttt 1260

tgatctcaac ggctacgacc cggcatacgc gggctctgtt ctctacggct ggtgcactcg 1320

cgcctttgga aagaggaaca ccgtctggct gtatggaccc gcgaccaccg gaaagaccaa 1380

catcgcggaa gccatctctc acaccgtgcc cttttatggc tgtgtgaact ggactaatga 1440

gaactttccc tttaatgact gtgtggaaaa aatgttgatc tggtgggagg agggaaagat 1500

gaccagcaag gtggtggaac ccgccaaggc catcttgggg gggtctagag tacgagtgga 1560

tcaaaaatgt aaatcctctg tacaagtaga ctctaccccg gtgattatca cctccaatac 1620

taacatgtgt gtggtggtgg atgggaactc cacgaccttt gaacaccagc agccgctgga 1680

agaccgcatg ttcagatttg aactcatgcg gcggctcccg ccagattttg gcaagattac 1740

caagcaggaa gtcaaagact tttttgcttg ggcaaaggtc aaccaggtgc cggtgactca 1800

cgagtttatg gttcccaaga aagtggcggg aactgagagg gcggagactt ctagaaaacg 1860

cccactggat gacgtcacca ataccaacta taaaagtccg gagaagcggg cccggctctc 1920

agttgttcct gagacgcctc gcagttcaga cgtgcctgta gagcccgctc ctctgcgacc 1980

tctcaactgg tcttccaggt atgaatgcag atgtgactat catgctaaat ttgactctgt 2040

aacgggggaa tgtgacgagt gtgaatattt gaatcggggc aaaaatggct gtatctttca 2100

taatgctaca cattgtcaaa tttgtcacgc tgttcctcca tgggaaaagg aaaatgtgtc 2160

agattttaat gattttgatg actgtaataa agagcagtaa ataaagtgag tagtcatgtc 2220

ttttgttgac caccctccag attggttgga atcgatcggc gacggctttc gtgaatttct 2280

cggccttgag gcgggtcccc cgaaacccaa ggccaatcaa cagaagcaag ataacgctcg 2340

aggtcttgtg cttcctgggt acaagtatct tggtcctggg aacggccttg ataagggcga 2400

tcctgtcaat tttgctgacg aggttgcccg agagcacgac ctctcctacc agaaacagct 2460

tgaggcgggc gataaccctt acctcaagta caaccacgcg gacgcagagt ttcaggagaa 2520

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gaggattctc gaacctcttg gcctggttga gacgccggat aaaacggcgc ctgcggcaaa 2640

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aggcaaacag cctgccagaa agagactcaa ctttgacgac gaacctggag ccggagacgg 2760

gcctccccca gaaggaccat cttccggagc tatgtctact gagactgaaa tgcgtgcagc 2820

agctggcgga aatggtggcg atgcgggaca aggtgccgag ggagtgggta atgcctccgg 2880

tgattggcat tgcgattcca cttggtcaga gagccacgtc accaccacct caacccgcac 2940

ctgggtcctg ccgacctaca acaaccacct gtacctgcgg ctcggctcga gcaacgccag 3000

cgacaccttc aacggattct ccacccccctg gggatacttt gactttaacc gcttccactg 3060

ccacttctcg ccaagagact ggcaaaggct catcaacaac cactggggac tgcgccccaa 3120

aagcatgcaa gtccgcatct tcaacatcca agttaaggag gtcacgacgt ctaacgggga 3180

gacgaccgta tccaacaacc tcaccagcac ggtccagatc tttgcggaca gcacgtacga 3240

gctcccgtac gtgatggatg caggtcagga gggcagcttg cctcctttcc ccaacgacgt 3300

gttcatggtg cctcagtacg ggtactgcgg actggtaacc ggaggcagct ctcaaaacca 3360

gacagacaga aatgccttct actgtctgga gtactttccc agccagatgc tgagaaccgg 3420

aaacaacttt gagatggtgt acaagtttga aaacgtgccc ttccactcca tgtacgctca 3480

cagccagagc ctggataggc tgatgaaccc gctgctggac cagtacctgt gggagctcca 3540

gtctaccacc tctggaggaa ctctcaacca gggcaattca gccaccaact ttgccaagct 3600

gaccaaaaca aacttttctg gctaccgcaa aaactggctc ccggggccca tgatgaagca 3660

gcagagattc tccaagactg ccagtcaaaa ctacaagatt ccccagggaa gaaacaacag 3720

tctgctccat tatgagacca gaactaccct cgacggaaga tggagcaatt ttgccccggg 3780

aacggccatg gcaaccgcag ccaacgacgc caccgacttc tctcaggccc agctcatctt 3840

tgcggggccc aacatcaccg gcaacaccac cacagatgcc aataacctga tgttcacttc 3900

agaagatgaa cttagggcca ccaacccccg ggacactgac ctgtttggcc acctggcaac 3960

caaccagcaa aacgccacca ccgttcctac cgtagacgac gtggacggag tcggcgtgta 4020

cccgggaatg gtgtggcagg acagagacat ttactaccaa gggcccattt gggccaaaat 4080

tccacacacg gatggacact ttcacccgtc tcctctcatt ggcggatttg gactgaaaag 4140

cccgcctcca caaatattca tcaaaaacac tcctgtaccc gccaatcccg caacgacctt 4200

ctctccggcc agaatcaaca gcttcatcac ccagtacagc accggacagg tggctgtcaa 4260

aatagaatgg gaaatccaga aggagcggtc caagagatgg aacccagagg tccagttcac 4320

gtccaactac ggagcacagg actcgcttct ctgggctccc gacaacgccg gagcctacaa 4380

agagcccagg gccattggat cccgatacct caccaaccac ctctagccca attctgttgc 4440

ataccctcaa taaaccgtgt attcgtttca gtaaaatact gcctcttgtg gtcattcggc 4500

gtacaacagc ttacaacaac aacaaaaccc ccttgctaga gagtgtggca ctccccccc 4560

tgtcgcgttc gctcgttcgc tggctcgatt gggggggtgg cagctcaaag agctgccaga 4620

cgacggccct ctgggccgtc gccccccaa tcgagccagc gaacgagcga acgcgacagg 4680

gggggagtg ccac 4694

<210> 526
<211> 390
<212> PRT
<213> Bovine Adeno-associated Virus

<400> 526
Met Ala Leu Val Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
1 5 10 15

Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
20 25 30

Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
35 40 45

Ile Met Ser Leu Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr
50 55 60

Val Pro Glu Asp Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu
65 70 75 80

Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys

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                85                  90                  95

Thr Arg Ala Phe Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

Cys Val Glu Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser
145                 150                 155                 160

Lys Val Val Glu Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val
            180                 185                 190

Ile Ile Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe
    210                 215                 220

Glu Leu Met Arg Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225                 230                 235                 240

Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
                245                 250                 255

Thr His Glu Phe Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala
            260                 265                 270

Glu Thr Ser Arg Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr
        275                 280                 285

Lys Ser Pro Glu Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro
```

290 295 300

Arg Ser Ser Asp Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn
305 310 315 320

Trp Ser Ser Arg Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp
325 330 335

Ser Val Thr Gly Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
340 345 350

Asn Gly Cys Ile Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala
355 360 365

Val Pro Pro Trp Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp
370 375 380

Asp Cys Asn Lys Glu Gln
385 390

<210> 527
<211> 610
<212> PRT
<213> Bovine Adeno-associated Virus

<400> 527
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Asn Phe Val Asp Trp Val Thr Gly
20 25 30

Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Ile
35 40 45

Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
50 55 60

Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65 70 75 80

```
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95

Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110

Ala Gln Leu Val Lys Val Val Phe Gln Asn Ile Glu Pro Arg Ile Asn
        115                 120                 125

Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140

Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160

Glu Leu Gln Trp Ala Trp Thr Asn Leu Glu Glu Tyr Lys Leu Ala Ala
                165                 170                 175

Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Gln Leu Glu
            180                 185                 190

Ser Ser Gln Arg Ser Gln Glu Ala Ser Ser Gln Arg Asp Val Ser Ala
        195                 200                 205

Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210                 215                 220

Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225                 230                 235                 240

Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245                 250                 255

Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys Ile Met Ser Leu
            260                 265                 270

Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr Val Pro Glu Asp
        275                 280                 285
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Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu Asn Gly Tyr Asp
    290                 295                 300

Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys Thr Arg Ala Phe
305                 310                 315                 320

Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325                 330                 335

Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro Phe Tyr Gly Cys
            340                 345                 350

Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Glu Lys
        355                 360                 365

Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser Lys Val Val Glu
    370                 375                 380

Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg Val Asp Gln Lys
385                 390                 395                 400

Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val Ile Ile Thr Ser
                405                 410                 415

Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
            420                 425                 430

His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe Glu Leu Met Arg
        435                 440                 445

Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
    450                 455                 460

Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465                 470                 475                 480

Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala Glu Thr Ser Arg
                485                 490                 495
```

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Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr Lys Ser Pro Glu
            500                 505                 510

Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro Arg Ser Ser Asp
        515                 520                 525

Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn Trp Ser Ser Arg
    530                 535                 540

Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp Ser Val Thr Gly
545                 550                 555                 560

Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
                565                 570                 575

Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala Val Pro Pro Trp
            580                 585                 590

Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp Asp Cys Asn Lys
        595                 600                 605

Glu Gln
    610


<210> 528
<211> 538
<212> PRT
<213> Bovine Adeno-associated Virus

<400> 528
Met Arg Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala
1               5                   10                  15

Glu Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
            20                  25                  30

Ser Glu Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro
        35                  40                  45

Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser
```

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    50                  55                  60

Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
65                  70                  75                  80

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
                85                  90                  95

Asn His Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn
            100                 105                 110

Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser
        115                 120                 125

Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu
    130                 135                 140

Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe
145                 150                 155                 160

Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val
                165                 170                 175

Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys
            180                 185                 190

Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu
        195                 200                 205

Met Val Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His
    210                 215                 220

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu
225                 230                 235                 240

Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn
                245                 250                 255

Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys Thr Asn Phe Ser Gly Tyr
```

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            260                 265                 270

Arg Lys Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser
        275                 280                 285

Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser
    290                 295                 300

Leu Leu His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn
305                 310                 315                 320

Phe Ala Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp
                325                 330                 335

Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly Pro Asn Ile Thr Gly Asn
            340                 345                 350

Thr Thr Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu
        355                 360                 365

Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr
    370                 375                 380

Asn Gln Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly
385                 390                 395                 400

Val Gly Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr
                405                 410                 415

Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His
            420                 425                 430

Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln
        435                 440                 445

Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe
    450                 455                 460

Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln
```

465 470 475 480

Val Ala Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg
485 490 495

Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser
500 505 510

Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala
515 520 525

Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
530 535

<210> 529
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 529
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1 5 10 15

Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
50 55 60

Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

```
Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
    130                 135                 140

Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205

Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255

Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285

Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300
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Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320

Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val His Ile Phe
                325                 330                 335

Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350

Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365

Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445

Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Asn
    450                 455                 460

Lys Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480

Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495

Gln Gly Gly Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510
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Asp Arg Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525

Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540

Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560

Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575

Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590

Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705                 710                 715                 720
```

Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730 735

<210> 530
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 530
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1 5 10 15

Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
50 55 60

Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
130 135 140

```
Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205

Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220

His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255

Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285

Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300

Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320

Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
                325                 330                 335

Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350
```

```
Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365

Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445

Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
    450                 455                 460

Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480

Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495

Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510

Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525

Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540

Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560
```

```
Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575

Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590

Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705                 710                 715                 720

Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730                 735
```

<210> 531
<211> 736
<212> PRT
<213> Bovine Adeno-associated Virus

<400> 531

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
```

```
1               5                   10                  15

Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
    50                  55                  60

Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
    130                 135                 140

Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175

Pro Gly Ala Gly Asp Gly Pro Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190

Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205

Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
```

```
    210                 215                 220

His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240

Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255

Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275                 280                 285

Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290                 295                 300

Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305                 310                 315                 320

Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
                325                 330                 335

Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
            340                 345                 350

Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355                 360                 365

Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370                 375                 380

Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385                 390                 395                 400

Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
                405                 410                 415

His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
```

```
            420                 425                 430

Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435                 440                 445

Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
    450                 455                 460

Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465                 470                 475                 480

Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
                485                 490                 495

Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
            500                 505                 510

Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515                 520                 525

Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530                 535                 540

Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545                 550                 555                 560

Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
                565                 570                 575

Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
            580                 585                 590

Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
```

625 630 635 640

Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
675 680 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
690 695 700

Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705 710 715 720

Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730 735

<210> 532
<211> 600
<212> PRT
<213> Bovine Adeno-associated Virus

<400> 532
Thr Ala Pro Ala Ala Lys Lys Arg Pro Leu Glu Gln Ser Pro Gln Glu
1 5 10 15

Pro Asp Ser Ser Ser Gly Val Gly Lys Lys Gly Lys Gln Pro Ala Arg
20 25 30

Lys Arg Leu Asn Phe Asp Asp Glu Pro Gly Ala Gly Asp Gly Pro Pro
35 40 45

Pro Glu Gly Pro Ser Ser Gly Ala Met Ser Thr Glu Thr Glu Met Arg
50 55 60

Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala Glu Gly
65 70 75 80

```
Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu
                85                  90                  95

Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr
            100                 105                 110

Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser Asp Thr
        115                 120                 125

Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
    130                 135                 140

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn His
145                 150                 155                 160

Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn Ile Gln
                165                 170                 175

Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser Asn Asn
            180                 185                 190

Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro
        195                 200                 205

Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe Pro Asn
    210                 215                 220

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val Thr Gly
225                 230                 235                 240

Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu
                245                 250                 255

Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Met Val
            260                 265                 270

Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His Ser Gln
        275                 280                 285
```

```
Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp Glu
    290                 295                 300

Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn Ser Ala
305                 310                 315                 320

Thr Asn Phe Ala Lys Leu Thr Lys Thr Asn Phe Ser Gly Tyr Arg Lys
                325                 330                 335

Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser Lys Thr
            340                 345                 350

Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser Leu Leu
        355                 360                 365

His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn Phe Ala
    370                 375                 380

Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp Phe Ser
385                 390                 395                 400

Gln Ala Gln Leu Ile Phe Ala Gly Pro Asn Ile Thr Gly Asn Thr Thr
                405                 410                 415

Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu Arg Ala
            420                 425                 430

Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr Asn Gln
        435                 440                 445

Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly Val Gly
    450                 455                 460

Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr Gln Gly
465                 470                 475                 480

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser
                485                 490                 495
```

```
Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln Ile Phe
            500                 505                 510


Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Pro
        515                 520                 525


Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala
    530                 535                 540


Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn
545                 550                 555                 560


Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser Leu Leu
                565                 570                 575


Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala Ile Gly
            580                 585                 590


Ser Arg Tyr Leu Thr Asn His Leu
        595                 600


<210> 533
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 533
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga       60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac      120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac      180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac      240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt      300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag      360
```

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ttggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 534
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 534
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540
```

```
Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 535
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 535
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

```
Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 536
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 536
```

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Glu Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 537
<211> 2181
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 537
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcacaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgcacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact attggggctt cagaccccgg 900

tctctcagag tcaaaatctt caacatccaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccaa 1020

ctcccgtacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc cccgcaggtc 1080

tttacgctgc cgcagtacgg ctacgcgacg ctgaaccgag acaacggaga caacccgaca 1140

gagcggagca gcttcttttg cctagagtac tttcccagca agatgctgag gacgggcaac 1200

aactttgagt ttacctacag ctttgaagag gtgcccttcc actgcagctt cgccccgagc 1260

cagaacctct ttaagctggc caacccgctg gtggaccagt acctgtaccg cttcgtgagc 1320

acctcggcca cgggcgccat ccagttccaa aagaacctgg cgggcagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacac gagctctggg 1440

gtcagcagca ccaacagagt cagcgtcaac aacttttccg tctcaaaccg gatgaacctg 1500

gaggggggca gctaccaagt gaacccccag cccaacggga tgacaaacac gctccaaggc 1560

agcaaccgct acgcgctgga aaacaccatg atcttcaacg ctcaaaacgc cacgccggga 1620

actacctcgg tgtacccaga ggacaatcta ctgctgacca gcgagagcga gactcagccc 1680

gtcaaccggg tggcttacaa cacgggcggt cagatggcca ccaacgccca gaacgccacc 1740

acggctccca cggtcgggac ctacaacctc caggaagtgc ttcctggcag cgtatggatg 1800

gagagggacg tgtacctcca aggacccatc tgggccaaga tcccagagac gggggcgcac 1860

tttcacccct ctccggccat gggcggattc ggactcaaac acccgccgcc catgatgctc 1920

atcaaaaaca cgccggtgcc cggcaacatc accagcttct cggacgtgcc cgtcagcagc 1980

ttcatcaccc agtacagcac cgggcaggtc accgtggaga tggaatggga gctcaaaaag 2040

gaaaactcca agaggtggaa cccagagatc cagtacacca acaactacaa cgacccccag 2100

tttgtggact ttgctccaga cggctccggc gaatacagaa ccaccagagc catcggaacc 2160

cgatacctca cccgacccct t 2181

<210> 538
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 538
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Gly Asp Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Ser Phe Glu Glu Val Pro Phe His Cys Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Ser Ala Thr Gly Ala Ile Gln
        435                 440                 445

Phe Gln Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Thr Ser Ser Gly
465                 470                 475                 480

Ser Ser Thr Asn Arg Val Ser Val Asn Asn Phe Ser Val Ser Asn Arg
                485                 490                 495

Met Asn Leu Glu Gly Ala Ser Tyr Gln Val Asn Pro Gln Pro Asn Gly
            500                 505                 510

Met Thr Asn Thr Leu Gln Gly Ser Asn Arg Tyr Ala Leu Glu Asn Thr
        515                 520                 525

Met Ile Phe Asn Ala Gln Asn Ala Thr Pro Gly Thr Thr Ser Val Tyr
    530                 535                 540
```

```
Pro Glu Asp Asn Leu Leu Leu Thr Ser Glu Ser Glu Thr Gln Pro Val
545                 550                 555                 560


Asn Arg Val Ala Tyr Asn Thr Gly Gly Gln Met Ala Thr Asn Ala Gln
                565                 570                 575


Asn Ala Thr Thr Ala Pro Thr Val Gly Thr Tyr Asn Leu Gln Glu Val
            580                 585                 590


Leu Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro
        595                 600                 605


Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro
    610                 615                 620


Ala Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile
625                 630                 635                 640


Lys Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro
                645                 650                 655


Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu
            660                 665                 670


Met Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
        675                 680                 685


Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala
    690                 695                 700


Pro Asp Gly Ser Gly Glu Tyr Arg Thr Thr Arg Ala Ile Gly Thr Arg
705                 710                 715                 720


Tyr Leu Thr Arg Pro Leu
                725


<210> 539
<211> 735
<212> PRT
```

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 539

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380
```

```
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415


Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430


Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445


Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460


Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480


Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495


Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510


Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525


Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540


Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590
```

```
Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 540
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 540
acggctccga ccggagacaa gcggaaaggc gaagacgaac ctcgtttgcc cgacacttct       60

tcacagactc ccaagaaaaa caagaagcct cgcaaggaaa gaccttccgg cggggcagaa      120

gatccgggcg aaggcacctc ttccaacgct ggagcagcag cacccgcctc tagtgtggga      180
```

tcatctatca tggctgaagg aggtggcggc ccagtgggcg atgcaggcca gggtgccgat 240

ggagtgggca attcctccgg aaattggcat tgcgattccc aatggctgga aaacggagtc 300

gtcactcgaa ccacccgaac ctgggtcttg cccagctaca acaaccacct gtacaaacga 360

atccaaggac ccagcggagg cgacaacaac aacaaattct ttggattcag cacccctgg 420

ggatactttg actacaatcg attccactgc cacttttccc cgcgagactg gcaacgactc 480

atcaacaaca actggggcat ccgtcccaaa gcgatgcgct ttagactctt taacatccag 540

gttaaagagg tcacggtcca agacttcaac accaccatcg gcaacaacct caccagtacg 600

gtccaggtct ttgcggacaa ggactaccaa ctgccgtacg tcctcggatc ggctaccgaa 660

ggcaccttcc cgccgttccc agcggatatc tacacgatcc cgcagtacgg gtactgcacg 720

ctaaactaca acaacgaggc ggtggatcgt tcggccttct actgtctgga ctactttccc 780

tcagacatgc tgcggacagg aaataacttt gagtttactt acaccttcga ggacgttcct 840

ttccatagca tgtttgccca caaccagacg ctagaccggc tgatgaatcc cctcgtggat 900

cagtacctct gggctttcag ctccgtcagc caagcaggct catctggacg agctcttcat 960

tactcgcggg cgactaaaac caacatggcg gctcaatata ggaactggtt acctgggcct 1020

ttcttccgtg atcagcaaat ctttacgggc gctagcaaca tcactaaaaa taacgtcttt 1080

agcgtttggg aaaaaggcaa gcaatgggaa ctcgacaatc ggaccaacct aatgcagccc 1140

ggtcctgcgg cagcgaccac ctttagcgga gaacctgacc gtcaagccat gcaaaacacg 1200

ctggctttta gcaggaccgt ctacgatcaa acgaccgcca cgaccgatcg taaccagata 1260

ctcatcacca acgaagacga aatcagaccc accaactcgg tcggtatcga cgcgtgggga 1320

gcagttccca ccaacaacca gtcgatcgtg acccccggca ctcgcgcggc cgtcaacaat 1380

caaggggcgc ttcccgggat ggtgtggcaa aacagagaca tttaccctac agggacccat 1440

ttggccaaaa ttcccgacac tgacaatcac ttccatccgt ccccgcttat tgggcggttt 1500

ggctgcaagc atccccctcc ccagattttc attaaaaaca cacccgtccc tgccaaccct 1560

tcggaaacgt tccagacggc caaagtggcc tccttcatca accagtactc gaccggacag 1620

tgcaccgtcg aaatcttttg ggaactcaag aaggaaacct ccaagcgctg gaaccccgaa 1680

atccagttca cctccaactt tggcaacgcg gccgacatcc agtttgccgt ctccgacacg 1740

ggatcctatt ccgaacctcg tcccatcggt acccgttacc ttaccaaacc tctgtaa 1797

<210> 541
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 541
atgaggtcgt actacgaggt catcgttcag ctgcccaacg acgtcgagag tcaggtacct 60

ggaatctccg attcgttcgt caactggatt acgtcgcgag aatggacgtt gcctgaggac 120

gccgattggg atttggacca ggtcgatcaa gttcaactga cgctcggcga caaaatccaa 180

cgggagattc gaactcattg ggggacgatg gccaaagaac cggactttca ctattttatc 240

caactggaac aaggtgaggt gttctttcat ttacacgtcc tgctggaaac gtgttccgta 300

aagccgatgg tactcggaag atatatccga catattcaac aaaaaattgt gagtaaagtc 360

tactgcgcca cgagcctacg atggaaggat ggatgcgtgg tgaccaagac caaaaatttc 420

gggggcgcga acaaggtccg ggccgagtcg tatattcccg cctacctgat cccgaaacag 480

caaccggaag tgcagtgggc gtggactaac gtgcccgagt atataaaagc gtgcttgcac 540

cgagaactgc gtgccagtct cgcgcgactt cacttcgagg aggcgggcgt ctcgcaatcc 600

aaggaaaatc tcgcgagaac tgcagacggc gctcccgtga tgccgacccg cgtcagcaaa 660

cgctacatgg agctcgtgga ttggctcgtg gagaagggga tcaccaccga gaaggaatgg 720

ctgctggaaa acagagaaag ctttcggagc tttcaggcct cgagcaactc ggcgcgtcag 780

atcaagacgg ccctgcaagg cgccattcag gagatgcttc tgaccaagac ggcggaggac 840

tacctcgtcg gaaaggatcc cgtctcggac gacgacatcc gtcagaaccg catctacaag 900

attctggaac tgaaccacta cgacccagcg tacgtgggga gtattttggt cgggtggtgc 960

cagaagaaat ggggcaagcg aaacacgctg tggctgttcg gacatgcgac caccggcaag 1020

accaacatcg cggaggctat tgcccatgct gtgccgttct atggatgcgt taactggacc 1080

aacgagaact ttccgttcaa cgactgcgtc gaaaaaatga ttatctggtg ggaggagggc 1140

aaaatgaccg ccaaagtggt ggaaacagcc aaggcgattc tgggaggatc tcgggtgaga 1200

gtggaccaaa aatgcaaagc ttcggttccg atcgaaccga cgccggtcat tattaccagt 1260

aacaccaaca tgtgttatgt catcgacggg aacacgacca cgttcgagca taagcagccg 1320

ttggaggaca ggatgtttaa gctcgaattg ctgactcggt tgcctgatga ctttggtaag 1380

gtgaccaaac aggaggtgcg tcaattcttc aggtggtctc aggatcacct gacccctgtg 1440

atcccagaat tcctagtgcg gaaggcggag tctcgcaaaa gacccgcccc ttccggggaa 1500

ggctatataa gcccgacaaa gcggcccgcg ctcgcagagc agcagcaggc gtcggagagc 1560

gcggacccgg ttcccaccag gtatcgtatc aaatgctcga aacattgcgg tatggataaa 1620

atgttgtttc cttgccaaat ttgtgaatcg atgaacagag atattaatat ttgtgctatt 1680

cataaaacga ccgactgtaa agagtgtttc cccgactacg gggataaaga tgatgtagaa 1740

ctacccccct gtacagaaca caacgtgtct cgttgttatc aatgtcattc gggcgaattg 1800

tatcgcgtga cttcggactc tgacgagaaa cctgcccccg agagtgatga aggcaccgag 1860

ccatcctatg ctccctgcac gattcaccac ctgatgggca agagtcacgg gttagtcact 1920

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gaacaataa 1989

<210> 542
<211> 1626
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 542
atgaggtcgt actacgaggt catcgttcag ctgcccaacg acgtcgagag tcaggtacct 60

ggaatctccg attcgttcgt caactggatt acgtcgcgag aatggacgtt gcctgaggac 120

gccgattggg atttggacca ggtcgatcaa gttcaactga cgctcggcga caaaatccaa 180

cgggagattc gaactcattg ggggacgatg gccaaagaac cggactttca ctattttatc 240

caactggaac aaggtgaggt gttctttcat ttacacgtcc tgctggaaac gtgttccgta 300

aagccgatgg tactcggaag atatatccga catattcaac aaaaaattgt gagtaaagtc 360

tactgcgcca cgagcctacg atggaaggat ggatgcgtgg tgaccaagac caaaaatttc 420

gggggcgcga acaaggtccg ggccgagtcg tatattcccg cctacctgat cccgaaacag 480

caaccggaag tgcagtgggc gtggactaac gtgcccgagt atataaaagc gtgcttgcac 540

cgagaactgc gtgccagtct cgcgcgactt cacttcgagg aggcgggcgt ctcgcaatcc 600

aaggaaaatc tcgcgagaac tgcagacggc gctcccgtga tgccgacccg cgtcagcaaa 660

cgctacatgg agctcgtgga ttggctcgtg gagaagggga tcaccaccga gaaggaatgg 720

ctgctggaaa acagagaaag ctttcggagc tttcaggcct cgagcaactc ggcgcgtcag 780

atcaagacgg ccctgcaagg cgccattcag gagatgcttc tgaccaagac ggcggaggac 840

tacctcgtcg gaaaggatcc cgtctcggac gacgacatcc gtcagaaccg catctacaag 900

attctggaac tgaaccacta cgacccagcg tacgtgggga gtattttggt cgggtggtgc 960

cagaagaaat ggggcaagcg aaacacgctg tggctgttcg gacatgcgac caccggcaag 1020

accaacatcg cggaggctat tgcccatgct gtgccgttct atggatgcgt taactggacc 1080

aacgagaact ttccgttcaa cgactgcgtc gaaaaaatga ttatctggtg ggaggagggc 1140

aaaatgaccg ccaaagtggt ggaaacagcc aaggcgattc tgggaggatc tcgggtgaga 1200

gtggaccaaa aatgcaaagc ttcggttccg atcgaaccga cgccggtcat tattaccagt 1260

aacaccaaca tgtgttatgt catcgacggg aacacgacca cgttcgagca taagcagccg 1320

ttggaggaca ggatgtttaa gctcgaattg ctgactcggt tgcctgatga ctttggtaag 1380

gtgaccaaac aggaggtgcg tcaattcttc aggtggtctc aggatcacct gacccctgtg 1440

atcccagaat tcctagtgcg gaaggcggag tctcgcaaaa gacccgcccc ttccggggaa 1500

ggctatataa gcccgacaaa gcggcccgcg ctcgcagagc agcagcaggc gtcggagagc 1560

gcggacccgg ttcccaccag attggttgga gcggttggtc aaaaagggag tgaatgctgc 1620

agctga 1626

<210> 543
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 543
atggagctcg tggattggct cgtggagaag gggatcacca ccgagaagga atggctgctg 60

gaaaacagag aaagctttcg gagctttcag gcctcgagca actcggcgcg tcagatcaag 120

acggccctgc aaggcgccat tcaggagatg cttctgacca agacggcgga ggactacctc 180

gtcggaaagg atcccgtctc ggacgacgac atccgtcaga accgcatcta caagattctg 240

gaactgaacc actacgaccc agcgtacgtg gggagtattt tggtcgggtg gtgccagaag 300

aaatggggca agcgaaacac gctgtggctg ttcggacatg cgaccaccgg caagaccaac 360

atcgcggagg ctattgccca tgctgtgccg ttctatggat gcgttaactg gaccaacgag 420

aactttccgt tcaacgactg cgtcgaaaaa atgattatct ggtgggagga gggcaaaatg 480

accgccaaag tggtggaaac agccaaggcg attctgggag gatctcgggt gagagtggac 540

caaaaatgca aagcttcggt tccgatcgaa ccgacgccgg tcattattac cagtaacacc 600

aacatgtgtt atgtcatcga cgggaacacg accacgttcg agcataagca gccgttggag 660

gacaggatgt ttaagctcga attgctgact cggttgcctg atgactttgg taaggtgacc 720

aaacaggagg tgcgtcaatt cttcaggtgg tctcaggatc acctgacccc tgtgatccca 780

gaattcctag tgcggaaggc ggagtctcgc aaaagacccg ccccttccgg ggaaggctat 840

ataagcccga caaagcggcc cgcgctcgca gagcagcagc aggcgtcgga gagcgcggac 900

ccggttccca ccaggtatcg tatcaaatgc tcgaaacatt gcggtatgga taaaatgttg 960

tttccttgcc aaatttgtga atcgatgaac agagatatta atatttgtgc tattcataaa 1020

acgaccgact gtaaagagtg tttccccgac tacggggata aagatgatgt agaactaccc 1080

ccctgtacag aacacaacgt gtctcgttgt tatcaatgtc attcgggcga attgtatcgc 1140

gtgacttcgg actctgacga gaaacctgcc cccgagagtg atgaaggcac cgagccatcc 1200

tatgctccct gcacgattca ccacctgatg ggcaagagtc acgggttagt cacttgcgcg 1260

gcgtgtcggt tgaaaaatag tacgttgcat gatgacttgg atgacggtga tctcgaacaa 1320

taa 1323

<210> 544
<211> 960
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 544
atggagctcg tggattggct cgtggagaag gggatcacca ccgagaagga atggctgctg 60

gaaaacagag aaagctttcg gagctttcag gcctcgagca actcggcgcg tcagatcaag 120

acggccctgc aaggcgccat tcaggagatg cttctgacca agacggcgga ggactacctc 180

gtcggaaagg atcccgtctc ggacgacgac atccgtcaga accgcatcta caagattctg 240

gaactgaacc actacgaccc agcgtacgtg gggagtattt tggtcgggtg gtgccagaag 300

aaatggggca agcgaaacac gctgtggctg ttcggacatg cgaccaccgg caagaccaac 360

atcgcggagg ctattgccca tgctgtgccg ttctatggat gcgttaactg gaccaacgag 420

aactttccgt tcaacgactg cgtcgaaaaa atgattatct ggtgggagga gggcaaaatg 480

accgccaaag tggtggaaac agccaaggcg attctgggag gatctcgggt gagagtggac 540

caaaaatgca aagcttcggt tccgatcgaa ccgacgccgg tcattattac cagtaacacc 600

aacatgtgtt atgtcatcga cgggaacacg accacgttcg agcataagca gccgttggag 660

gacaggatgt ttaagctcga attgctgact cggttgcctg atgactttgg taaggtgacc 720

aaacaggagg tgcgtcaatt cttcaggtgg tctcaggatc acctgacccc tgtgatccca 780

gaattcctag tgcggaaggc ggagtctcgc aaaagacccg ccccttccgg ggaaggctat 840

ataagcccga caaagcggcc cgcgctcgca gagcagcagc aggcgtcgga gagcgcggac 900

ccggttccca ccagattggt tggagcggtt ggtcaaaaag ggagtgaatg ctgcagctga 960

<210> 545
<211> 1608
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 545

atggctgaag gaggtggcgg cccagtgggc gatgcaggcc agggtgccga tggagtgggc 60

aattcctccg gaaattggca ttgcgattcc caatggctgg aaaacggagt cgtcactcga 120

accacccgaa cctgggtctt gcccagctac aacaaccacc tgtacaaacg aatccaagga 180

cccagcggag gcgacaacaa caacaaattc tttggattca gcacccccctg gggatacttt 240

gactacaatc gattccactg ccacttttcc ccgcgagact ggcaacgact catcaacaac 300

aactggggca tccgtcccaa agcgatgcgc tttagactct ttaacatcca ggttaaagag 360

gtcacggtcc aagacttcaa caccaccatc ggcaacaacc tcaccagtac ggtccaggtc 420

tttgcggaca aggactacca actgccgtac gtcctcggat cggctaccga aggcaccttc 480

ccgccgttcc cagcggatat ctacacgatc ccgcagtacg ggtactgcac gctaaactac 540

aacaacgagg cggtggatcg ttcggccttc tactgtctgg actactttcc ctcagacatg 600

ctgcggacag gaaataactt tgagtttact tacaccttcg aggacgttcc tttccatagc 660

atgtttgccc acaaccagac gctagaccgg ctgatgaatc ccctcgtgga tcagtacctc 720

tgggctttca gctccgtcag ccaagcaggc tcatctggac gagctcttca ttactcgcgg 780

gcgactaaaa ccaacatggc ggctcaatat aggaactggt tacctgggcc tttcttccgt 840

gatcagcaaa tctttacggg cgctagcaac atcactaaaa ataacgtctt tagcgtttgg 900

gaaaaaggca agcaatggga actcgacaat cggaccaacc taatgcagcc cggtcctgcg 960

gcagcgacca cctttagcgg agaacctgac cgtcaagcca tgcaaaacac gctggctttt 1020

agcaggaccg tctacgatca aacgaccgcc acgaccgatc gtaaccagat actcatcacc 1080

aacgaagacg aaatcagacc caccaactcg gtcggtatcg acgcgtgggg agcagttccc 1140

accaacaacc agtcgatcgt gacccccggc actcgcgcgg ccgtcaacaa tcaaggggcg 1200

cttcccggga tggtgtggca aaacagagac atttacccta cagggaccca tttggccaaa 1260

attcccgaca ctgacaatca cttccatccg tccccgctta ttgggcggtt tggctgcaag 1320

catccccctc cccagatttt cattaaaaac acacccgtcc ctgccaaccc ttcggaaacg 1380

ttccagacgg ccaaagtggc ctccttcatc aaccagtact cgaccggaca gtgcaccgtc 1440

gaaatctttt gggaactcaa gaaggaaacc tccaagcgct ggaaccccga aatccagttc 1500

acctccaact ttggcaacgc ggccgacatc cagtttgccg tctccgacac gggatcctat 1560

tccgaacctc gtcccatcgg tacccgttac cttaccaaac ctctgtaa 1608

<210> 546
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 546
atgtctctca tttctgatgc gattccagat tggttggagc ggttggtcaa aaagggagtg 60

aatgctgcag ctgatttcta ccatttggaa agcggtcctc ctcgtcctaa ggcaaatcag 120

caaactcaag aatctcttga aaaggacgat tcgagaggtc tcgtgttccc aggctacaat 180

tatctaggcc ctttcaacgg tctagataaa ggagaacccg tcaacgaggc agacgctgcc 240

gccttagaac acgacaaggc ttacgacctc gaaatcaagg acgggcacaa cccgtacttt 300

gagtacaacg aggccgacag acgtttccag gaacgtctca aagacgatac ctcctttgga 360

ggcaatttag gtaaagccat cttccaggcc aaaaagaggg ttctcgaacc ctttggtctg 420

gtggaagact caaagacggc tccgaccgga gacaagcgga aaggcgaaga cgaacctcgt 480

ttgcccgaca cttcttcaca gactcccaag aaaaacaaga agcctcgcaa ggaaagacct 540

tccggcgggg cagaagatcc gggcgaaggc acctcttcca acgctggagc agcagcaccc 600

gcctctagtg tgggatcatc tatcatggct gaaggaggtg gcggcccagt gggcgatgca 660

ggccagggtg ccgatggagt gggcaattcc tccggaaatt ggcattgcga ttcccaatgg 720

ctggaaaacg gagtcgtcac tcgaaccacc cgaacctggg tcttgcccag ctacaacaac 780

cacctgtaca aacgaatcca aggacccagc ggaggcgaca acaacaacaa attctttgga 840

ttcagcaccc cctggggata ctttgactac aatcgattcc actgccactt ttccccgcga 900

gactggcaac gactcatcaa caacaactgg ggcatccgtc ccaaagcgat gcgctttaga 960

ctctttaaca tccaggttaa agaggtcacg gtccaagact tcaacaccac catcggcaac 1020

aacctcacca gtacggtcca ggtctttgcg gacaaggact accaactgcc gtacgtcctc 1080

ggatcggcta ccgaaggcac cttcccgccg ttcccagcgg atatctacac gatcccgcag 1140

tacgggtact gcacgctaaa ctacaacaac gaggcggtgg atcgttcggc cttctactgt 1200

ctggactact ttccctcaga catgctgcgg acaggaaata actttgagtt tacttacacc 1260

ttcgaggacg ttcctttcca tagcatgttt gcccacaacc agacgctaga ccggctgatg 1320

aatcccctcg tggatcagta cctctgggct ttcagctccg tcagccaagc aggctcatct 1380

ggacgagctc ttcattactc gcgggcgact aaaaccaaca tggcggctca atataggaac 1440

tggttacctg ggcctttctt ccgtgatcag caaatcttta cgggcgctag caacatcact 1500

aaaaataacg tctttagcgt ttgggaaaaa ggcaagcaat gggaactcga caatcggacc 1560

aacctaatgc agcccggtcc tgcggcagcg accaccttta gcggagaacc tgaccgtcaa 1620

gccatgcaaa acacgctggc ttttagcagg accgtctacg atcaaacgac cgccacgacc 1680

gatcgtaacc agatactcat caccaacgaa gacgaaatca gacccaccaa ctcggtcggt 1740

atcgacgcgt ggggagcagt tcccaccaac aaccagtcga tcgtgacccc cggcactcgc 1800

gcggccgtca acaatcaagg ggcgcttccc gggatggtgt ggcaaaacag agacatttac 1860

cctacaggga cccatttggc caaaattccc gacactgaca atcacttcca tccgtccccg 1920

cttattgggc ggtttggctg caagcatccc cctccccaga ttttcattaa aaacacaccc 1980

gtccctgcca acccttcgga aacgttccag acggccaaag tggcctcctt catcaaccag 2040

tactcgaccg gacagtgcac cgtcgaaatc ttttgggaac tcaagaagga aacctccaag 2100

cgctggaacc ccgaaatcca gttcacctcc aactttggca acgcggccga catccagttt 2160

gccgtctccg acacgggatc ctattccgaa cctcgtccca tcggtacccg ttaccttacc 2220

aaacctctgt aa 2232

<210> 547
<211> 535
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 547

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Met Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala
1               5                  10                  15

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp
            20                  25                  30

Leu Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro
        35                  40                  45

Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly
    50                  55                  60

Asp Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe
65                  70                  75                  80

Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
                85                  90                  95

Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg
            100                 105                 110

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Phe Asn Thr
        115                 120                 125

Thr Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys
    130                 135                 140

Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe
145                 150                 155                 160

Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys
                165                 170                 175

Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys
            180                 185                 190

Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu
```

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        195                 200                 205

Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His
    210                 215                 220

Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu
225                 230                 235                 240

Trp Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu
                245                 250                 255

His Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn
            260                 265                 270

Trp Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala
        275                 280                 285

Ser Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys
    290                 295                 300

Gln Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala
305                 310                 315                 320

Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn
                325                 330                 335

Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr
            340                 345                 350

Asp Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr
        355                 360                 365

Asn Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln
    370                 375                 380

Ser Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala
385                 390                 395                 400

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr
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405 410 415

His Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro
420 425 430

Leu Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile
435 440 445

Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala
450 455 460

Lys Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val
465 470 475 480

Glu Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro
485 490 495

Glu Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe
500 505 510

Ala Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr
515 520 525

Arg Tyr Leu Thr Lys Pro Leu
530 535

<210> 548
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 548
Met Glu Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys
1 5 10 15

Glu Trp Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser
20 25 30

```
Ser Asn Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln
        35                  40                  45

Glu Met Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp
    50                  55                  60

Pro Val Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu
65                  70                  75                  80

Glu Leu Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly
                85                  90                  95

Trp Cys Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly
            100                 105                 110

His Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala
        115                 120                 125

Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe
    130                 135                 140

Asn Asp Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met
145                 150                 155                 160

Thr Ala Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg
                165                 170                 175

Val Arg Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr
            180                 185                 190

Pro Val Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly
        195                 200                 205

Asn Thr Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe
    210                 215                 220

Lys Leu Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr
225                 230                 235                 240
```

```
Lys Gln Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr
                245                 250                 255

Pro Val Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg
            260                 265                 270

Pro Ala Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala
        275                 280                 285

Leu Ala Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr
    290                 295                 300

Arg Tyr Arg Ile Lys Cys Ser Lys His Cys Gly Met Asp Lys Met Leu
305                 310                 315                 320

Phe Pro Cys Gln Ile Cys Glu Ser Met Asn Arg Asp Ile Asn Ile Cys
                325                 330                 335

Ala Ile His Lys Thr Thr Asp Cys Lys Glu Cys Phe Pro Asp Tyr Gly
            340                 345                 350

Asp Lys Asp Asp Val Glu Leu Pro Pro Cys Thr Glu His Asn Val Ser
        355                 360                 365

Arg Cys Tyr Gln Cys His Ser Gly Glu Leu Tyr Arg Val Thr Ser Asp
    370                 375                 380

Ser Asp Glu Lys Pro Ala Pro Glu Ser Asp Glu Gly Thr Glu Pro Ser
385                 390                 395                 400

Tyr Ala Pro Cys Thr Ile His His Leu Met Gly Lys Ser His Gly Leu
                405                 410                 415

Val Thr Cys Ala Ala Cys Arg Leu Lys Asn Ser Thr Leu His Asp Asp
            420                 425                 430

Leu Asp Asp Gly Asp Leu Glu Gln
        435                 440
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<210> 549
<211> 319
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 549
Met Glu Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys
1 5 10 15

Glu Trp Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser
20 25 30

Ser Asn Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln
35 40 45

Glu Met Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp
50 55 60

Pro Val Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu
65 70 75 80

Glu Leu Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly
85 90 95

Trp Cys Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly
100 105 110

His Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala
115 120 125

Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe
130 135 140

Asn Asp Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met
145 150 155 160

```
Thr Ala Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg
                165                 170                 175


Val Arg Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr
            180                 185                 190


Pro Val Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly
        195                 200                 205


Asn Thr Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe
    210                 215                 220


Lys Leu Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr
225                 230                 235                 240


Lys Gln Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr
                245                 250                 255


Pro Val Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg
            260                 265                 270


Pro Ala Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala
        275                 280                 285


Leu Ala Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr
    290                 295                 300


Arg Leu Val Gly Ala Val Gly Gln Lys Gly Ser Glu Cys Cys Ser
305                 310                 315


<210> 550
<211> 662
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 550
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Met Arg Ser Tyr Tyr Glu Val Ile Val Gln Leu Pro Asn Asp Val Glu
1               5                  10                  15

Ser Gln Val Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ile Thr Ser
            20                  25                  30

Arg Glu Trp Thr Leu Pro Glu Asp Ala Asp Trp Asp Leu Asp Gln Val
        35                  40                  45

Asp Gln Val Gln Leu Thr Leu Gly Asp Lys Ile Gln Arg Glu Ile Arg
    50                  55                  60

Thr His Trp Gly Thr Met Ala Lys Glu Pro Asp Phe His Tyr Phe Ile
65                  70                  75                  80

Gln Leu Glu Gln Gly Glu Val Phe Phe His Leu His Val Leu Leu Glu
                85                  90                  95

Thr Cys Ser Val Lys Pro Met Val Leu Gly Arg Tyr Ile Arg His Ile
            100                 105                 110

Gln Gln Lys Ile Val Ser Lys Val Tyr Cys Ala Thr Ser Leu Arg Trp
        115                 120                 125

Lys Asp Gly Cys Val Val Thr Lys Thr Lys Asn Phe Gly Gly Ala Asn
    130                 135                 140

Lys Val Arg Ala Glu Ser Tyr Ile Pro Ala Tyr Leu Ile Pro Lys Gln
145                 150                 155                 160

Gln Pro Glu Val Gln Trp Ala Trp Thr Asn Val Pro Glu Tyr Ile Lys
                165                 170                 175

Ala Cys Leu His Arg Glu Leu Arg Ala Ser Leu Ala Arg Leu His Phe
            180                 185                 190

Glu Glu Ala Gly Val Ser Gln Ser Lys Glu Asn Leu Ala Arg Thr Ala
        195                 200                 205
```

```
Asp Gly Ala Pro Val Met Pro Thr Arg Val Ser Lys Arg Tyr Met Glu
    210                 215                 220

Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys Glu Trp
225                 230                 235                 240

Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser Ser Asn
                245                 250                 255

Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln Glu Met
            260                 265                 270

Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp Pro Val
        275                 280                 285

Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly Trp Cys
305                 310                 315                 320

Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly His Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr Pro Val
                405                 410                 415
```

```
Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly Asn Thr
            420                 425                 430

Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe Lys Leu
        435                 440                 445

Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr Pro Val
465                 470                 475                 480

Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg Pro Ala
                485                 490                 495

Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala Leu Ala
            500                 505                 510

Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr Arg Tyr
        515                 520                 525

Arg Ile Lys Cys Ser Lys His Cys Gly Met Asp Lys Met Leu Phe Pro
    530                 535                 540

Cys Gln Ile Cys Glu Ser Met Asn Arg Asp Ile Asn Ile Cys Ala Ile
545                 550                 555                 560

His Lys Thr Thr Asp Cys Lys Glu Cys Phe Pro Asp Tyr Gly Asp Lys
                565                 570                 575

Asp Asp Val Glu Leu Pro Pro Cys Thr Glu His Asn Val Ser Arg Cys
            580                 585                 590

Tyr Gln Cys His Ser Gly Glu Leu Tyr Arg Val Thr Ser Asp Ser Asp
        595                 600                 605

Glu Lys Pro Ala Pro Glu Ser Asp Glu Gly Thr Glu Pro Ser Tyr Ala
    610                 615                 620
```

Pro Cys Thr Ile His His Leu Met Gly Lys Ser His Gly Leu Val Thr
625 630 635 640

Cys Ala Ala Cys Arg Leu Lys Asn Ser Thr Leu His Asp Asp Leu Asp
645 650 655

Asp Gly Asp Leu Glu Gln
660

<210> 551
<211> 541
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 551
Met Arg Ser Tyr Tyr Glu Val Ile Val Gln Leu Pro Asn Asp Val Glu
1 5 10 15

Ser Gln Val Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ile Thr Ser
20 25 30

Arg Glu Trp Thr Leu Pro Glu Asp Ala Asp Trp Asp Leu Asp Gln Val
35 40 45

Asp Gln Val Gln Leu Thr Leu Gly Asp Lys Ile Gln Arg Glu Ile Arg
50 55 60

Thr His Trp Gly Thr Met Ala Lys Glu Pro Asp Phe His Tyr Phe Ile
65 70 75 80

Gln Leu Glu Gln Gly Glu Val Phe Phe His Leu His Val Leu Leu Glu
85 90 95

Thr Cys Ser Val Lys Pro Met Val Leu Gly Arg Tyr Ile Arg His Ile
100 105 110

Gln Gln Lys Ile Val Ser Lys Val Tyr Cys Ala Thr Ser Leu Arg Trp

```
        115                 120                 125

Lys Asp Gly Cys Val Val Thr Lys Thr Lys Asn Phe Gly Gly Ala Asn
    130                 135                 140

Lys Val Arg Ala Glu Ser Tyr Ile Pro Ala Tyr Leu Ile Pro Lys Gln
145                 150                 155                 160

Gln Pro Glu Val Gln Trp Ala Trp Thr Asn Val Pro Glu Tyr Ile Lys
                165                 170                 175

Ala Cys Leu His Arg Glu Leu Arg Ala Ser Leu Ala Arg Leu His Phe
            180                 185                 190

Glu Glu Ala Gly Val Ser Gln Ser Lys Glu Asn Leu Ala Arg Thr Ala
        195                 200                 205

Asp Gly Ala Pro Val Met Pro Thr Arg Val Ser Lys Arg Tyr Met Glu
    210                 215                 220

Leu Val Asp Trp Leu Val Glu Lys Gly Ile Thr Thr Glu Lys Glu Trp
225                 230                 235                 240

Leu Leu Glu Asn Arg Glu Ser Phe Arg Ser Phe Gln Ala Ser Ser Asn
                245                 250                 255

Ser Ala Arg Gln Ile Lys Thr Ala Leu Gln Gly Ala Ile Gln Glu Met
            260                 265                 270

Leu Leu Thr Lys Thr Ala Glu Asp Tyr Leu Val Gly Lys Asp Pro Val
        275                 280                 285

Ser Asp Asp Asp Ile Arg Gln Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

Asn His Tyr Asp Pro Ala Tyr Val Gly Ser Ile Leu Val Gly Trp Cys
305                 310                 315                 320

Gln Lys Lys Trp Gly Lys Arg Asn Thr Leu Trp Leu Phe Gly His Ala
```

```
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Glu Lys Met Ile Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Thr Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ala Ser Val Pro Ile Glu Pro Thr Pro Val
                405                 410                 415

Ile Ile Thr Ser Asn Thr Asn Met Cys Tyr Val Ile Asp Gly Asn Thr
            420                 425                 430

Thr Thr Phe Glu His Lys Gln Pro Leu Glu Asp Arg Met Phe Lys Leu
        435                 440                 445

Glu Leu Leu Thr Arg Leu Pro Asp Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

Glu Val Arg Gln Phe Phe Arg Trp Ser Gln Asp His Leu Thr Pro Val
465                 470                 475                 480

Ile Pro Glu Phe Leu Val Arg Lys Ala Glu Ser Arg Lys Arg Pro Ala
                485                 490                 495

Pro Ser Gly Glu Gly Tyr Ile Ser Pro Thr Lys Arg Pro Ala Leu Ala
            500                 505                 510

Glu Gln Gln Gln Ala Ser Glu Ser Ala Asp Pro Val Pro Thr Arg Leu
        515                 520                 525

Val Gly Ala Val Gly Gln Lys Gly Ser Glu Cys Cys Ser
```

530 535 540

<210> 552
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 552
Met Ser Leu Ile Ser Asp Ala Ile Pro Asp Trp Leu Glu Arg Leu Val
1 5 10 15

Lys Lys Gly Val Asn Ala Ala Ala Asp Phe Tyr His Leu Glu Ser Gly
20 25 30

Pro Pro Arg Pro Lys Ala Asn Gln Gln Thr Gln Glu Ser Leu Glu Lys
35 40 45

Asp Asp Ser Arg Gly Leu Val Phe Pro Gly Tyr Asn Tyr Leu Gly Pro
50 55 60

Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Glu Ala Asp Ala Ala
65 70 75 80

Ala Leu Glu His Asp Lys Ala Tyr Asp Leu Glu Ile Lys Asp Gly His
85 90 95

Asn Pro Tyr Phe Glu Tyr Asn Glu Ala Asp Arg Arg Phe Gln Glu Arg
100 105 110

Leu Lys Asp Asp Thr Ser Phe Gly Gly Asn Leu Gly Lys Ala Ile Phe
115 120 125

Gln Ala Lys Lys Arg Val Leu Glu Pro Phe Gly Leu Val Glu Asp Ser
130 135 140

Lys Thr Ala Pro Thr Gly Asp Lys Arg Lys Gly Glu Asp Glu Pro Arg
145 150 155 160

```
Leu Pro Asp Thr Ser Ser Gln Thr Pro Lys Lys Asn Lys Lys Pro Arg
                165                 170                 175

Lys Glu Arg Pro Ser Gly Gly Ala Glu Asp Pro Gly Glu Gly Thr Ser
            180                 185                 190

Ser Asn Ala Gly Ala Ala Ala Pro Ala Ser Ser Val Gly Ser Ser Ile
        195                 200                 205

Met Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala
    210                 215                 220

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp
225                 230                 235                 240

Leu Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro
                245                 250                 255

Ser Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly
            260                 265                 270

Asp Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe
        275                 280                 285

Asp Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
    290                 295                 300

Leu Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg
305                 310                 315                 320

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Phe Asn Thr
                325                 330                 335

Thr Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys
            340                 345                 350

Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe
        355                 360                 365
```

```
Pro Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys
    370                 375                 380

Thr Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys
385                 390                 395                 400

Leu Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu
                405                 410                 415

Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His
            420                 425                 430

Asn Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu
        435                 440                 445

Trp Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu
    450                 455                 460

His Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn
465                 470                 475                 480

Trp Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala
                485                 490                 495

Ser Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys
            500                 505                 510

Gln Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala
        515                 520                 525

Ala Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn
    530                 535                 540

Thr Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr
545                 550                 555                 560

Asp Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr
                565                 570                 575
```

```
Asn Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln
            580                 585                 590

Ser Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr
    610                 615                 620

His Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro
625                 630                 635                 640

Leu Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala
            660                 665                 670

Lys Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val
        675                 680                 685

Glu Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe
705                 710                 715                 720

Ala Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Lys Pro Leu
            740
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<210> 553
<211> 598
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 553

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Thr Ala Pro Thr Gly Asp Lys Arg Lys Gly Glu Asp Glu Pro Arg Leu
1               5                  10                  15

Pro Asp Thr Ser Ser Gln Thr Pro Lys Lys Asn Lys Lys Pro Arg Lys
            20                  25                  30

Glu Arg Pro Ser Gly Gly Ala Glu Asp Pro Gly Glu Gly Thr Ser Ser
        35                  40                  45

Asn Ala Gly Ala Ala Ala Pro Ala Ser Ser Val Gly Ser Ser Ile Met
    50                  55                  60

Ala Glu Gly Gly Gly Gly Pro Val Gly Asp Ala Gly Gln Gly Ala Asp
65                  70                  75                  80

Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu
                85                  90                  95

Glu Asn Gly Val Val Thr Arg Thr Thr Arg Thr Trp Val Leu Pro Ser
            100                 105                 110

Tyr Asn Asn His Leu Tyr Lys Arg Ile Gln Gly Pro Ser Gly Gly Asp
        115                 120                 125

Asn Asn Asn Lys Phe Phe Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp
    130                 135                 140

Tyr Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu
145                 150                 155                 160

Ile Asn Asn Asn Trp Gly Ile Arg Pro Lys Ala Met Arg Phe Arg Leu
                165                 170                 175

Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Phe Asn Thr Thr
            180                 185                 190
```

```
Ile Gly Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Lys Asp
        195                 200                 205

Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Phe Pro
    210                 215                 220

Pro Phe Pro Ala Asp Ile Tyr Thr Ile Pro Gln Tyr Gly Tyr Cys Thr
225                 230                 235                 240

Leu Asn Tyr Asn Asn Glu Ala Val Asp Arg Ser Ala Phe Tyr Cys Leu
                245                 250                 255

Asp Tyr Phe Pro Ser Asp Met Leu Arg Thr Gly Asn Asn Phe Glu Phe
            260                 265                 270

Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Met Phe Ala His Asn
        275                 280                 285

Gln Thr Leu Asp Arg Leu Met Asn Pro Leu Val Asp Gln Tyr Leu Trp
    290                 295                 300

Ala Phe Ser Ser Val Ser Gln Ala Gly Ser Ser Gly Arg Ala Leu His
305                 310                 315                 320

Tyr Ser Arg Ala Thr Lys Thr Asn Met Ala Ala Gln Tyr Arg Asn Trp
                325                 330                 335

Leu Pro Gly Pro Phe Phe Arg Asp Gln Gln Ile Phe Thr Gly Ala Ser
            340                 345                 350

Asn Ile Thr Lys Asn Asn Val Phe Ser Val Trp Glu Lys Gly Lys Gln
        355                 360                 365

Trp Glu Leu Asp Asn Arg Thr Asn Leu Met Gln Pro Gly Pro Ala Ala
    370                 375                 380

Ala Thr Thr Phe Ser Gly Glu Pro Asp Arg Gln Ala Met Gln Asn Thr
385                 390                 395                 400
```

```
Leu Ala Phe Ser Arg Thr Val Tyr Asp Gln Thr Thr Ala Thr Thr Asp
                405                 410                 415

Arg Asn Gln Ile Leu Ile Thr Asn Glu Asp Glu Ile Arg Pro Thr Asn
            420                 425                 430

Ser Val Gly Ile Asp Ala Trp Gly Ala Val Pro Thr Asn Asn Gln Ser
        435                 440                 445

Ile Val Thr Pro Gly Thr Arg Ala Ala Val Asn Asn Gln Gly Ala Leu
    450                 455                 460

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Pro Thr Gly Thr His
465                 470                 475                 480

Leu Ala Lys Ile Pro Asp Thr Asp Asn His Phe His Pro Ser Pro Leu
                485                 490                 495

Ile Gly Arg Phe Gly Cys Lys His Pro Pro Pro Gln Ile Phe Ile Lys
            500                 505                 510

Asn Thr Pro Val Pro Ala Asn Pro Ser Glu Thr Phe Gln Thr Ala Lys
        515                 520                 525

Val Ala Ser Phe Ile Asn Gln Tyr Ser Thr Gly Gln Cys Thr Val Glu
    530                 535                 540

Ile Phe Trp Glu Leu Lys Lys Glu Thr Ser Lys Arg Trp Asn Pro Glu
545                 550                 555                 560

Ile Gln Phe Thr Ser Asn Phe Gly Asn Ala Ala Asp Ile Gln Phe Ala
                565                 570                 575

Val Ser Asp Thr Gly Ser Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg
            580                 585                 590

Tyr Leu Thr Lys Pro Leu
        595
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<210> 554
<211> 4694
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 554
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agcgaccgct tcgcggtcgc ggcccgagtg agcgagcgag cctgtcttgg aaactggcca 120

gcactccggt gaggtaatgc cgtcacgtgg tcgggaatgg gaacgggaaa tctcgcgaga 180

acgtaaacaa atataagacg gcgccacacg gcgctgcgtc atacgcgcgc gcgcaccggc 240

gagatgaggt cgtactacga ggtcatcgtt cagctgccca acgacgtcga gagtcaggta 300

cctggaatct ccgattcgtt cgtcaactgg attacgtcgc gagaatggac gttgcctgag 360

gacgccgatt gggatttgga ccaggtcgat caagttcaac tgacgctcgg cgacaaaatc 420

caacgggaga ttcgaactca ttgggggacg atggccaaag aaccggactt tcactatttt 480

atccaactgg aacaaggtga ggtgttcttt catttacacg tcctgctgga aacgtgttcc 540

gtaaagccga tggtactcgg aagatatatc cgacatattc aacaaaaaat tgtgagtaaa 600

gtctactgcg ccacgagcct acgatggaag gatggatgcg tggtgaccaa gaccaaaaat 660

ttcgggggcg cgaacaaggt ccgggccgag tcgtatattc ccgcctacct gatcccgaaa 720

cagcaaccgg aagtgcagtg ggcgtggact aacgtgcccg agtatataaa agcgtgcttg 780

caccgagaac tgcgtgccag tctcgcgcga cttcacttcg aggaggcggg cgtctcgcaa 840

tccaaggaaa atctcgcgag aactgcagac ggcgctcccg tgatgccgac ccgcgtcagc 900

aaacgctaca tggagctcgt ggattggctc gtggagaagg ggatcaccac cgagaaggaa 960

tggctgctgg aaaacagaga aagctttcgg agctttcagg cctcgagcaa ctcggcgcgt 1020

cagatcaaga cggccctgca aggcgccatt caggagatgc ttctgaccaa gacggcggag 1080

gactacctcg tcggaaagga tcccgtctcg gacgacgaca tccgtcagaa ccgcatctac 1140

aagattctgg aactgaacca ctacgaccca gcgtacgtgg ggagtatttt ggtcgggtgg 1200

tgccagaaga aatggggcaa gcgaaacacg ctgtggctgt tcggacatgc gaccaccggc 1260

aagaccaaca tcgcggaggc tattgcccat gctgtgccgt tctatggatg cgttaactgg 1320

accaacgaga actttccgtt caacgactgc gtcgaaaaaa tgattatctg gtgggaggag 1380

ggcaaaatga ccgccaaagt ggtggaaaca gccaaggcga ttctgggagg atctcgggtg 1440

agagtggacc aaaaatgcaa agcttcggtt ccgatcgaac cgacgccggt cattattacc 1500

agtaacacca acatgtgtta tgtcatcgac gggaacacga ccacgttcga gcataagcag 1560

ccgttggagg acaggatgtt taagctcgaa ttgctgactc ggttgcctga tgactttggt 1620

aaggtgacca aacaggaggt gcgtcaattc ttcaggtggt ctcaggatca cctgacccct 1680

gtgatcccag aattcctagt gcggaaggcg gagtctcgca aaagacccgc cccttccggg 1740

gaaggctata taagcccgac aaagcggccc gcgctcgcag agcagcagca ggcgtcggag 1800

agcgcggacc cggttcccac caggtatcgt atcaaatgct cgaaacattg cggtatggat 1860

aaaatgttgt ttccttgcca aatttgtgaa tcgatgaaca gagatattaa tatttgtgct 1920

attcataaaa cgaccgactg taaagagtgt ttccccgact acggggataa agatgatgta 1980

gaactacccc cctgtacaga acacaacgtg tctcgttgtt atcaatgtca ttcgggcgaa 2040

ttgtatcgcg tgacttcgga ctctgacgag aaacctgccc ccgagagtga tgaaggcacc 2100

gagccatcct atgctccctg cacgattcac cacctgatgg gcaagagtca cgggttagtc 2160

acttgcgcgg cgtgtcggtt gaaaaatagt acgttgcatg atgacttgga tgacggtgat 2220

ctcgaacaat aaatgattga aatgtagcca tgtctctcat ttctgatgcg attccagatt 2280

ggttggagcg gttggtcaaa aagggagtga atgctgcagc tgatttctac catttggaaa 2340

gcggtcctcc tcgtcctaag gcaaatcagc aaactcaaga atctcttgaa aaggacgatt 2400

cgagaggtct cgtgttccca ggctacaatt atctaggccc tttcaacggt ctagataaag 2460

gagaacccgt caacgaggca gacgctgccg ccttagaaca cgacaaggct tacgacctcg 2520

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ccggaaattg gcattgcgat tcccaatggc tggaaaacgg agtcgtcact cgaaccaccc 3000

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gaggcgacaa caacaacaaa ttctttggat tcagcacccc ctggggatac tttgactaca 3120

atcgattcca ctgccacttt tccccgcgag actggcaacg actcatcaac aacaactggg 3180

gcatccgtcc caaagcgatg cgctttagac tctttaacat ccaggttaaa gaggtcacgg 3240

tccaagactt caacaccacc atcggcaaca acctcaccag tacggtccag gtctttgcgg 3300

acaaggacta ccaactgccg tacgtcctcg gatcggctac cgaaggcacc ttcccgccgt 3360

tcccagcgga tatctacacg atcccgcagt acgggtactg cacgctaaac tacaacaacg 3420

aggcggtgga tcgttcggcc ttctactgtc tggactactt tccctcagac atgctgcgga 3480

caggaaataa ctttgagttt acttacacct tcgaggacgt tcctttccat agcatgtttg 3540

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tcagctccgt cagccaagca ggctcatctg gacgagctct tcattactcg cgggcgacta 3660

aaaccaacat ggcggctcaa tataggaact ggttacctgg gcctttcttc cgtgatcagc 3720

aaatctttac gggcgctagc aacatcacta aaaataacgt ctttagcgtt tgggaaaaag 3780

gcaagcaatg ggaactcgac aatcggacca acctaatgca gcccggtcct gcggcagcga 3840

ccacctttag cggagaacct gaccgtcaag ccatgcaaaa cacgctggct tttagcagga 3900

ccgtctacga tcaaacgacc gccacgaccg atcgtaacca gatactcatc accaacgaag 3960

acgaaatcag acccaccaac tcggtcggta tcgacgcgtg gggagcagtt cccaccaaca 4020

accagtcgat cgtgaccccc ggcactcgcg cggccgtcaa caatcaaggg gcgcttcccg 4080

ggatggtgtg gcaaaacaga gacatttacc ctacagggac ccatttggcc aaaattcccg 4140

acactgacaa tcacttccat ccgtccccgc ttattgggcg gtttggctgc aagcatcccc 4200

ctccccagat tttcattaaa aacacacccg tccctgccaa cccttcggaa acgttccaga 4260

cggccaaagt ggcctccttc atcaaccagt actcgaccgg acagtgcacc gtcgaaatct 4320

tttgggaact caagaaggaa acctccaagc gctggaaccc cgaaatccag ttcacctcca 4380

actttggcaa cgcggccgac atccagtttg ccgtctccga cacgggatcc tattccgaac 4440

ctcgtcccat cggtacccgt taccttacca aacctctgta aattaaaccc ttcaataaac 4500

cgtttatgcg taactgtatt tccgtctcct gtcgttattc agtcacatga tgcggcatta 4560

cctcaccgga gtgctggcca gtttccaaga caggctcgct cgctcactcg ggccggggcc 4620

ccaaaggggc ccctagcgac cgcttcgcgg tcgcggcccg agtgagcgag cgagcctgtc 4680

ttggaaactg gcca 4694

<210> 555
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 555
atggctgctg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgcggagttc 300

cagcagcggc ttcagggcga cacatcgttt gggggcaacc tcggcagagc agtcttccag 360

gccaaaaaga gggttcttga acctcttggt ctggttgagc aagcgggtga gacggctcct 420

ggaaagaaga gaccgttgat tgaatccccc cagcagcccg actcctccac gggtatcggc 480

aaaaaaggca agcagccggc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc agtaggacgc tcttcatttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtaccgg aaacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 556
<211> 736
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 556
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
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Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400


Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415


Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430


Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445


Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460


Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590
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```
Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 557
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 557
atggcttccg atggttatct tccagattgg ctcgaggaca acctctctga gggcatccgc       60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac      120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac      180
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aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca gagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attctactgg ccaagtcagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgtcccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 558
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 558
Met Ala Ser Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Arg Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
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Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510
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```
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720
```

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 559
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 559
atggctgctg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggtga caacccctac ctcaagtaca accacgccga cgcggagttc 300

cagcagcggc ttcagggcga cacatcgttt gggggcaacc tcggcagagc agtcttccag 360

gccaaaaaga gggttcttga acctcttggt ctggttgagc aagcgggtga gacggctcct 420

ggaaagaaga gaccgttgat tgaatccccc cagcagcccg actcctccac gggtatcggc 480

aaaaaaggca agcagccggc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc agtaggacgc tcttcatttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtaccgg aaacaacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagt ctggaccgtc tcatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ctgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgccatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 560
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 560
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
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Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Thr Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
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Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 561
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 561
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcaatcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgat 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca taaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac attgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtccccagta a 2211

<210> 562
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 562
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg

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    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
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            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
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545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Ile Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Gln
725 730 735

<210> 563
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 563
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gtgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 564
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 564
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
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Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Cys Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 565
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 565
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gaatggtggg acttgaaacc tggagccccg aaacccaaag tcaaccagca aaagcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggacgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ctgaaagatt tgggactgtg 1740

gcagtcaatc tccagagcag cagcacagac cctgcgaccg gagatgtgca tgccatggga 1800

gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 566
<211> 736

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 566
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Val Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Thr Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590
```

```
Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 567
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"


<220>
<221> modified_base
<222> (955)..(955)
<223> a, c, g, or t
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<220>
<221> modified_base
<222> (971)..(972)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (981)..(981)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (986)..(986)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1235)..(1235)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1694)..(1696)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1698)..(1698)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1763)..(1765)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1778)..(1778)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (2204)..(2204)
<223> a, c, g, or t

<400> 567
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gaatggtggg acttgaaacc tggagccccg aaacccaaag tcaaccagca aaagcaggac 120

aacgctcggg gtcttgtgct tccgggttac aaatacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac cttcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc ttggacgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaataaca attggggatt ccggcccaag agactcaact tcaaactctt caacntccaa 960

gtcaaggagg nnacgacgaa ngatgncgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt acctncagct acacttttga ggacgttcct 1260

ttccacagca gctacgctca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccaactggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag agannncnaa gccactaacc ccgtggccac tgaaagattt gggactgtgg 1740

cagtcaatct ccaagcagca cannnaccct gcgaccgnag atgtgcatgc catgggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

attcctcaca cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag 1920

cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag 1980

ttttcggcta caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat 2100

acatctaact atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat 2160

actgagcctc gccccattgg cacccgttac ctcacccgtc cccngtaa 2208

<210> 568
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 568
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Val Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Gln Val
305                 310                 315                 320

Lys Glu Thr Thr Asp Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                325                 330                 335

Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
            340                 345                 350

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
        355                 360                 365

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val
    370                 375                 380

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
385                 390                 395                 400

Arg Thr Gly Asn Asn Phe Thr Ser Tyr Thr Phe Glu Asp Val Pro Phe
                405                 410                 415

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
            420                 425                 430

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser
        435                 440                 445

Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Thr
    450                 455                 460

Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg
465                 470                 475                 480

Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe
                485                 490                 495

Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile
            500                 505                 510
```

```
Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys
        515                 520                 525

Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly
    530                 535                 540

Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Ala
545                 550                 555                 560

Thr Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Leu
                565                 570                 575

Gln Ser Ser Pro Ala Thr Asp Val His Ala Met Gly Ala Leu Pro Gly
            580                 585                 590

Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605

Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly
    610                 615                 620

Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr
625                 630                 635                 640

Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu
            660                 665                 670

Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln
        675                 680                 685

Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp
    690                 695                 700

Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
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Thr Arg Pro

<210> 569
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 569
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggtc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacgct ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 570
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 570
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

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Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Ala Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 571
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 571
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcaaac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcgggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac gaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

acagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 572
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 572
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg

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    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asn Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
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            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Arg Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
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545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 573
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 573
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaata actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgat 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acggacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcactcaat actccacagg acaagtgagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 574
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 574
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
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Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 575
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 575
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
```

305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asn Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp

```
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Gln
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725 730 735

<210> 576
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 576
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggaacgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cggaaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atcagtaa 2208

<210> 577
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 577
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctatgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg atccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaagttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtatgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggtaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacagacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca agtgtggaca ttgaaaaggt catgattaca 1680

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cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga agttcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

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<210> 578
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 578
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1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
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Gly Phe Arg Pro Lys Arg Leu Lys Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asp Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
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Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Ser Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
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Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 579
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 579
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atgactgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

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ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

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cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcaactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

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gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 580
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

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cgtttcagtt gaactgcggc c 2601

<210> 581
<211> 2601

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggactcg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

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taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

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gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

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cgtttcagtt gaactgcggc c 2601

<210> 582
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 582

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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcctccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

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<211> 2601
<212> DNA
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<220>
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<211> 2601
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<211> 2580
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

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gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

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cgtttcagtt gaactgcggc c 2601

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<211> 2601
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<213> Artificial Sequence

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<221> source
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polynucleotide"

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tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

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caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

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<211> 2601
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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

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<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

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<210> 592
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 593
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 593
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgactgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgac aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggggа cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

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cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

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caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccagtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattgcaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 594
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 594
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cagaattcaa atatctgctt cactcacggt gtcaaagact gtttagagtg ctttcccgtg 180

tcagaatctc aacccgtttc tgtcgtcaaa aaggcgtatc agaaactgtg ctacattcat 240

cacatcatgg gaaaggtgcc agacgcttgc actgcttgcg acctggtcaa tgtggacttg 300

gatgtctgtg tttctgaaca ataaatgact taaaccaggt atggctgccg atggttatct 360

tccagattgg ctcgaggaca accttagtga aggaattcgc gagtggtggg ctttgaaacc 420

tggagcccct caacccaagg caaatcaaca acatcaagac aacgctcgag gtcttgtgct 480

tccgggttac aaataccttg gacccggcaa cggactcgat aaggggggagc cggtcaacgc 540

agcagacgcg gcggccctcg agcacgacaa ggcctacgac cagcagctca aggccggaga 600

caacccgtac ctcaagtaca accacgccga cgccgagttc caggagcggc tcaaagaaga 660

tacgtctttt gggggcaacc tcgggcgagc agtcttccag gccaaaaaga ggcttcttga 720

acctcttggt ctggttgagg aagcggctaa gacggctcct ggaaagaaga ggcctgtaga 780

gcagtctcct caggaaccgg actcctccgc gggtattggc aaatcgggtg cacagcccgc 840

taaaaagaga ctcaatttcg gtcagactgg cgacacagag tcagtcccag accctcaacc 900

aatcggagaa cctcccgcag ccccctcagg tgtgggatct cttacaatgg cttcaggtgg 960

tggcgcacca gtggcagaca ataacgaagg tgccgatgga gtgggtagtt cctcgggaaa 1020

ttggcattgc gattcccaat ggctgggggа cagagtcatc accaccagca cccgaacctg 1080

ggccctgccc acctacaaca atcacctcta caagcaaatc tccaacagca catctggagg 1140

atcttcaaat gacaacgcct acttcggcta cagcaccccc tgggggtatt ttgacttcaa 1200

cagattccac tgccacttct caccacgtga ctggcagcga ctcatcaaca acaactgggg 1260

attccggcct aagcgactca acttcaagct cttcaacatt caggtcaaag aggttacgga 1320

caacaatgga gtcaagacca tcgccaataa ccttaccagc acggtccagg tcttcacgga 1380

ctcagactat cagctcccgt acgtgctcgg gtcggctcac gagggctgcc tcccgccgtt 1440

cccagcggac gttttcatga ttcctcagta cgggtatctg acgcttaatg atggaagcca 1500

ggccgtgggt cgttcgtcct tttactgcct ggaatatttc ccgtcgcaaa tgctaagaac 1560

gggtaacaac ttccagttca gctacgagtt tgagaacgta cctttccata gcagctacgc 1620

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ttcttgggct ctcaatggac gtaatagctt gatgaatcct ggacctgcta tggccagcca 1920

caaagaagga gaggaccgtt tctttccttt gtctggatct ttaatttttg gcaaacaagg 1980

aactggaaga gacaacgtgg atgcggacaa agtcatgata accaacgaag aagaaattaa 2040

aactactaac ccggtagcaa cggagtccta tggacaagtg gccacaaacc accagagtgc 2100

ccaagcacag gcgcagaccg gctgggttca aaaccaagga atacttccgg gtatggtttg 2160

gcaggacaga gatgtgtacc tgcaaggacc catttgggcc aaaattcctc acacggacgg 2220

caactttcac ccttctccgc tgatgggagg gtttggaatg aagcacccgc ctcctcagat 2280

cctcatcaaa aacacacctg tacctgcgga tcctccaacg gccttcaaca aggacaagct 2340

gaactctttc atcacccagt attctactgg ccaagtcagc gtggagatcg agtgggagct 2400

gcagaaggaa aacagcaagc gctggaaccc ggagatccag tacacttcca actattacaa 2460

gtctaataat gttgaatttg ctgttaatac tgaaggtgta tatagtgaac cccgccccat 2520

tggcaccaga tacctgactc gtaatctgta attgcttgtt aatcaataaa ccgtttaatt 2580

cgtttcagtt gaactgcggc c 2601

<210> 595
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 595

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Met Thr Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
```

195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Gln Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu

```
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
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610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 596
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 596
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Gly Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Gly Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 597
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 597
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
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```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Asp
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
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Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 598
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 598
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Leu Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Ser Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 599
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polypeptide"

<400> 599

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
```

```
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Lys Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 600
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 600
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Arg Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 601
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 601
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Val Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 602
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 602
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Arg Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 603
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polypeptide"

<400> 603

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Cys Gly Gly
```

195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu

405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 604
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 604
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Ile Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Tyr Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 605
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 605
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro His Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Asn
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Met Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 606
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 606
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 607
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polypeptide"

<400> 607

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
```

195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu

```
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Arg Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 608
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 608
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ala Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 609
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 609
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Ile Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510
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```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Cys Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
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Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 610
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 610
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270


Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285


Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
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```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Arg Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
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Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 611
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 611

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctgggaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

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<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccgcttct caccacgtga ctggcagcga 900

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aagcacccgc ctcctcagat cctcatcaaa aacgcccctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 613
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 613
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aaggggggagc cggtcagcgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 614
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 614

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

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aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

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tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct 1560

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 615
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

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aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcggctca acttcaagct cttcaacatt 960

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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cacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 616
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 616
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aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

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aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaggct cttcaacatt 960

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 617
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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ctcatcaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

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<210> 618
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

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ctcatcaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

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<210> 619
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagccatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 620
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

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aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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gaccaatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 621
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa tctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 622
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 622
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ccggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 623
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcggg gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ccggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcggcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 624
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 624
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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 625
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caagaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 626
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1325)..(1325)
<223> a, c, g, or t

<400> 626
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

gaccnatact tgcactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

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accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg atatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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<210> 627
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 628
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 628
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aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 629
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 629
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agccgacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 630
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 630
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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

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aaatcgggtg cacagcccgc taagaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatggtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 631
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 631
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tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 632
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc aattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaag aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 633
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac agataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggtaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtatcggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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<210> 634
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 634
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aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 635
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggagg caacccgtgc ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

agatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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<210> 636
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 636
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aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gcctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 637
<211> 2208

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 637
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gccaaaaaga ggcctcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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<210> 638
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcacga ttcctcagta cgggtatctg 1140

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ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta 1260

cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc 1320

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tgggccccga tacctgactc gtaatttt 2208

<210> 639
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacaacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgagatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 640
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 640
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggcgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acctcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcgagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg 1380

ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 641
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccccccagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcggaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atactttcgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 642
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 642
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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ctaaaattca gtgtggccgg acccagcaac atggctgtcc agggaagaaa ctacatacct 1440

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 643
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 643
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

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tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 644
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 644
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtgca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acctcgacta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcgg 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 645
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 645
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 646
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 646

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccgggga caacccgcac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcccgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taagaagaga ctcaatttcg gtcagactgg cgacactgag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggagtg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaggct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 647
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 647
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 648
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 648
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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

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tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 649
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 649

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gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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ttaatttctg gcaaacaagg aactggaaga gacaacgtgg atgcgaacaa agtcatgata 1680

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 650
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 650
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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatag cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct tttcaacatt 960

cgggtcaaag aggttacgga caacaatgga gtcaagacca tcaccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgcttgg gtcggctcac 1080

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gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 651
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggcg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

ccagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 652
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 652
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgggttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag tccctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctg 2208

<210> 653
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
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<222> (377)..(377)
<223> a, c, g, or t

<400> 653
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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gccaaaaaga ggcttcntga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcggggaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

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aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 654
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 654
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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

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cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

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atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 655
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 655

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gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct ggactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggtgatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

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<210> 656
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 656
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtggggcct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgtcgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

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aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ccacaaagct tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 657
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 657
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagagac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

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ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

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atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcgttc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 658
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 658

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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ccgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgggg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tcccatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 659
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 659
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgcgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 660
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 660
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cggctcagag 540

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgacttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 661
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 661
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caagagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgctg tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

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tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

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<210> 662
<211> 2208
<212> DNA
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<210> 665
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polynucleotide"

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gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 668
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 668
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc acgtctgttc agcccaaaaa ctggctacct 1440

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ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgggc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 669
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 669
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg ccccaggaaa ttggcattgc gactccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcacagcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acaggcgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 670
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 670
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cagactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaggaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcgcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatatagc ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gggcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgccatgatt 1680

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 671
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 671
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

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gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 672
<211> 2208

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 672
atggctgccg atggttatct cccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcagcgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaagagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ccaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

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tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 673
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 673
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgctatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagaacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctg 2208

<210> 674
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 674
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gcagtcaatt tccagagcag caacacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 675
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 675
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tacaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gcagtcaatt tccagagcag cgacacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 676
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 676
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcagggc 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccaaca ctcgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gttacgggca cagccagagc ctggaccggc tgatgaatct tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtttgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 677
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 677
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccaaca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 678
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 678
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacgggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtccgttc agcccaaaaa ctggctacct 1440

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ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

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aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 679
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (305)..(305)
<223> a, c, g, or t

<400> 679
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggngcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

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gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcgg cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggccacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag caacacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 680
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 680
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aggacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcga cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gcagtcaatt tccagagcag cagcccagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatagtgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 681
<211> 2208

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 681
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaacc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagactacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

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gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 682
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 682
atggctgccg atggttatcc tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagtcccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

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ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

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gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 683
<211> 2196
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 683
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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gttcaagcct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

ccatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

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ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

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ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctt 2196

<210> 684
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 684
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

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tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

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gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactctcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 685
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 685
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

ctatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggaact tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 686
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 686
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gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacgatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

cccaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caataccagt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 687
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 687
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacctaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacgggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggattc agagtaccaa ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtccgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaatactg cattggacaa tgtcatgatc 1680

acagatgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cccgcgaccg gagatgtgca tgttatggga 1800

gccttacctg gcatggtgtg gcaagacaga gacgtatacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcaaat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccttg 2208

<210> 688
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 688
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc gggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctg 2205

<210> 689
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 689
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Asp Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Val Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Gly Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
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Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Pro
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
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Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 690
<211> 736
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 690
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Arg Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Ile Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Leu Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
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Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 691
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 691
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
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            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Ser Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
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225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Ser Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
```

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        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asp Val Asp Ala Asp Lys Val Ile Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 692
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 692
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Gly Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Gly Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gly Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Ser Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 693
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 693
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser His Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly His Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Gly Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 694
<211> 736
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 694
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn Arg Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Pro Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 695
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 695
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

```
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
```

435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
515 520 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala

645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 696
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 696
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 697
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 697
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Leu Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Lys Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 698
<211> 736
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 698
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590
```

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 699
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 699
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Gly Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser

```
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 700
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 700
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys Arg Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Ala Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 701
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 701
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 702
<211> 736
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 702
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Thr Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 703
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 703
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Ser Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser

```
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Ala Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln His Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 704
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 704
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Arg Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Ser Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 705
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 705
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Arg Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Ala Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe
                405                 410                 415

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
    450                 455                 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
        515                 520                 525

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
    530                 535                 540
```

```
Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr
545                 550                 555                 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
            580                 585                 590

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655

Pro Pro Thr Ala Phe Asn Lys Asp Glu Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 706
<211> 735
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 706
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Asp Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe
                405                 410                 415

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
        435                 440                 445

Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
    450                 455                 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
465                 470                 475                 480

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
            500                 505                 510

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
        515                 520                 525

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr
545                 550                 555                 560

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
                565                 570                 575

Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
            580                 585                 590
```

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
645 650 655

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 707
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 707
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Ala Ile
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser

```
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Thr
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 708
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 708
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Thr Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Gly Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 709
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 709
Met Ala Ala Asp Gly Tyr Phe Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Ser Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Leu
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Val Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 710
<211> 736
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 710
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Ala Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 711
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 711
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
```

```
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Pro Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
```

225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Arg Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser

```
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
```

645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 712
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 712
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Leu Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 713
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 713
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 714
<211> 736
<212> PRT
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> MOD_RES
<222> (442)..(442)
<223> Any naturally occurring amino acid

<400> 714
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Thr Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Xaa Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Asp Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 715
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 715

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu His Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser Tyr Lys
        515                 520                 525

Glu Gly Glu Asp Ser Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Thr Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 716
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 716
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Gly Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asp Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 717
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 717
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Arg Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Cys Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

His Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu

725 730 735

<210> 718
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 718
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Gly Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 719
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

<400> 719

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Arg Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 720
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 720
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asn Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Gly Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 721
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 721
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Val Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Gly Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 722
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 722
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 723
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

<400> 723

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Gly Asn Pro Cys Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Arg Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Ala Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asp Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asp Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Gly Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 724
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 724
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Pro Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 725
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 725
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asn Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Pro Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Arg Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile

305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Thr Met Ala Ser His Lys

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 726
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 726
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Val His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Thr Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Pro Arg Tyr Leu Thr Arg Asn Phe
                725                 730                 735


<210> 727
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

<400> 727

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asn Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Arg Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 728
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 728
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Glu Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Ser Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Ala Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 729
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 729
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Pro Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Ser Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Ser Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Ser Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 730
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 730
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 731
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 731

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 732
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 732
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Asp Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Gly Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 733
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 733
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Cys Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 734
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 734
Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro His Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Arg Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 735
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 735

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 736
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 736
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Thr Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Ile
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 737
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 737
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Ser Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asn Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Glu Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

725 730 735

<210> 738
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 738
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Ile Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Arg Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Arg Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Thr Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Arg Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575
```

```
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 739
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

<400> 739

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Gly Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Ala Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 740
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 740
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Gly Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Val Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460
```

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495


Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540


Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 741
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (126)..(126)
<223> Any naturally occurring amino acid

<400> 741
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Arg Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Xaa Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Pro
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Val
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 742
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 742
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Leu Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560


Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 743
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 743
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asp Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Val Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 744
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 744
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Val Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Leu Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 745
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 745
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Arg Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 746
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 746
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Pro Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Gly Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 747
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 747
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Arg Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Pro Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 748
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 748
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Gly Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Pro Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 749
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 749
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Val Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 750
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 750
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Gln Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Thr Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asp Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 751
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 751
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Pro Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly His Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Thr Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 752
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 752
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Glu Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Thr Gly Thr Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Thr Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asp Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 753
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 753
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Leu Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asp Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 754
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 754
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Ala Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Val Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 755
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 755
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asn Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Pro Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Ser Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 756
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 756
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Thr Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Gly Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 757
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 757
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Pro Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Gly Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 758
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 758
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Arg Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Arg Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Ser Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Gly Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Ala Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 759
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 759
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Gly Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro

```
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Ser Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Thr Leu Pro Gly Met Val Trp Gln
```

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 760
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 760
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Ser Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Glu Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 761
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 761
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Gly Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 762
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 762
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asn Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 763
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 763
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asp Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 764
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 764
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Gly Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Asn Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Gly His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Leu Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Phe Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 765
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 765
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Asn Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Met Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Ala Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 766
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 766
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 767
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> MOD_RES
<222> (102)..(102)
<223> Any naturally occurring amino acid

<400> 767
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Xaa Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Gly Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly His Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Ser Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Asn Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 768
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 768
```

```
Met Ala Ala Asp Gly Tyr Phe Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Arg Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Pro Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 769
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 769
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Thr Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
```

```
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
```

465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Tyr
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 770
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 770
Met Ala Ala Asp Gly Tyr Pro Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Val Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 771
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 771
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Ala Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Pro Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
                725                 730


<210> 772
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 772
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```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

Thr Asp Gly His Ser His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 773
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 773
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
```

```
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Leu Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
```

```
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Thr Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 774
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 774
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Ser Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Pro Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Gln Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 775
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 775
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575
```

```
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 776
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 776
```

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Arg
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 777
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 777
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgcctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tccttttact gcccggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcaccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 778
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 778
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aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

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actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

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tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 779
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 779

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aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

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aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

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tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

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<210> 780
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<223> a, c, g, or t

<400> 780
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caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

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gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccatctcta caagcaaatc 780

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gactttcagc ccggccaagt ttgcttcatt tatcactcag tactccactg gacaggtcag 2040

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<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

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caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

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<210> 782
<211> 2212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<210> 783
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 783
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gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

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actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 784
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 784
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gaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

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tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

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cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgctttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

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tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

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acggatgaag aagagattcg taccaccaat cctgtggcaa cagtgcagta tggaactgtg 1740

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gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 785
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 785

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aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaagg ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

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aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgt tcgggtcggc gcaccaaggc 1080

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cacagcagct acgctcacag ccagagttcg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgctttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgaa cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

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gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 786
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 786
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aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

gaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca gccacctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

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cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

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gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

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aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

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actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 787
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 787
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aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg gagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

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gtctcccgcc gtttccagcg gacgccttca tggtccctca gtatggatac ctcaccctga 1140

acaacggaag tcaagcggtg ggacgctcat ccttttactg cctggagtac ttcccttcgc 1200

agatgctaag gactggaaat aacttccaat tcagctatac cctcgaggat gtacctttc 1260

acagcagcta cgctcacagc cagagtttgg atcgcttgat gaatcctctt attgatcagt 1320

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tgctttttag ccaggctggg cctcagtcta tgtctttgca ggccagaaat tggctacctg 1440

ggccctgcta ccggcaacag agactttcaa agactgctaa cgacaacaac aacagtaact 1500

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gaccagctat ggccagtcac aaaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

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aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 788
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 788

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gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

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cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

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gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 789
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 789
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ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

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gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

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aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

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cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 790
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacgag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

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aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

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cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

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tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 791
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 791

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gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acggaactgg agcaggcgac 540

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gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

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tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattccc cacccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggcgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

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actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

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cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc gacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

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tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

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<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 792
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gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

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tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

aacacctaca acggattctc cacccccctgg ggatactttg acttcaaccg cttccactgc 840

cacttctcac cacgtgactg gcagcgactc atcaacaaca actggggcat gcgacccaaa 900

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aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

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cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

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gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 793
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 793
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gctcggggtc ttgtgcttca gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc ccttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

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cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

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gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 794
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 794
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaggctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

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aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

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acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 795
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atcctccggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgcta gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

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gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 796
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 796
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgaca ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagagc 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 797
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 797
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg tccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggа cagagtcgtc accaagtcca cccgaacctg ggtgccgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctattggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 798
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 798
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacaccga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

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tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 799
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 799
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacggggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

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tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 800
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 800
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggaggggggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaag cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 801
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 801
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg tccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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gattccacgt ggatgggggа cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

gagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctattggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 802
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 802
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacagcgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatgggggа cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

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aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accgccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 803
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 803
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtaccccc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacagg accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 804
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 804
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcctctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat gaagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 805
<211> 2175

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 805
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tttttgggcc ttgaggcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca ccccgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

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acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 806
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 806
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag caccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

cacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 807
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 807
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca gcgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

acgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cagactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 808
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 808
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc gcgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggcg gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatac caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 809
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 809
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggtagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcggca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggggcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccctcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 810
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 810
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

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aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgagccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatgcaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 811
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 811
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatcct caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtgggccagt acttgtaccg cttcgtgagc 1320

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 812
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 812
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg cctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accatcatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgcccccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 813
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 813
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcctc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 814
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 814

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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg ccaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcgggcgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

ggctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataata ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 815
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 815
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccgcc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 816
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 816
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gccgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 817
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 817

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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 818
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 818
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagcctccca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgccgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt cgccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 819
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 819
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

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gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 820
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 820
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

ttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gctgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag ccaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aaccttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccggagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 821
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 821
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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aggcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgggactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgcgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa gggaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 822
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 822
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac gtccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggtgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 823
<211> 2175
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (1652)..(1652)

<223> a, c, g, or t

<400> 823

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tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg cccggaccga ggaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

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gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaa 2175

<210> 824
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 824
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt 60

gagtggtggg ctctgaaacc tggagtccct caacccaaag cgaaccaaca acaccaggac 120

aaccgtcggg gtcttgtgct tccgggttac aaatacctcg gacccggtaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga ggatccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga tcagtctcct caggaaccgg actcatcatc tggtgttggc 480

aaatcgggca aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg cgactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag cccccacaag tttgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

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cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 1380

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 1440

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 1500

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 1560

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 1620

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 1680

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1740

gcaaataact tgcagagctc aaatacagct cccacgacta gaactgtcaa tgatcagggg 1800

gccttacctg gcatggtgtg gcaagatcgt gacgtgtacc ttcaaggacc tatctgggca 1860

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1920

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1980

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 2040

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 2100

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 2160

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgta a 2211

<210> 825
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 825
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg actcgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgagc acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc ggagttccag 300

cagcggcttc agggcgacac atcgtttggg ggcaacctcg gcagagcagt cttccaggcc 360

aaaaagaggg ttcttgaacc tcttggtctg gttgagcaag cgggtgagac ggctcctgga 420

aagaagagac cgttgattga atccccccag cagcccgact cctccacggg tatcggcaaa 480

aaaggcaagc agccggctaa aaagaagctc gttttcgaag acgaaactgg agcaggcgac 540

ggacccccctg agggatcaac ttccggagcc atgtctgatg acagtgagat gcgtgcagca 600

gctggcggag ctgcagtcga gggcggacaa ggtgccgatg gagtgggtaa tgcctcgggt 660

gattggcatt gcgattccac ctggtctgag ggccacgtca cgaccaccag caccagaacc 720

tgggtcttgc ccacctacaa caaccacctc tacaagcgac tcggagagag cctgcagtcc 780

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gccatgcggg tcaaaatctt caacatccag gtcaaggagg tcacgacgtc gaacggcgag 960

acaacggtgg ctaataacct taccagcacg gttcagatct ttgcggactc gtcgtacgaa 1020

ctgccgtacg tgatggatgc gggtcaagag ggcagcctgc ctccttttcc caacgacgtc 1080

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actgacagaa atgccttcta ctgcctggag tactttcctt cgcagatgct gcggactggc 1200

aacaactttg aaattacgta cagttttgag aaggtgcctt tccactcgat gtacgcgcac 1260

agccagagcc tggaccggct gatgaaccct ctcatcgacc agtacctgtg gggactgcaa 1320

tcgaccacca ccggaaccac cctgaatgcc gggactgcca ccaccaactt taccaagctg 1380

cggcctacca acttttccaa ctttaaaaag aactggctgc ccgggccttc aatcaagcag 1440

cagggcttct caaagactgc caatcaaaac tacaagatcc ctgccaccgg gtcagacagt 1500

ctcatcaaat acgagacgca cagcactctg gacggaagat ggagtgccct gacccccgga 1560

cctccaatgg ccacggctgg acctgcggac agcaagttca gcaacagcca gctcatcttt 1620

gcggggccta aacagaacgg caacacggcc accgtacccg ggactctgat cttcacctct 1680

gaggaggagc tggcagccac caacgccacc gatacggaca tgtggggcaa cctacctggc 1740

ggtgaccaga gcaacagcaa cctgccgacc gtggacagac tgacagcctt gggagccgtg 1800

cctggaatgg tctggcaaaa cagagacatt tactaccagg gtcccatttg ggccaagatt 1860

cctcataccg atggacactt tcacccctca ccgctgattg gtgggtttgg gctgaaacac 1920

ccgcctcctc aaatttttat caagaacacc ccggtacctg cgaatcctgc aacgaccttc 1980

agctctactc cggtaaactc cttcattact cagtacagca ctggccaggt gtcggtgcag 2040

attgactggg agatccagaa ggagcggtcc aaacgctgga accccgaggt ccagtttacc 2100

tccaactacg gacagcaaaa ctctctgttg tgggctcccg atgcggctgg gaaatacact 2160

gagcctaggg ctatcggtac ccgctacctc acccaccacc tgtaa 2205

<210> 826
<211> 2234
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 826

atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaaccgtgta ttcgtgtcag 2220

taaaatactg cctc 2234

<210> 827
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 827
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Pro Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 828
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 828
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Val Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
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<210> 829
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 829
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145   150   155   160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Gly Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
```

```
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Gly Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Cys Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
```

580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 830
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 830
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Ala Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Gly Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Ser
                725                 730                 735


<210> 831
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 831
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Leu Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Gly Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210> 832
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 832
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Cys Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160


Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Ser
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asp Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 833
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 833
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asn Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
```

```
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
```

580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 834
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 834
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asp Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Val Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 835
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 835
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Gly Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270
```

```
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Phe Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Ser Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Thr Ala Ala Ser Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr Thr
            580                 585                 590

Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685
```

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 836
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 836
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Glu Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 837
<211> 668
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 837
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Gly Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145   150   155   160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Ser His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Ile Leu Thr Leu Thr Asp Ser Thr
        275                 280                 285

Ala Thr Ser His His Val Thr Gly Ser Asp Ser Leu Thr Thr Thr Gly
    290                 295                 300

Asp Ser Gly Pro Arg Asn Ser Ala Ser Ser Ser Ser Thr Ser Lys Leu
305                 310                 315                 320

Lys Arg Ser Arg Arg Thr Met Ala Arg Arg Leu Leu Pro Ile Thr Leu
                325                 330                 335

Pro Ala Arg Phe Lys Cys Leu Arg Thr Arg Ser Ile Ser Ser Arg Thr
            340                 345                 350

Cys Ser Gly Arg Arg Thr Lys Ala Val Ser Arg Arg Phe Gln Arg Thr
        355                 360                 365

Pro Ser Trp Ser Leu Ser Met Asp Thr Ser Pro Thr Thr Glu Val Lys
```

```
    370                 375                 380

Arg Trp Asp Ala His Pro Phe Thr Ala Trp Ser Thr Ser Leu Arg Arg
385                 390                 395                 400

Cys Gly Leu Glu Ile Thr Ser Asn Ser Ala Ile Pro Ser Arg Met Tyr
                405                 410                 415

Leu Phe Thr Ala Ala Thr Leu Thr Ala Arg Val Trp Ile Ala Ile Leu
            420                 425                 430

Leu Leu Ile Ser Ile Cys Thr Thr Thr Glu Arg Lys Glu Gln Pro Leu
        435                 440                 445

Glu Gln Pro Thr Asn His Gly Cys Phe Leu Ala Arg Leu Gly Leu Ser
    450                 455                 460

Leu Cys Leu Cys Arg Pro Glu Ile Gly Tyr Leu Gly Pro Ala Thr Gly
465                 470                 475                 480

Asn Arg Asp Phe Gln Arg Leu Leu Thr Thr Thr Thr Thr Val Thr Phe
                485                 490                 495

Leu Gly Gln Arg Pro Ala Asn Ile Ile Ser Met Ala Ala Thr Arg Trp
            500                 505                 510

Ile Gln Asp Gln Leu Trp Pro Val Thr Arg Thr Met Lys Lys Asn Phe
        515                 520                 525

Ser Leu Cys Thr Ala Ile Arg Gly Pro Tyr Leu Ala Trp Cys Gly Lys
    530                 535                 540

Ile Val Thr Cys Thr Phe Lys Asp Leu Ser Gly Gln Arg Phe Leu Thr
545                 550                 555                 560

Arg Met Asp Thr Phe Ile Leu Leu Leu Trp Glu Ala Leu Asp Asn Ile
                565                 570                 575

Arg Leu Leu Lys Ser Ser Lys Ile Leu Arg Tyr Arg Gln Ile Leu Arg
```

580 585 590

Arg Leu Ser Ala Arg Pro Ser Leu Leu His Leu Ser Leu Ser Thr Pro
595 600 605

Leu Asp Arg Ser Ala Trp Lys Leu Ser Gly Ser Tyr Arg Lys Lys Thr
610 615 620

Ala Asn Val Gly Ile Gln Arg Phe Ser Thr Leu Pro Thr Thr Thr Ser
625 630 635 640

Leu Leu Met Trp Thr Leu Leu Thr Leu Met Val Phe Ile Val Asn Leu
645 650 655

Ala Leu Leu Glu Pro Gly Ile Ser His Glu Thr Cys
660 665

<210> 838
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 838
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

```
Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Thr Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Leu Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495
```

```
Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700
```

```
Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 839
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 839
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15


Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30


Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60


Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80


Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125
```

```
Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Leu Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Val Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
```

```
Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asp Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540
```

```
Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 840
<211> 734
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 840
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Glu Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
130 135 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145 150 155 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
165 170 175

```
Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380
```

```
Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400


Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415


Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430


Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445


Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460


Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480


Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495


Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510


Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525


Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540


Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560


Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575


Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590
```

```
Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605


Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620


Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640


Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655


Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670


Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685


Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700


Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 841
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 841
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15


Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
```

```
            20                  25                  30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Gly Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
```

225 230 235 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
245 250 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Pro Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305 310 315 320

Thr Thr Ala Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
325 330 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
340 345 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
355 360 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
370 375 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
405 410 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
420 425 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu

```
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
```

645 650 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 842
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 842
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

```
Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Arg Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495
```

```
Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700
```

```
Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720


Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730


<210> 843
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 843
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                   10                  15


Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30


Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Gln Gly
        35                  40                  45


Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60


Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80


Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125
```

```
Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Arg Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
```

```
Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Arg Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540
```

```
Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 844
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 844
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Arg Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Glu Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 845
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 845
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Ser Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

```
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
```

```
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
```

645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 846
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 846
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Ser
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 847
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 847
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Pro Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Val Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Pro Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Cys Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 848
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 848
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Ala Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 849
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 849
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Gly Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Ala Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln

```
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
```

645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 850
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 850
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Val Pro Pro Gln Pro Asn Gly Met Thr Asn
            500                 505                 510

Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe
        515                 520                 525

Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly
    530                 535                 540

Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val
545                 550                 555                 560

Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr
                565                 570                 575

Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly
            580                 585                 590

Ser Val Trp Met Glu Gly Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605

Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
    610                 615                 620

Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625                 630                 635                 640

Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
                645                 650                 655

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
            660                 665                 670

Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
        675                 680                 685

Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
    690                 695                 700
```

Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705 710 715 720

Arg Pro Leu

<210> 851
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 851
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Val Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Glu Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 852
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 852

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Ser Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175
```

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

```
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Ala Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 853
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 853
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Pro Glu Ala Gly Pro Pro Lys Pro Lys
```

20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro

```
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
```

```
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Thr Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Pro Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
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645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 854
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 854
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Leu Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Lys Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 855
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 855
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Pro Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 856
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 856
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr His Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Ser Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Arg Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 857
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 857
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

```
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
```

```
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Ser Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Thr Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Arg Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
```

645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 858
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 858
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Ala Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Gly Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Thr Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 859
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 859
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Val Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Gly Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Gly Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Leu Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 860
<211> 723
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 860
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Ala
595 600 605

Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
610 615 620

Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625 630 635 640

Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
645 650 655

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
660 665 670

Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
675 680 685

Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
690 695 700

Thr Gly Glu Cys Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705 710 715 720

Arg Pro Leu

<210> 861
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 861
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Leu Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Gly
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln

```
        435                 440                 445

Phe Asn Glu Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
```

645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Ala Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 862
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 862
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Ile Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 863
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 863
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Leu Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 864
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 864
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Ala
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Gly
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
165 170 175

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Gly Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

```
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 865
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 865
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
```

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

```
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Ala
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
```

```
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
```

645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 866
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 866
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Pro Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

```
Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 867
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 867
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30


Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45


Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60


Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80


Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110


Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125
```

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 868
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 868

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Pro Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175
```

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Pro Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

```
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 869
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 869
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                   10                  15


Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
```

```
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
```

225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln

```
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
```

645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 870
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 870
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

```
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Ala Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285
```

```
Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Ala
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Leu Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495
```

```
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Val His Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700
```

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 871
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 871
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

```
Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Gly Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335
```

```
Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540
```

```
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Ala Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Gly Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 872
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 872

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175
```

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

```
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Val His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu
```

<210> 873
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> MOD_RES
<222> (551)..(551)
<223> Any naturally occurring amino acid

<400> 873

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205
```

```
Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415
```

```
Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Ser Met Leu Ile Thr Xaa Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620
```

```
Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu



<210> 874
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 874
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460
```

```
Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540


Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575


Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590


Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 875
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 875
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn

```
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
```

305 310 315 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
325 330 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
340 345 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
355 360 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
370 375 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385 390 395 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
405 410 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
420 425 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
435 440 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
450 455 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465 470 475 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
485 490 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
500 505 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro

```
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
```

725 730

<210> 876
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 876
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145 150 155 160

```
Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala Asp
        195                 200                 205

Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Met
    210                 215                 220

Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro Ser
225                 230                 235                 240

Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp Gly
                245                 250                 255

Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
            260                 265                 270

Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln Arg
        275                 280                 285

Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val Lys
    290                 295                 300

Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr Thr
305                 310                 315                 320

Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Asp
                325                 330                 335

Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys Leu
            340                 345                 350

Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr Ala
        355                 360                 365
```

```
Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser Phe
    370                 375                 380

Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn Asn
385                 390                 395                 400

Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser Phe
                405                 410                 415

Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp Gln
            420                 425                 430

Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln Phe
        435                 440                 445

Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp Phe
    450                 455                 460

Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly Val
465                 470                 475                 480

Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu Leu
                485                 490                 495

Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr Asn
            500                 505                 510

Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile Phe
        515                 520                 525

Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu Gly
    530                 535                 540

Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val
545                 550                 555                 560

Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr
                565                 570                 575
```

```
Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly
            580                 585                 590

Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
        595                 600                 605

Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly
    610                 615                 620

Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr
625                 630                 635                 640

Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser
                645                 650                 655

Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp
            660                 665                 670

Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr
        675                 680                 685

Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser
    690                 695                 700

Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr
705                 710                 715                 720

Arg Pro Leu
```

<210> 877
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 877

```
Met Ala Glu Gly Gly Gly Gly Ala Met Gly Asp Ser Ser Gly Gly Ala
1               5                  10                  15

Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Gln Trp
            20                  25                  30

Met Gly Asn Thr Val Ile Thr Lys Thr Thr Arg Thr Trp Val Leu Pro
        35                  40                  45

Ser Tyr Asn Asn His Ile Tyr Lys Ala Ile Thr Ser Gly Thr Ser Gln
    50                  55                  60

Asp Ala Asn Val Gln Tyr Ala Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
65                  70                  75                  80

Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
                85                  90                  95

Leu Ile Asn Asn His Trp Gly Ile Arg Pro Lys Ser Leu Lys Phe Lys
            100                 105                 110

Ile Phe Asn Val Gln Val Lys Glu Val Thr Thr Gln Asp Gln Thr Lys
        115                 120                 125

Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Asp
    130                 135                 140

Glu His Gln Leu Pro Tyr Val Leu Gly Ser Ala Thr Glu Gly Thr Met
145                 150                 155                 160

Pro Pro Phe Pro Ser Asp Val Tyr Ala Leu Pro Gln Tyr Gly Tyr Cys
                165                 170                 175

Thr Met His Thr Asn Gln Asn Gly Ala Arg Phe Asn Asp Arg Ser Ala
            180                 185                 190

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
        195                 200                 205
```

```
Asn Phe Glu Phe Thr Phe Asp Phe Glu Glu Val Pro Phe His Ser Met
    210                 215                 220

Phe Ala His Ser Gln Asp Leu Asp Arg Leu Met Asn Pro Leu Val Asp
225                 230                 235                 240

Gln Tyr Leu Trp Asn Phe Asn Glu Val Asp Ser Ser Arg Asn Ala Gln
                245                 250                 255

Phe Lys Lys Ala Val Lys Gly Ala Tyr Gly Thr Met Gly Arg Asn Trp
            260                 265                 270

Leu Pro Gly Pro Lys Phe Leu Asp Gln Arg Val Arg Ala Tyr Thr Gly
        275                 280                 285

Gly Thr Asp Asn Tyr Ala Asn Trp Asn Ile Trp Ser Asn Gly Asn Lys
    290                 295                 300

Val Asn Leu Lys Asp Arg Gln Tyr Leu Leu Gln Pro Gly Pro Val Ser
305                 310                 315                 320

Ala Thr Tyr Thr Glu Gly Glu Ala Ser Ser Leu Pro Ala Gln Asn Ile
                325                 330                 335

Leu Gly Ile Ala Lys Asp Pro Tyr Arg Ser Gly Ser Thr Thr Ala Gly
            340                 345                 350

Ile Ser Asp Ile Met Val Thr Glu Glu Gln Glu Val Ala Pro Thr Asn
        355                 360                 365

Gly Val Gly Trp Lys Pro Tyr Gly Arg Thr Val Thr Asn Glu Gln Asn
    370                 375                 380

Thr Thr Thr Ala Pro Thr Ser Ser Asp Leu Asp Val Leu Gly Ala Leu
385                 390                 395                 400

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Leu Gln Gly Pro Ile
                405                 410                 415
```

```
Gly Ala Lys Ile Pro Lys Thr Asp Gly Lys Phe His Pro Ser Pro Asn
            420                 425                 430


Leu Gly Gly Phe Gly Leu His Asn Pro Pro Pro Gln Val Phe Ile Lys
        435                 440                 445


Asn Thr Pro Val Pro Ala Asp Pro Pro Val Glu Tyr Val His Gln Lys
    450                 455                 460


Trp Asn Ser Tyr Ile Thr Gln Tyr Ser Thr Gly Gln Cys Thr Val Glu
465                 470                 475                 480


Met Val Trp Glu Leu Arg Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
                485                 490                 495


Ile Gln Phe Thr Ser Asn Phe Ser Asn Arg Thr Ser Ile Met Phe Ala
            500                 505                 510


Pro Asn Glu Thr Gly Gly Tyr Val Glu Asp Arg Leu Ile Gly Thr Arg
        515                 520                 525


Tyr Leu Thr Gln Asn Leu
    530


<210> 878
<211> 554
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 878
Met Thr Ser Val Asn Ser Ala Glu Ala Ser Thr Gly Ala Gly Gly Gly
1               5                   10                  15


Gly Ser Asn Pro Val Lys Ser Met Trp Ser Glu Gly Ala Thr Phe Ser
            20                  25                  30
```

```
Ala Asn Ser Val Thr Cys Thr Phe Ser Arg Gln Phe Leu Ile Pro Tyr
        35                  40                  45

Asp Pro Glu His His Tyr Lys Val Phe Ser Pro Ala Ala Ser Ser Cys
    50                  55                  60

His Asn Ala Ser Gly Lys Glu Ala Lys Val Cys Thr Ile Ser Pro Ile
65                  70                  75                  80

Met Gly Tyr Ser Thr Pro Trp Arg Tyr Leu Asp Phe Asn Ala Leu Asn
                85                  90                  95

Leu Phe Phe Ser Pro Leu Glu Phe Gln His Leu Ile Glu Asn Tyr Gly
            100                 105                 110

Ser Ile Ala Pro Asp Ala Leu Thr Val Thr Ile Ser Glu Ile Ala Val
        115                 120                 125

Lys Asp Val Thr Asp Lys Thr Gly Gly Gly Val Gln Val Thr Asp Ser
    130                 135                 140

Thr Thr Gly Arg Leu Cys Met Leu Val Asp His Glu Tyr Lys Tyr Pro
145                 150                 155                 160

Tyr Val Leu Gly Gln Gly Gln Asp Thr Leu Ala Pro Glu Leu Pro Ile
                165                 170                 175

Trp Val Tyr Phe Pro Pro Gln Tyr Ala Tyr Leu Thr Val Gly Asp Val
            180                 185                 190

Asn Thr Gln Gly Ile Ser Gly Asp Ser Lys Lys Leu Ala Ser Glu Glu
        195                 200                 205

Ser Ala Phe Tyr Val Leu Glu His Ser Ser Phe Gln Leu Leu Gly Thr
    210                 215                 220

Gly Gly Thr Ala Thr Met Ser Tyr Lys Phe Pro Pro Val Pro Pro Glu
225                 230                 235                 240
```

```
Asn Leu Glu Gly Cys Ser Gln His Phe Tyr Glu Met Tyr Asn Pro Leu
                245                 250                 255

Tyr Gly Ser Arg Leu Gly Val Pro Asp Thr Leu Gly Gly Asp Pro Lys
            260                 265                 270

Phe Arg Ser Leu Thr His Glu Asp His Ala Ile Gln Pro Gln Asn Phe
        275                 280                 285

Met Pro Gly Pro Leu Val Asn Ser Val Ser Thr Lys Glu Gly Asp Ser
    290                 295                 300

Phe Asn Thr Gly Ala Gly Lys Ala Leu Thr Gly Leu Ser Thr Gly Thr
305                 310                 315                 320

Ser Gln Asn Thr Arg Ile Ser Leu Arg Pro Gly Pro Val Ser Gln Pro
                325                 330                 335

Tyr His His Trp Asp Thr Asp Lys Tyr Val Thr Gly Ile Asn Ala Ile
            340                 345                 350

Ser His Gly Gln Thr Thr Tyr Gly Asn Ala Glu Asp Lys Glu Tyr Gln
        355                 360                 365

Gln Gly Val Gly Arg Phe Pro Asn Glu Lys Glu Gln Leu Lys Gln Leu
    370                 375                 380

Gln Gly Leu Asn Met His Thr Tyr Phe Pro Asn Lys Gly Thr Gln Gln
385                 390                 395                 400

Tyr Thr Asp Gln Ile Glu Arg Pro Leu Met Val Gly Ser Val Trp Asn
                405                 410                 415

Arg Arg Ala Leu His Tyr Glu Ser Gln Leu Trp Ser Lys Ile Pro Asn
            420                 425                 430

Leu Asp Asp Ser Phe Lys Thr Gln Phe Ala Ala Leu Gly Gly Trp Gly
        435                 440                 445
```

Leu His Gln Pro Pro Pro Gln Ile Phe Leu Lys Ile Leu Pro Gln Ser
450 455 460

Gly Pro Ile Gly Gly Ile Lys Ser Met Gly Ile Thr Thr Leu Val Gln
465 470 475 480

Tyr Ala Val Gly Ile Met Thr Val Thr Met Thr Phe Lys Leu Gly Pro
485 490 495

Arg Lys Ala Thr Gly Arg Trp Asn Pro Gln Pro Gly Val Tyr Pro Pro
500 505 510

His Ala Ala Gly His Leu Pro Tyr Val Leu Tyr Asp Pro Thr Ala Thr
515 520 525

Asp Ala Lys Gln His His Arg His Gly Tyr Glu Lys Pro Glu Glu Leu
530 535 540

Trp Thr Ala Lys Ser Arg Val His Pro Leu
545 550

<210> 879
<211> 587
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 879
Met Ser Asp Gly Thr Ser Gln Pro Asp Gly Gly Asn Ala Val His Ser
1 5 10 15

Ala Ala Arg Val Glu Arg Ala Ala Asp Gly Pro Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Val Gly Val Ser Thr Gly Ser Tyr Asp
35 40 45

Asn Gln Thr His Tyr Arg Phe Leu Gly Asp Gly Trp Val Glu Ile Thr

```
    50                  55                  60

Ala Leu Ala Thr Arg Leu Val His Leu Asn Met Pro Lys Ser Glu Asn
65                  70                  75                  80

Tyr Cys Arg Ile Arg Val His Asn Thr Thr Asp Thr Ser Val Lys Gly
                85                  90                  95

Asn Met Ala Lys Asp Asp Ala His Glu Gln Ile Trp Thr Pro Trp Ser
            100                 105                 110

Leu Val Asp Ala Asn Ala Trp Gly Val Trp Leu Gln Pro Ser Asp Trp
        115                 120                 125

Gln Tyr Ile Cys Asn Thr Met Ser Gln Leu Asn Leu Val Ser Leu Asp
    130                 135                 140

Gln Glu Ile Phe Asn Val Val Leu Lys Thr Val Thr Glu Gln Asp Ser
145                 150                 155                 160

Gly Gly Gln Ala Ile Lys Ile Tyr Asn Asn Asp Leu Thr Ala Cys Met
                165                 170                 175

Met Val Ala Val Asp Ser Asn Asn Ile Leu Pro Tyr Thr Pro Ala Ala
            180                 185                 190

Asn Ser Met Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Ala
        195                 200                 205

Ser Pro Tyr Arg Tyr Tyr Phe Cys Val Asp Arg Asp Leu Ser Val Thr
    210                 215                 220

Tyr Glu Asn Gln Glu Gly Thr Ile Glu His Asn Val Met Gly Thr Pro
225                 230                 235                 240

Lys Gly Met Asn Ser Gln Phe Phe Thr Ile Glu Asn Thr Gln Gln Ile
                245                 250                 255

Thr Leu Leu Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Tyr Tyr Phe
```

```
            260                 265                 270

Asp Thr Asn Pro Val Lys Leu Thr His Thr Trp Gln Thr Asn Arg Gln
        275                 280                 285

Leu Gly Gln Pro Pro Leu Leu Ser Thr Phe Pro Glu Ala Asp Thr Asp
    290                 295                 300

Ala Gly Thr Leu Thr Ala Gln Gly Ser Arg His Gly Ala Thr Gln Met
305                 310                 315                 320

Glu Val Asn Trp Val Ser Glu Ala Ile Arg Thr Arg Pro Ala Gln Val
                325                 330                 335

Gly Phe Cys Gln Pro His Asn Asp Phe Glu Ala Ser Arg Ala Gly Pro
            340                 345                 350

Phe Ala Ala Pro Lys Val Pro Ala Asp Val Thr Gln Gly Met Asp Arg
        355                 360                 365

Glu Ala Asn Gly Ser Val Arg Tyr Ser Tyr Gly Lys Gln His Gly Glu
    370                 375                 380

Asn Trp Ala Ala His Gly Pro Ala Pro Glu Arg Tyr Thr Trp Asp Glu
385                 390                 395                 400

Thr Asn Phe Gly Ser Gly Arg Asp Thr Arg Asp Gly Phe Ile Gln Ser
                405                 410                 415

Ala Pro Leu Val Val Pro Pro Pro Leu Asn Gly Ile Leu Thr Asn Ala
            420                 425                 430

Asn Pro Ile Gly Thr Lys Asn Asp Ile His Phe Ser Asn Val Phe Asn
        435                 440                 445

Ser Tyr Gly Pro Leu Thr Thr Phe Ser His Pro Ser Pro Val Tyr Pro
    450                 455                 460

Gln Gly Gln Ile Trp Asp Lys Glu Leu Asp Leu Glu His Lys Pro Arg
```

465 470 475 480

Leu His Ile Thr Ala Pro Phe Val Cys Lys Asn Asn Ala Pro Gly Gln
485 490 495

Met Leu Val Arg Leu Gly Pro Asn Leu Thr Asp Gln Tyr Asp Pro Asn
500 505 510

Gly Ala Thr Leu Ser Arg Ile Val Thr Tyr Gly Thr Phe Phe Trp Lys
515 520 525

Gly Lys Leu Thr Met Arg Ala Lys Leu Arg Ala Asn Thr Thr Trp Asn
530 535 540

Pro Val Tyr Gln Val Ser Val Glu Asp Asn Gly Asn Ser Tyr Met Ser
545 550 555 560

Val Thr Lys Trp Leu Pro Thr Ala Thr Gly Asn Met Gln Ser Val Pro
565 570 575

Leu Ile Thr Arg Pro Val Ala Arg Asn Thr Tyr
580 585

<210> 880
<211> 584
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 880
Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
1 5 10 15

Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
20 25 30

Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
35 40 45

```
Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
    50                  55                  60

Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
65                  70                  75                  80

Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
                85                  90                  95

Ala Leu Asp Asp Ile His Val Glu Ile Val Thr Pro Trp Ser Leu Val
            100                 105                 110

Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
        115                 120                 125

Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
    130                 135                 140

Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro
145                 150                 155                 160

Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
                165                 170                 175

Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
            180                 185                 190

Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
        195                 200                 205

Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
    210                 215                 220

Thr Ser Gly Thr Pro Thr Asn Val Tyr His Gly Thr Asp Pro Asp Asp
225                 230                 235                 240

Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
                245                 250                 255
```

```
Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro
            260                 265                 270

Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
        275                 280                 285

Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly
    290                 295                 300

Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
305                 310                 315                 320

Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
                325                 330                 335

Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
            340                 345                 350

Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
        355                 360                 365

Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His
    370                 375                 380

Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
385                 390                 395                 400

Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln
                405                 410                 415

Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro
            420                 425                 430

Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
        435                 440                 445

Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
    450                 455                 460
```

```
Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
465                 470                 475                 480


Arg Leu His Ile Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly
                485                 490                 495


Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Gln Tyr Asp Pro
            500                 505                 510


Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp
        515                 520                 525


Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr
    530                 535                 540


Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn
545                 550                 555                 560


Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser
                565                 570                 575


Gln Leu Ala Pro Arg Lys Leu Tyr
            580


<210> 881
<211> 548
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 881
Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln Thr Glu Phe Lys
1               5                   10                  15


Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn Ser Ser Arg Leu
            20                  25                  30
```

```
Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Arg Arg Val Val Val
        35                  40                  45

Asn Asn Met Asp Lys Thr Ala Val Asn Gly Asn Met Ala Leu Asp Asp
    50                  55                  60

Ile His Ala Gln Ile Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala
65                  70                  75                  80

Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr
                85                  90                  95

Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val
            100                 105                 110

Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val
        115                 120                 125

Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn
    130                 135                 140

Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu Gly
145                 150                 155                 160

Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr Tyr Phe
                165                 170                 175

Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr Ser Gly Thr
            180                 185                 190

Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp Val Gln Phe Tyr
        195                 200                 205

Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg Thr Gly Asp Glu
    210                 215                 220

Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro Cys Arg Leu Thr
225                 230                 235                 240
```

```
His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro Pro Phe Leu Asn
                245                 250                 255

Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly Asp Ile Gly Val
            260                 265                 270

Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly Asn Thr Asn Tyr
        275                 280                 285

Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val Gly Tyr Ser Ala
    290                 295                 300

Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro Phe Lys Thr Pro
305                 310                 315                 320

Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala
                325                 330                 335

Asp Gly Asn Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr
            340                 345                 350

Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile Ala His Gln
        355                 360                 365

Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln Asn Ile Asn Phe
    370                 375                 380

Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro Ile
385                 390                 395                 400

Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr Tyr Gly
                405                 410                 415

Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro Asn Gly Gln
            420                 425                 430

Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro Arg Leu His Val
        435                 440                 445
```

```
Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly Gln Leu Phe Val
    450                 455                 460


Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro Asp Ala Ser Ala
465                 470                 475                 480


Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp Trp Lys Gly Lys
                485                 490                 495


Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr Trp Asn Pro Ile
            500                 505                 510


Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn Tyr Val Pro Ser
        515                 520                 525


Asn Ile Gly Gly Met Lys Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro
    530                 535                 540


Arg Lys Leu Tyr
545


<210> 882
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 882
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460
```

```
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495


Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510


Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540


Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 883
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 883
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys

```
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
```

725 730 735

<210> 884
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 884
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Glu Pro Asp Ser Ser Ser Gly Thr
145 150 155 160

```
Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn
                485                 490                 495

Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575
```

```
Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala
            580                 585                 590

Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 885
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

<400> 885

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 886
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 886
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460
```

```
Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480


Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495


Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510


Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525


Lys Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540


Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560


Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Arg Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590


Ala Thr Glu Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
            660                 665                 670
```

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 887
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 887
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

```
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
```

```
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
```

705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 888
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 888
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

```
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 889
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 889

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asp Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 890
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 890
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 891
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 891
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
```

```
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Val Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
```

```
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asn Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
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705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 892
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 892
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaagacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 893
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 893

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415
```

```
Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu



<210> 894
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 894
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
```

245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu

```
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
```

660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 895
<211> 4472
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 895
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attacgtcat aggggagtgg tcctgtatta gctgtcacgt gagtgctttt gcgacatttt 120

gcgacaccac gtggccattc atggtatata tggccgagtg agcgagcagg atctccattt 180

tgaccgcgaa atttgaacga gcagcagcca tgccgggctt ctacgagatc gtgcttaagg 240

tgccgagcga cctggacgag cacctgccgg gcatttctga ctcgtttgtg aactgggtgg 300

cagagaagga atgggagctg cccccggatt ctgacatgga tcggaatctg attgagcagg 360

cacccctgac cgtggccgag aagctacagc gcgacttcct ggtccaatgg cgccgcgtga 420

gtaaggcccc ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc 480

tccatattct ggtagagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc 540

agattcggga caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact 600

ggttcgcggt gacaaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt 660

gctacatccc caactacctg ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta 720

acatggagga gtatataagc gcgtgcttga acctggccga gcgcaaacgg ctcgtggcgc 780

agcacctgac ccacgtcagc cagacccagg agcagaacaa ggagaatctg aacccgaatt 840

ctgacgcgcc tgtcatccgg tcaaaaacct ccgcgcgcta catggagctg gtcgggtggc 900

tggtggaccg gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca 960

tctccttcaa cgccgcctcc aactcgcggt ctcagatcaa ggccgcgctg gacaatgccg 1020

gcaagatcat ggcgctgacc aaatccgcgc ccgactacct ggtaggcccc gctctgcccg 1080

cggacattaa atccaaccgc atctaccgca tcctggagct gaatggctac gaccctgcct 1140

acgccggttc cgtctttctc ggctgggccc agaaaaagtt tggcaaaagg aacaccatct 1200

ggctgtttgg gccggccacc acgggcaaga ccaacatcgc ggaagccatc gcccacgccg 1260

tgcccttcta cggctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 1320

acaagatggt gatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca 1380

aggccattct cggcggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga 1440

tcgatcccac ccccgtgatc gtcacctcca acaccaacat gtgcgccgtg attgacggga 1500

acagcaccac cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactta 1560

cccgccgtct ggagcacgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc 1620

gctgggcgca ggatcacgtg accgaggtgg cgcatgagtt ctacgtcaga aagggtggag 1680

ctaacaaaag acccgccccc gatgacgcgg atataagcga gcccaagcgg gcctgcccct 1740

cagtcgcgga tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt 1800

accaaaacaa atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaaaacat 1860

gcgagagaat gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag 1920

aatgtttccc tggcgtgtca gaatctcaac cggtcgtcag aaaaaagacg tatcggaaac 1980

tctgtgcgat tcatcatctg ctggggcggg cacccgagat tgcttgctcg gcctgcgacc 2040

tggtcaacgt ggacctggat gactgtgttt ctgagcaata aatgacttaa accaggtatg 2100

gctgccgatg gttatcttcc agattggctc gaggacaacc tctctgaggg cattcgcgag 2160

tggtgggacc tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacaac 2220

ggccggggtc tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag 2280

ggggagcccg tcaacgcggc ggacgcagcg gccctcgagc acgacaaggc ctacgaccag 2340

cagctccaag cgggtgacaa tccgtacctg cggtataatc acgccgacgc cgagtttcag 2400

gagcgtctgc aagaagatac gtcttttggg ggcaacctcg ggcgcgcagt cttccaggcc 2460

aaaaagcggg ttctcgaacc tctgggcctg gttgaatcgc cggttaagac ggctcctgga 2520

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aagaaaggcc agcagcccgc aaaaaagaga ctcaattttg ggcagactgg cgactcagag 2640

tcagtccccg accctcaacc aatcggagaa ccaccagcag gcccctctgg tctgggatct 2700

ggtacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 2760

gtgggtagtt cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 2820

accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcaaatc 2880

tccaacggga cctcgggagg aagcaccaac gacaacacct acttcggcta cagcaccccc 2940

tgggggtatt ttgacttcaa cagattccac tgccactttt caccacgtga ctggcagcga 3000

ctcatcaaca acaactgggg attccggccc aagaggctca acttcaagct cttcaacatc 3060

caagtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 3120

acgattcagg tctttacgga ctcggaatac cagctcccgt acgtgctcgg ctcggcgcac 3180

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cgggtacctg 3240

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ccttctcaaa tgctgagaac gggcaacaac tttgaattca gctacaactt cgaggacgtg 3360

cccttccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa ccctctcatc 3420

gaccagtact tgtactacct gtcccggact caaagcacgg gcggtactgc aggaactcag 3480

cagttgctat tttctcaggc cgggcctaac aacatgtcgg ctcaggccaa gaactggcta 3540

cccggtccct gctaccggca gcaacgcgtc tccacgacac tgtcgcagaa caacaacagc 3600

aactttgcct ggacgggtgc caccaagtat catctgaatg gcagagactc tctggtgaat 3660

cctggcgttg ccatggctac ccacaaggac gacgaagagc gatttttttcc atccagcgga 3720

gtcttaatgt ttgggaaaca gggagctgga aaagacaacg tggactatag cagcgtgatg 3780

ctaaccagcg aggaagaaat aaagaccacc aacccagtgg ccacagaaca gtacggcgtg 3840

gtggccgata acctgcaaca gcaaaacgcc gctcctattg taggggccgt caatagtcaa 3900

ggagccttac ctggcatggt gtggcagaac cgggacgtgt acctgcaggg tcccatctgg 3960

gccaagattc ctcatacgga cggcaacttt catccctcgc cgctgatggg aggctttgga 4020

ctgaagcatc cgcctcctca gatcctgatt aaaaacacac ctgttcccgc ggatcctccg 4080

accaccttca atcaggccaa gctggcttct ttcatcacgc agtacagtac cggccaggtc 4140

agcgtggaga tcgagtggga gctgcagaag gagaacagca aacgctggaa cccagagatt 4200

cagtacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa tactgagggt 4260

acttattccg agcctcgccc cattggcacc cgttacctca cccgtaatct gtaattacat 4320

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctcctgt ccttcttatc 4380

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acttacgtca tcgggttacc cctagtgatg ga 4472

<210> 896
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 896
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460
```

```
Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480


Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495


Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510


Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525


His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540


Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560


Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575


Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590


Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670
```

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 897
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 897
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
```

```
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
```

```
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Arg Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
```

705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 898
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 898
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Arg Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 899
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 899
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

```
Gly Lys Arg Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365
```

```
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Arg Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

```
Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 900
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 900
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Arg Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

```
Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400
```

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Arg Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 901
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 901

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
```

```
            20                  25                  30

Lys Ala Asn Gln Gln Arg Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Arg Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Arg Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Arg Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Arg Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Arg Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
405 410 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu

```
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Arg Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Arg Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
```

645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Arg Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 902
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 902
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacaag gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaagacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctg 2214

<210> 903
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 903
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcaagaaag agactcaatt ttgggcagac tggcgactca 540

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cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

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gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

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agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacagg gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggag acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaggacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 904
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 904
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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagagag gccagcagcc cgcaagaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccagga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacagg gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

atgctaacca gcgaggaaga aataaggacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 905
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 905
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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaggcaggac 120

aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagagag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

atccaagtca aggaggtcac gcagaatgaa ggcaccagga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtgct cggctcggcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

gtgcccttcc acagcagcta cgcgcacagc cagagcctgg accggctgat gaaccctctc 1320

atcgaccagt acttgtacta cctgtcccgg actcaaagca cgggcggtac tgcaggaact 1380

cagcagttgc tattttctca ggccgggcct aacaacatgt cggctcaggc caagaactgg 1440

ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

aatcctggcg ttgccatggc tacccacagg gacgacgaag agcgattttt tccatccagc 1620

ggagtcttaa tgtttgggag acagggagct ggaagagaca acgtggacta tagcagcgtg 1680

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caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caagctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 906
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 906
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aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgcgc agtcttccag 360

gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagagag gccagcagcc cgcaaaaaag agactcaatt ttgggcagac tggcgactca 540

gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgcac ctgggccctg cccacctaca acaaccacct ctacaggcaa 780

atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

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ctacccggtc cctgctaccg gcagcaacgc gtctccacga cactgtcgca gaacaacaac 1500

agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

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caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caggctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 907
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 907

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aacggccggg gtctggtgct tcctggctac aggtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacag ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

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gccaaaaagc gggttctcga acctctgggc ctggttgaat cgccggttag gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

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gagtcagtcc ccgaccctca accaatcgga gaaccaccag cagccccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

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atctccaacg ggacctcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagaggc tcaacttcaa gctcttcaac 960

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ctgactctga acaatggcag tcaggctgtg ggccggtcgt ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgaat tcagctacaa cttcgaggac 1260

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agcaactttg cctggacggg tgccaccaag tatcatctga atggcagaga ctctctggtg 1560

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gtggtggccg ataacctgca acagcaaaac gccgctccta ttgtaggggc cgtcaatagt 1800

caaggagcct tacctggcat ggtgtggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcatac ggacggcaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaagc atccgcctcc tcagatcctg attaaaaaca cacctgttcc cgcggatcct 1980

ccgaccacct tcaatcaggc caggctggct tctttcatca cgcagtacag taccggccag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaaacgctg gaacccagag 2100

attcagtaca cttccaacta ctacaaatct acaaatgtgg actttgctgt caatactgag 2160

ggtacttatt ccgagcctcg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 908
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 908
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
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Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495
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Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Gln Arg Gly Glu Ser Gly
            580                 585                 590

His Gly Tyr Phe Ala Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly
        595                 600                 605

Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly
    610                 615                 620

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser
625                 630                 635                 640

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu
                645                 650                 655

Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala
            660                 665                 670

Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
        675                 680                 685

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
    690                 695                 700
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Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp
705 710 715 720

Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly
725 730 735

Thr Arg Tyr Leu Thr Arg Asn Leu
740

<210> 909
<211> 8359
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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
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Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
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Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
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Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Thr Asn Asp Asn Thr
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Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
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His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
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Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
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Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
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Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
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Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
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Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
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Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
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Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
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Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
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Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
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Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
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Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
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Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
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Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
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35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525
```

```
Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Val Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
```

Leu

<210> 913
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 913
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctctac gggcatcggc 480

aagaaaggcc agcagcccgc gaaaaagaga ctcaactttg ggcagactgg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccaacagcc aatcgggagg aagcaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgatggc accacgacca tcgccaataa ccttaccagc 1020

acggttcagg tctttacgga ctcggaatac cagctcccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cgggtacctg 1140

actctgaaca atggcagtca ggccgtgggc cgttcctcct tctactgcct ggagtacttt 1200

ccttctcaaa tgctgagaac gggcaacaac tttgagttca gctacacgtt tgaggacgtg 1260

ccttttcaca gcagctacgc gcacagccaa agcctggacc ggctgatgaa ccccctcatc 1320

gaccagtacc tgtactacct gtctcggact cagaccacgg gaggtaccgc aggaaatcgg 1380

acgttgcaat tttctcaggc cgggcctagt agcatggcga atcaggccaa aaactggcta 1440

cccgggccct gctaccggca gcaacgcgtc tccaagacaa cgaatcaaaa taacaacagc 1500

aactttgcct ggaccggtgc caccaagtat catctgaatg gcagagactc tctggtaaat 1560

cccggtgtcg ctatggcaac ccacaaggac gacgaagacc gatttttttcc gtccagcgga 1620

gtcttaatat ttgggaaaca gggagctgga aatgacaacg tggaccttga caacgttatg 1680

ataaccagtg aggaagaaat taaaaccacc aacccagtgg ccacagaaga gtacggcgtg 1740

gtggccacta acctgcaatc ggcaaacacc gctcctcaaa cagggaccgt caacagtcaa 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcctatctgg 1860

gccaagattc ctcacacgga cggaaacttt catccctcgc cgctgatggg aggctttgga 1920

ctgaaacacc cgcctcctca gatcctgatt aagaatacac ctgttcccgc gaatcctcca 1980

actaccttca gtccagctaa gtttgcgtcg ttcatcacgc agtacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaaa gaaaacagca aacgctggaa cccagagatt 2100

caatacactt ccaactacaa caaatctaca aatgtggact ttgctgttga cacagaaggc 2160

gtttattctg agcctcgccc catcggcacc cgttacctca cccgtaatct g 2211

<210> 914
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 914
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
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    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
```

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            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Ile Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Val Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala
            580                 585                 590

Pro Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
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625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 915
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 915
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccaaaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gacgaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccgtcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttcaat tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

cagacgttgc agttttctca ggccgggcct agcagcatgg cgaatcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga caacgaatca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcgtcctca tatttggcaa gcagggagct ggaaatgaca acgtggacta tagcaacgtg 1680

atgataacca gcgaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggcta ctaacctaca gtcggcaaac accgctcctc aaacggggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 916
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 916
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320
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Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
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Asn Leu

<210> 917
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 917
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttcaat tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

cagacgttgc agttttctca ggccgggcct agcaacatgg cgaatcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga caacgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tatttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctcctc aaatagggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 918
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 918
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 919
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 919
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tggtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttgagt tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc caaaaactgg 1440

ctgcctggac cctgctacag acagcagcgc gtctccacga cactgtcgca aaacaacaac 1500

agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcatcctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 920
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 920
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
```

```
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540
```

```
Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 921
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 921
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacttcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgagt tcagctacac gtttgaggac 1260

gtgccttttc acagcagcta cgcgcacagc caaagcctgg accggctgat gaacccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

cagcagttgc tattttctca ggccgggcct agtaacatgt cggctcaggc caaaaactgg 1440

ctacccgggc cctgctaccg gcagcaacgc gtctccacga cactgtcgca aaataacaac 1500

agcaactttg cctggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacccacaag gacgacgaag agcgattttt tccgtccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aattaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac accgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggaaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc taagctggcg tcgttcatca cgcagtacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaagaaaaca gcaaacgctg gaacccagag 2100

attcaataca cttccaacta ctacaaatct acaaatgtgg actttgctgt taacacagaa 2160

ggcacttatt ctgagcctcg ccccatcggc acccgttacc tcacccgtaa tctg 2214

<210> 922
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 922
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala

```
        435                 440                 445

Arg Thr Gln Ser Thr Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Ala Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Val Val Ser Ser Asn Leu Gln Ser Ala Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
```

645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Asp Lys Ser Thr Asn Val Asp Phe Ala Val Asp Ser Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 923
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 923
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccaaaaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

attaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtc aaagtgcagg tagtaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctgc ggttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020

acggttcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctacctg 1140

actctcaaca atggcagtca gtctgtggga cgttcctcct tctactgcct ggagtacttc 1200

ccctctcaga tgctgagaac gggcaacaac tttgagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc acacagccag agcctggacc ggctgatgaa tcccctcatc 1320

gaccagtact tgtactacct ggccagaaca cagagtacca caggaggcac agctggcaat 1380

cgggaactgc agttttacca ggccgggcct tcaactatgg ccgaacaagc caagaattgg 1440

ttacctggac cttgctaccg gcaacaaaga gtctccaaaa cgctggatca aaacaacaac 1500

agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt 1560

aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca gctaacaaaa ctacattgga aaatgtgtta 1680

atgacaaatg aagaagaaat taaaactact aatcctgtag ccacggaaga atacggggta 1740

gtcagcagca acttacaatc ggctaatact gcaccccaga cacaaactgt caacagccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg 1980

gaggtgttta ctcctgccaa gtttgcttcg ttcatcacac agtacagcac cggacaagtc 2040

agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt 2100

cagtacacct ccaactatga taagtcgact aatgtggact ttgccgttga cagcgagggt 2160

gtttactctg agcctcgccc tattggcact cgttacctca cccgtaatct g 2211

<210> 924
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 924
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

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Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335
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Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Ala Gln Asn Arg Glu Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540
```

```
Gln Gly Ala Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560


Asp Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575


Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590


Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605


Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Ala Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 925
<211> 2205
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 925
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctcttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagtcaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcag ccccctctgg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtcaat caggggccag caacgacaac cactacttcg gctacagcac cccctggggg 840

tattttgatt tcaacagatt ccactgccat ttctcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcaacttca agctcttcaa catccaagtc 960

aaggaggtca cgacgaatga tggcaccacg accatcgcta ataaccttac cagcacggtt 1020

caagtcttca cggactcgga gtaccagttg ccgtacgtcc tcggctctgc gcaccagggc 1080

tgcctccctc cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc 1140

aacaatggca gccaggcagt gggacggtca tccttttact gcctggaata tttcccatcg 1200

cagatgctga gaacgggcaa taactttacc ttcagctaca ccttcgagga cgtgcctttc 1260

cacagcagct acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag 1320

tacctgtatt acctgagcag aactcagact acgtccggaa ctgcccaaaa cagggagttg 1380

cagtttagcc aggcgggtcc atctagcatg gctaatcagg ccaaaaactg gctacctgga 1440

ccctgttacc ggcagcagcg cgtttctaaa acagcaaatg acaacaacaa cagcaacttt 1500

gcctggactg gtgctacaaa atatcacctt aatgggcgtg attctttagt caaccctggc 1560

cctgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcttg 1620

atttttggaa agcagggcgc cggagcttca aacgttgatt tggacaatgt catgatcaca 1680

gacgaagagg aaatcaaaac cactaacccc gtggccaccg aacaatatgg gactgtggca 1740

accaatctcc agagcagcaa cacagcccct gcgaccggaa ctgtgaattc tcagggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

attcctcaca cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag 1920

cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccgacaacg 1980

ttttcgcctg caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga aatacagtat 2100

acatctaact ataataaatc tgccaacgtt gatttcactg tggacaccaa tggagtttat 2160

agtgagcctc gccccattgg cacccgttac ctcacccgta acctg 2205

<210> 926
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 926
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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```
Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Pro Ser Ser Met Ala Gln Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

```
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 927
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 927
atggctgctg acggttatct tccagattgg ctcgaggaca acctttctga aggcattcgt       60

gagtggtggg atctgaaacc tggagcccct caacccaaag cgaaccaaca acaccaggac      120

gacggtcggg gtcttgtgct tccgggttac aaatacctcg gacccttaa cggactcgac       180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac      240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt      300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag      360

gccaaaaaga gggtccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct      420

ggaaagaaga ggcctgtaga acagtctcct caggaaccgg actcatcatc tggtattggc      480

aaatcgggcc aacagcctgc cagaaaaaga ctaaatttcg gtcagactgg agactcagag      540

tcagtcccag accctcaacc tctcggagaa ccaccagcag ccccctcagg tgtgggatct      600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga      660

gtgggtaatt cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc      720
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accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagaaa ctcaacttca agctcttcaa catccaagtt 960

aaagaggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 1020

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 1080

tgtctcccgc cgtttccagc ggacgtcttc atgatccctc agtatggata cctcaccctg 1140

aacaacggaa gtcaagcggt gggacgctca tcctttttact gcctggagta cttcccttcg 1200

cagatgctaa ggactggaaa taacttcaca ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgagcag aacgcaaaca acctctggaa caacccaaca atcacggctg 1380

caatttagcc aggctgggcc ttcgtctatg gctcagcagg ccaaaaattg gctacctggg 1440

ccctgctacc ggcaacagag agtttcaaag actgctaacg acaacaacaa cagtaacttt 1500

gcttggacag gggccaccaa atatcatctc aatggccgcg actcgctggt gaatccagga 1560

ccagctatgg ccagtcacaa ggacgatgaa gaaaaatttt tccctatgca cggcgttcta 1620

atatttggca aacaagggac aggggcaagt aacgtagatt tagataatgt aatgattacg 1680

gatgaagaag agattcgtac caccaatcct gtggcaacag agcagtatgg aactgtggca 1740

actaacttgc agagctcaaa tacagctccc gcgactggaa ctgtcaatag tcaggggggcc 1800

ttacctggca tggtgtggca agatcgtgac gtgtaccttc aaggacctat ctgggcaaag 1860

attcctcaca cggatggaca ctttcatcct tctcctctga tgggaggctt tggactgaaa 1920

catccgcctc ctcaaatctt gatcaaaaat actccggtac cggcaaatcc tccgacgact 1980

ttcagcccgg ccaagtttgc ttcatttatc actcagtact ccactggaca ggtcagcgtg 2040

gaaattgagt gggagctaca gaaagaaaac agcaaacgtt ggaatccaga gattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tagacactaa tggtgtttat 2160

agtgaacctc gccctattgg aacccggtat ctcacacgaa acttg 2205

<210> 928

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 928
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
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Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590
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```
Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 929
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 929
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 930
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 930
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 931
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 931
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
```

```
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
```

```
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 932

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 932
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590
```

```
Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 933
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 933
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 934
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 934
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270
```

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Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

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Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
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Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 935
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 935
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

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        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
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325 330 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
435 440 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly

530 535 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
580 585 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 936

<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 936
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctcttc gggcatcggc 480

aagaaaggcc agcagcccgc gaaaaagaga ctcaactttg ggcagacagg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaacg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccagccaat cgggagcaag caccaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcacc acgaccatcg ccaataacct taccagcacg 1020

gttcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg gtacctgact 1140

ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga gtactttcct 1200

tctcaaatgc tgagaacggg caacaacttt gagttcagct acacgtttga ggacgtgcct 1260

tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc cctcatcgac 1320

cagtacctgt actacctgtc tcggactcag accacgagtg gtaccgcagg aaatcggacg 1380

ttgcaatttt ctcaggccgg gcctagtagc atggcgaatc aggccaaaaa ctggctaccc 1440

gggccctgct accggcagca acgcgtctcc aagacagcga atcaaaataa caacagcaac 1500

tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct ggtaaatccc 1560

ggtcccgcta tggcaaccca caaggacgac gaagacaaat tttttccgat gagcggagtc 1620

ttaatatttg ggaaacaggg agctggaaat agcaacgtgg accttgacaa cgttatgata 1680

accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta cggcacggtg 1740

gccactaacc tgcaatcgtc aaacaccgct cctgctacag ggaccgtcaa cagtcaagga 1800

gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc tatctgggcc 1860

aagattcctc acacggacgg acactttcat ccctcgccgc tgatgggagg ctttggactg 1920

aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgaa tcctccaact 1980

accttcagtc cagctaagtt tgcgtcgttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actacaacaa atctacaaat gtggactttg ctgttgacac aaatggcgtt 2160

tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta a 2211

<210> 937
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 937
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

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Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
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Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
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Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
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Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 938
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 938
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cgcgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgag tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa caggcaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc atgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacacac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 939
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 939
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cgcgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgag tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa caggcaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc atgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacacac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 940
<211> 2202
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 940
atgactgacg gttaccttcc agattggcta gaggacaacc tctctgaagg cgttcgagag 60

tggtgggcgc tgcaacctgg agcccctaaa cccaaggcaa atcaacaaca tcaggacaac 120

gctcggggtc ttgtgcttcc gggttacaaa tacctcggac ccggcaacgg acttgacaag 180

ggggaacccg tcaacgcagc ggacgcggca gccctcgaac acgacaaggc ctacgaccag 240

cagctcaagg ccggtgacaa cccctacctc aagtacaacc acgccgacgc cgagtttcag 300

gagcgtcttc aagaagatac gtcttttggg ggcaacctcg gacgagcagt cttccaggcc 360

aaaaagagga tccttgagcc tctgggtctg gttgaggaag cggctaagac ggctcctgga 420

aaaaagagac ctgtagagca atctccagca gaaccggact cctcttcggg catcggcaaa 480

tcaggccagc agcccgctag aaaaagactg aattttggtc agactggcga cacagagtca 540

gtcccagacc ctcaaccact cggacaacct cccgcagccc cctctggtgt gggatctact 600

acaatggctt caggcggtgg cgcaccaatg gcagacaata acgagggtgc cgatggagtg 660

ggtaattcct caggaaattg gcattgcgat tcccaatggc tgggcgacag agtcatcacc 720

accagcaccc gcacctgggc cctgcccacc tacaacaatc acctctacaa gcaaatctcc 780

agccaatcag gagccaccaa cgacaaccac tactttggct acagcacccc ctgggggtat 840

tttgacttca acagattcca ctgccacttt tcaccacgtg actggcaaag actcatcaac 900

aacaactggg gattccgacc caagagactc aacttcaagc tctttaacat tcaagtcaaa 960

gaggtcacgc agaatgacgg tacgacgacg attgccaata accttaccag cacggttcag 1020

gtgtttactg actccgagta ccagctcccg tacgtcctcg gctcggcgca tcagggatgc 1080

ctcccgccgt tcccagcaga cgtcttcatg gtcccacagt atggatacct caccctgaac 1140

aacgggagtc aggcggtagg acgctcttcc ttttactgcc tggagtactt tccttctcag 1200

atgctgcgta ctggaaacaa ctttcagttt agctacactt ttgaagacgt gcctttccac 1260

agcagctacg ctcacagcca aagtctggac cgtctcatga atcctctgat cgaccagtac 1320

ctgtactatc tgaacaggac acaaacagcc agtggaactc agcagtctcg gctactgttt 1380

agccaagctg gacccaccag tatgtctctt caagctaaaa actggctgcc tggaccttgc 1440

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actggtgcca ccaaatatca tctgaatggc cgggactcat tggtgaaccc gggccctgct 1560

atggccagtc acaaggatga caaagaaaag tttttcccca tgcatggaac cctgatattt 1620

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gaagaaatcc gcaccaccaa tcccgtggct acggagcagt acgggactgt gtcaaataat 1740

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cacaccgatg gacactttca tccttctcca ctgatgggag gttttgggct caaacacccg 1920

cctcctcaga tcatgatcaa aaacactccc gttccagcca atcctcccac aaactttagt 1980

gcggcaaagt ttgcttcctt catcacacag tactccacgg ggcaggtcag cgtggagatc 2040

gagtgggagc tgcagaagga gaacagcaaa cgctggaatc ccgaaattca gtacacttcc 2100

aactacaaca aatctgttaa tgtggacttt actgtggaca ctaatggtgt gtattcagag 2160

cctcgcccca ttggcaccag atacctgact cgtaatctgt aa 2202

<210> 941
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 941
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 942
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 942
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

aagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggagagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcaatacgg ctacctgacg 1140

ctcaacaatg gcagccaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 943
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 943
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

aacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc acttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

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caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagt 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 944
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 944
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaagc gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acaaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aaccagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agctcaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

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gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aaacacccgc ctcctcagat cctcatcaaa aacacacctg ttcctgcgaa tcctccggcg 1980

gagttttcag ctacaaagtt tgcttcattc atcacccaat actccacagg acaagtgagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaagc gctggaatcc cgaagtgcag 2100

tacacatcca attatgcaaa atctgccaac gttgatttta ccgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt taccttaccc gtcccctgta a 2211

<210> 945
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 945
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcgccc caagaaccag actcctcatc gggcatcggc 480

aaatcaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatt 720

accaccagca cccgaacctg ggccctgccc acctataaca accacctcta caaacaaatc 780

tccagcgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg attttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

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ttccacagca gctacgcgca cagccaaagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacttgt attacctaaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga ctggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcttcaca caaagacgac gaagacaagt tctttccaat gagcggtgtc 1620

atgatttttg gcaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc aatttgggcc 1860

aaaattcctc acacagatgg acactttcac ccgtctcctc ttatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagt 2040

gtggaaattg aatgggagtt gcagaaagaa aacagcaagc gttggaatcc cgaagtgcag 2100

tacacatcta attatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 946
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 946
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcaccc caagaaccag actcctcctc gggcattggc 480

aaatcaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tttgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa cgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

gttcaagtct tctcggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctgacg 1140

ctcaacaatg gcagcaaagc cgtgggacgt tcatcctttt actgcctgga atatttccct 1200

tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

caatacctgt attacctgaa cagaactcaa aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgtgggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt atcggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaat 1500

tttacctgga ctggtgcttc aaaatataac ctcaatgggc gtgaatccat catcaaccct 1560

ggcactgcta tggcctcaca caaagacgac gaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaagagag cgccggagct tcaaacactg cattggacaa tgtcatgatt 1680

acagacgaag aggaaattaa agccactaac cctgtggcca ccgaaagatt tgggaccgtg 1740

gcagtcaatt tccagagcag cagcacagac cctgcgaccg gagatgtgca tgttatggga 1800

gcattacctg gcatggtgtg gcaagataga gacgtgtacc tgcagggtcc catttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc ttatgggcgg ctttggactc 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt actccacagg acaagtgagc 2040

gtggaaattg aatgggagtt gcagaaagaa aacagtaagc gctggaatcc cgaagtgcag 2100

tacacatcta attatgcaaa atctgccaac gttgacttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 947
<211> 2970
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 947
agatgaccgc caaggtcgta gagtccgcca aggccattct gggcggcagc aaggtgcgcg 60

tggaccaaaa atgcaaggcc tctgcgcaga tcgaccccac ccccgtgatc gtcacctcca 120

acaccaacat gtgcgccgtg attgacggga acagcaccac cttcgagcac cagcagcccc 180

tgcaggaccg gatgttcaag tttgaactca cccgccgcct cgactacgac tttggcaagg 240

tcaccaagca ggaagtcaag gacttttcc ggtgggcggc tgatcacgtg actgacgtgg 300

ctcatgagtt ttacgtcaca aagggtggag ctaagaaaag gcccgccccc tctgacgagg 360

atataagcga gcccaagcgg ccgcgcgtgt catttgcgca gccggagacg tcagacgcgg 420

aagctcccgg agacttcgcc gacaggtacc aaaacaaatg ttctcgtcac gcgggtatgc 480

tgcagatgct ctttccctgc aagacgtgcg agagaatgaa tcagaattcc aacgtctgct 540

tcacgcacgg tcagaaagat tgcggggagt gctttcccgg gtcagaatct caaccggttt 600

ctgtcgtcag aaaaacgtat cagaaactgt gcatccttca tcagctccgg ggggcacccg 660

agatcgcctg ctctgcttgc gaccaactca accccgattt ggacgattgc caatttgagc 720

aataaatgac tgaaatcagg tatggctgct gacggttatc ttccagattg gctcgaggac 780

aacctctctg aaggcattcg cgagtggtgg gcgctgaaac ctggagctcc acaacccaag 840

gccaaccaac agcatcagga caacggcagg ggtcttgtgc ttcctgggta caagtacctc 900

ggacccttca acggactcga caagggagag ccggtcaacg aggcagacgc cgcggccctc 960

gagcacgaca aggcctacga caagcagctc gagcaggggg acaacccgta tctcaagtac 1020

aaccacggcg acgccgagtt ccagcagcgc ttggcgaccg acacctcttt tgggggcaac 1080

ctcgggcgag cagtcttcca ggccaaaaag aggattctcg agcctctggg tctggttgaa 1140

gagggcgtta aaacggctcc tggaaagaaa cgcccattag aaaagactcc aaatcggccg 1200

accaacccgg actctgggaa ggccccggcc aagaaaaagc aaaaagacgg cgaaccagcc 1260

gactctgcta gaaggacact cgactttgaa gactctggag caggagacgg acccccctgag 1320

ggatcatctt ccggagaaat gtctcatgat gctgagatgc gtgcggcgcc aggcggaaat 1380

gctgtcgagg cgggacaagg tgccgatgga gtgggtaatg cctccggtga ttggcattgc 1440

gattccacct ggtcagaggg ccgagtcacc accaccagca cccgaacctg ggtcctaccc 1500

acgtacaaca accacctgta cctgcgaatc ggaacaacgg ccaacagcaa cacctacaac 1560

ggattctcca ccccctgggg atactttgac tttaaccgct tccactgcca cttttcccca 1620

cgcgactggc agcgactcat caacaacaac tggggactca ggccgaaatc gatgcgtgtt 1680

aaaatcttca acatacaggt caaggaggtc acgacgtcaa acggcgagac tacggtcgct 1740

aataacctta ccagcacggt tcagatcttt gcggattcga cgtatgaact cccatacgtg 1800

atggacgccg gtcaggaggg gagctttcct ccgtttccca acgacgtctt tatggttccc 1860

caatacggat actgcggagt tgtcactgga aaaaaccaga accagacaga cagaaatgcc 1920

ttttactgcc tggaatactt tccatcccaa atgctaagaa ctggcaacaa ttttgaagtc 1980

agttaccaat ttgaaaaagt tcctttccat tcaatgtacg cgcacagcca gagcctggac 2040

agaatgatga atcctttact ggatcagtac ctgtggcatc tgcaatcgac cactaccgga 2100

aattccctta atcaaggaac agctaccacc acgtacggga aaattaccac tggagacttt 2160

gcctactaca ggaaaaactg gttgcctgga gcctgcatta aacaacaaaa attttcaaag 2220

aatgccaatc aaaactacaa gattcccgcc agcgggggag acgccctttt aaagtatgac 2280

acgcatacca ctctaaatgg gcgatggagt aacatggctc ctggacctcc aatggcaacc 2340

gcaggtgccg gggactcgga ttttagcaac agccagctga tctttgccgg acccaatccg 2400

agcggtaaca cgaccacatc ttcaaacaat ttgttgttta cctcagaaga ggagattgcc 2460

acaacaaacc cacgagacac ggacatgttt ggacagattg cagataataa tcaaaatgcc 2520

accaccgccc ctcacatcgc taacctggac gctatgggaa ttgttcccgg aatggtctgg 2580

caaaacagag acatctacta ccagggccct atttgggcca aggtccctca cacggacgga 2640

cactttcacc cttcgccgct gatgggagga tttggactga aacacccgcc tccacagatt 2700

ttcatcaaaa acacccccgt acccgccaat cccaatacta cctttagcgc tgcaaggatt 2760

aattcttttc tgacgcagta cagcaccgga caagttgccg ttcagatcga ctgggaaatt 2820

cagaaggagc attccaaacg ctggaatccc gaagttcaat ttacttcaaa ctacggcact 2880

caaaattcta tgctgtgggc tcccgacaat gctggcaact accacgaact ccgggctatt 2940

gggtcccgtt tcctcaccca ccacttgtaa 2970

<210> 948
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 948
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Ser Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Gly Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly His Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr His Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210> 949
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 949
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Ser Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Gly Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly His Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr His Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
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<210> 950
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 950

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Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1               5                  10                  15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20                  25                  30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Val Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
```

```
                165                 170                 175

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
            180                 185                 190

Ala Pro Ser Gly Val Gly Ser Thr Thr Met Ala Ser Gly Gly Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300

Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320

Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335

Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
```

```
    370                 375                 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400

Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln
        435                 440                 445

Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460

Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480

Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn Ser
                485                 490                 495

Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510

Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp Lys
        515                 520                 525

Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu Gly
    530                 535                 540

Thr Asn Ala Asn Asn Ala Asp Leu Glu Asn Val Met Ile Thr Asp Glu
545                 550                 555                 560

Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Thr
                565                 570                 575

Val Ser Asn Asn Leu Gln Asn Ser Asn Ala Gly Pro Thr Thr Gly Thr
```

580 585 590

Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg Asp
595 600 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
610 615 620

His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625 630 635 640

Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro
645 650 655

Thr Asn Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
675 680 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys
690 695 700

Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu
705 710 715 720

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 951
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 951
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 952
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 952
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Lys Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210> 953
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 953
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr His Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 954
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 954
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
```

```
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Leu Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
```

580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 955
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 955
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Gly Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 956
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 956
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Leu Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Lys Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

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Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210> 957
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 957
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Ala Thr Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Lys Thr Pro Asn Arg Pro Thr Asn Pro Asp Ser Gly Lys
145                 150                 155                 160

Ala Pro Ala Lys Lys Lys Gln Lys Asp Gly Glu Pro Ala Asp Ser Ala
                165                 170                 175

Arg Arg Thr Leu Asp Phe Glu Asp Ser Gly Ala Gly Asp Gly Pro Pro
            180                 185                 190

Glu Gly Ser Ser Ser Gly Glu Met Ser His Asp Ala Glu Met Arg Ala
        195                 200                 205

Ala Pro Gly Gly Asn Ala Val Glu Ala Gly Gln Gly Ala Asp Gly Val
    210                 215                 220

Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly
225                 230                 235                 240

Arg Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr Asn
                245                 250                 255

Asn His Leu Tyr Leu Arg Ile Gly Thr Thr Ala Asn Ser Asn Thr Tyr
            260                 265                 270

Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Leu Arg Pro Lys Ser Met Arg Val Lys Ile Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro Tyr
            340                 345                 350

Val Met Asp Ala Gly Gln Glu Gly Ser Phe Pro Pro Phe Pro Asn Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Val Val Thr Gly Lys
    370                 375                 380

Asn Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Val Ser Tyr Gln
                405                 410                 415

Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Met Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp His Leu Gln
        435                 440                 445

Ser Thr Thr Thr Gly Asn Ser Leu Asn Gln Gly Thr Ala Thr Thr Thr
    450                 455                 460

Tyr Gly Lys Ile Thr Thr Gly Asp Phe Ala Tyr Tyr Arg Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Ala Cys Ile Lys Gln Gln Lys Phe Ser Lys Asn Ala Asn
                485                 490                 495

Gln Asn Tyr Lys Ile Pro Ala Ser Gly Gly Asp Ala Leu Leu Lys Tyr
            500                 505                 510

Asp Thr His Thr Thr Leu Asn Gly Arg Trp Ser Asn Met Ala Pro Gly
        515                 520                 525
```

```
Pro Pro Met Ala Thr Ala Gly Ala Gly Asp Ser Asp Phe Ser Asn Ser
    530                 535                 540

Gln Leu Ile Phe Ala Gly Pro Asn Pro Ser Gly Asn Thr Thr Thr Ser
545                 550                 555                 560

Ser Asn Asn Leu Leu Phe Thr Ser Glu Glu Glu Ile Ala Thr Thr Asn
                565                 570                 575

Pro Arg Asp Thr Asp Met Phe Gly Gln Ile Ala Asp Asn Asn Gln Asn
            580                 585                 590

Ala Thr Thr Ala Pro His Ile Ala Asn Leu Asp Ala Met Gly Ile Val
        595                 600                 605

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
    610                 615                 620

Trp Ala Lys Val Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
625                 630                 635                 640

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
                645                 650                 655

Asn Thr Pro Val Pro Ala Asn Pro Asn Thr Thr Phe Ser Ala Ala Arg
            660                 665                 670

Ile Asn Ser Phe Leu Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Gln
        675                 680                 685

Ile Asp Trp Glu Ile Gln Lys Glu His Ser Lys Arg Trp Asn Pro Glu
    690                 695                 700

Val Gln Phe Thr Ser Asn Tyr Gly Thr Gln Asn Ser Met Leu Trp Ala
705                 710                 715                 720

Pro Asp Asn Ala Gly Asn Tyr His Glu Leu Arg Ala Ile Gly Ser Arg
                725                 730                 735
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Phe Leu Thr His His Leu
740

<210> 958
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 958
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa ggcggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcag ccccctcagg tctgggacct 600

aatacaatgg cttcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggca cctcgggagg aagcaccaac gacaacacct attttggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcactttt caccacgtga ctggcaacga 900

ctcatcaaca acaattgggg attccggccc aaaagactca acttcaagct gttcaacatc 960

caggtcaagg aagtcacgac gaacgaaggc accaagacca tcgccaataa tctcaccagc 1020

accgtgcagg tctttacgga ctcggagtac cagttaccgt acgtgctagg atccgctcac 1080

cagggatgtc tgcctccgtt cccggcggac gtcttcatgg ttcctcagta cggctattta 1140

actttaaaca atggaagcca agccctggga cgttcctcct tctactgtct ggagtatttc 1200

ccatcgcaga tgctgagaac cggcaacaac tttcagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctggaca ggctgatgaa tcccctcatc 1320

gaccagtacc tgtactacct ggtcagaacg caaacgactg gaactggagg gacgcagact 1380

ctggcattca gccaagcggg tcctagctca atggccaacc aggctagaaa ttgggtgccc 1440

ggaccttgct accggcagca gcgcgtctcc acgacaacca accagaacaa caacagcaac 1500

tttgcctgga cgggagctgc caagtttaag ctgaacggcc gagactctct aatgaatccg 1560

ggcgtggcaa tggcttccca caaggatgac gacgaccgct tcttcccttc gagcggggtc 1620

ctgatttttg gcaagcaagg agccgggaac gatggagtgg attacagcca agtgctgatt 1680

acagatgagg aagaaatcaa ggctaccaac cccgtggcca cagaagaata tggagcagtg 1740

gccatcaaca accaggccgc caatacgcag gcgcagaccg gactcgtgca caaccagggg 1800

gtgattcccg gcatggtgtg gcagaataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacggacgg caactttcac ccgtctcccc tgatgggcgg ctttggactg 1920

aagcacccgc ctcctcaaat tctcatcaag aacacaccgg ttccagcgga cccgccgctt 1980

accttcaacc aggccaagct gaactctttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaatcg agtgggagct gcagaaagaa aacagcaaac gctggaatcc agagattcaa 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgtcaacac ggagggggtt 2160

tatagcgagc ctcgccccat tggcacccgt tacctcaccc gcaacctgta a 2211

<210> 959
<211> 2592
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 959
ctggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatggaagtg 420

cagctccaag ccagtggtgg cggactggtg caggcaggag gcagcttgag gctcagctgt 480

gccgccagcg gcttcaagat cacccactac accatgggct ggttccggca ggcccctggc 540

aaggagaggg agttcgtgag caggattacc tggggtggtg acaacacctt ctacagcaac 600

agcgtgaagg gcaggttcac catcagcagg gacaacgcca agaacaccgt gtacctgcag 660

atgaacagcc tgaagcccga ggacaccgcc gactactact gtgcagccgg cagtaccagc 720

accgctaccc ccctgagggt ggactactgg ggcaaaggca ctcaggtgac agtgtcttca 780

ggagggggtg gcagcgctcc tggaaagaaa cgtccggtag agcagtcgcc acaagagcca 840

gactcctcct cgggcatcgg caagacaggc cagcagcccg ctaaaaagag actcaatttt 900

ggtcagactg gcgactcaga gtcagtcccc gatccacaac ctctcggaga acctccagca 960

gccccctcag gtctgggacc taatacaatg gcttcaggcg gtggcgctcc aatggcagac 1020

aataacgaag gcgccgacgg agtgggtaat tcctcgggaa attggcattg cgattccaca 1080

tggctggggg acagagtcat caccaccagc acccgaacct gggccctgcc cacctacaac 1140

aaccacctct acaagcaaat ctccaacggc acctcgggag gaagcaccaa cgacaacacc 1200

tattttggct acagcacccc ctgggggtat tttgacttca acagattcca ctgtcacttt 1260

tcaccacgtg actggcaacg actcatcaac aacaattggg gattccggcc caaaagactc 1320

aacttcaagc tgttcaacat ccaggtcaag gaagtcacga cgaacgaagg caccaagacc 1380

atcgccaata atctcaccag caccgtgcag gtctttacgg actcggagta ccagttaccg 1440

tacgtgctag gatccgctca ccagggatgt ctgcctccgt tcccggcgga cgtcttcatg 1500

gttcctcagt acggctattt aactttaaac aatggaagcc aagccctggg acgttcctcc 1560

ttctactgtc tggagtattt cccatcgcag atgctgagaa ccggcaacaa ctttcagttc 1620

agctacacct tcgaggacgt gcctttccac agcagctacg cgcacagcca gagcctggac 1680

aggctgatga atcccctcat cgaccagtac ctgtactacc tggtcagaac gcaaacgact 1740

ggaactggag ggacgcagac tctggcattc agccaagcgg gtcctagctc aatggccaac 1800

caggctagaa attgggtgcc cggaccttgc taccggcagc agcgcgtctc cacgacaacc 1860

aaccagaaca acaacagcaa ctttgcctgg acgggagctg ccaagtttaa gctgaacggc 1920

cgagactctc taatgaatcc gggcgtggca atggcttccc acaaggatga cgacgaccgc 1980

ttcttccctt cgagcggggt cctgattttt ggcaagcaag gagccgggaa cgatggagtg 2040

gattacagcc aagtgctgat tacagatgag gaagaaatca aggctaccaa ccccgtggcc 2100

acagaagaat atggagcagt ggccatcaac aaccaggccg ccaatacgca ggcgcagacc 2160

ggactcgtgc acaaccaggg ggtgattccc ggcatggtgt ggcagaatag agacgtgtac 2220

ctgcagggtc ccatctgggc caaaattcct cacacggacg gcaactttca cccgtctccc 2280

ctgatgggcg gctttggact gaagcacccg cctcctcaaa ttctcatcaa gaacacaccg 2340

gttccagcgg acccgccgct taccttcaac caggccaagc tgaactcttt catcacgcag 2400

tacagcaccg gacaggtcag cgtggaaatc gagtgggagc tgcagaaaga aaacagcaaa 2460

cgctggaatc cagagattca atacacttcc aactactaca aatctacaaa tgtggacttt 2520

gctgtcaaca cggagggggt ttatagcgag cctcgcccca ttggcacccg ttacctcacc 2580

cgcaacctgt aa 2592

<210> 960
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 960
ctggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatggaggtg 420

cagctgcagg cttctggagg aggactggtg caggctggag ggagtctgag gctgtcttgc 480

agtgcctcag tgaggacttt ctccatctac gccatgggct ggtttaggca ggctcccggg 540

aaggagcgcg aattcgtggc cggaatcaac cggtctggcg acgtgaccaa gtacgctgat 600

ttcgtgaaag gccggtttag catttccaga gacaacgcca agaatatggt gtatctgcag 660

atgaactccc tgaaacctga agacacagct ctgtactatt gtgccgctac ttgggcctac 720

gataccgtgg gggctctgac atcaggatat aatttttggg gccaggggac ccaggtgaca 780

gtgagctccg gaggaggagg aagcgctcct ggaaagaaac gtccggtaga gcagtcgcca 840

caagagccag actcctcctc gggcatcggc aagacaggcc agcagcccgc taaaaagaga 900

ctcaattttg gtcagactgg cgactcagag tcagtccccg atccacaacc tctcggagaa 960

cctccagcag ccccctcagg tctgggacct aatacaatgg cttcaggcgg tggcgctcca 1020

atggcagaca ataacgaagg cgccgacgga gtgggtaatt cctcgggaaa ttggcattgc 1080

gattccacat ggctgggggа cagagtcatc accaccagca cccgaacctg ggccctgccc 1140

acctacaaca accacctcta caagcaaatc tccaacggca cctcgggagg aagcaccaac 1200

gacaacacct attttggcta cagcaccccc tgggggtatt ttgacttcaa cagattccac 1260

tgtcactttt caccacgtga ctggcaacga ctcatcaaca acaattgggg attccggccc 1320

aaaagactca acttcaagct gttcaacatc caggtcaagg aagtcacgac gaacgaaggc 1380

accaagacca tcgccaataa tctcaccagc accgtgcagg tctttacgga ctcggagtac 1440

cagttaccgt acgtgctagg atccgctcac cagggatgtc tgcctccgtt cccggcggac 1500

gtcttcatgg ttcctcagta cggctattta actttaaaca atggaagcca agccctggga 1560

cgttcctcct tctactgtct ggagtatttc ccatcgcaga tgctgagaac cggcaacaac 1620

tttcagttca gctacacctt cgaggacgtg cctttccaca gcagctacgc gcacagccag 1680

agcctggaca ggctgatgaa tcccctcatc gaccagtacc tgtactacct ggtcagaacg 1740

caaacgactg gaactggagg gacgcagact ctggcattca gccaagcggg tcctagctca 1800

atggccaacc aggctagaaa ttgggtgccc ggaccttgct accggcagca gcgcgtctcc 1860

acgacaacca accagaacaa caacagcaac tttgcctgga cgggagctgc caagtttaag 1920

ctgaacggcc gagactctct aatgaatccg ggcgtggcaa tggcttccca caaggatgac 1980

gacgaccgct tcttcccttc gagcggggtc ctgatttttg gcaagcaagg agccgggaac 2040

gatggagtgg attacagcca agtgctgatt acagatgagg aagaaatcaa ggctaccaac 2100

cccgtggcca cagaagaata tggagcagtg gccatcaaca accaggccgc caatacgcag 2160

gcgcagaccg gactcgtgca caaccagggg gtgattcccg gcatggtgtg gcagaataga 2220

gacgtgtacc tgcagggtcc catctgggcc aaaattcctc acacggacgg caactttcac 2280

ccgtctcccc tgatgggcgg ctttggactg aagcacccgc ctcctcaaat tctcatcaag 2340

aacacaccgg ttccagcgga cccgccgctt accttcaacc aggccaagct gaactctttc 2400

atcacgcagt acagcaccgg acaggtcagc gtggaaatcg agtgggagct gcagaaagaa 2460

aacagcaaac gctggaatcc agagattcaa tacacttcca actactacaa atctacaaat 2520

gtggactttg ctgtcaacac ggagggggtt tatagcgagc ctcgccccat tggcacccgt 2580

tacctcaccc gcaacctgta a 2601

<210> 961
<211> 2367
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 961
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatgccaagc 420

agtgtaatcg atgcgctgca gtacaagctg gagggcacca cgaggctgac caggaagagg 480

ggtctgaagc tggccacggc cctcagcctt agcaataagt tcgtagaggg cagccccagc 540

ggcggcggcg gcagcggcgg cggcggcagc gctcctggaa agaaacgtcc ggtagagcag 600

tcgccacaag agccagactc ctcctcgggc atcggcaaga caggccagca gcccgctaaa 660

aagagactca attttggtca gactggcgac tcagagtcag tccccgatcc acaacctctc 720

ggagaacctc cagcagcccc ctcaggtctg ggacctaata caatggcttc aggcggtggc 780

gctccaatgg cagacaataa cgaaggcgcc gacggagtgg gtaattcctc gggaaattgg 840

cattgcgatt ccacatggct gggggacaga gtcatcacca ccagcacccg aacctgggcc 900

ctgcccacct acaacaacca cctctacaag caaatctcca acggcacctc gggaggaagc 960

accaacgaca acacctattt tggctacagc acccccctggg ggtattttga cttcaacaga 1020

ttccactgtc acttttcacc acgtgactgg caacgactca tcaacaacaa ttggggattc 1080

cggcccaaaa gactcaactt caagctgttc aacatccagg tcaaggaagt cacgacgaac 1140

gaaggcacca agaccatcgc caataatctc accagcaccg tgcaggtctt tacggactcg 1200

gagtaccagt taccgtacgt gctaggatcc gctcaccagg gatgtctgcc tccgttcccg 1260

gcggacgtct tcatggttcc tcagtacggc tatttaactt taaacaatgg aagccaagcc 1320

ctgggacgtt cctccttcta ctgtctggag tatttcccat cgcagatgct gagaaccggc 1380

aacaactttc agttcagcta caccttcgag gacgtgcctt tccacagcag ctacgcgcac 1440

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agaacgcaaa cgactggaac tggagggacg cagactctgg cattcagcca agcgggtcct 1560

agctcaatgg ccaaccaggc tagaaattgg gtgcccggac cttgctaccg gcagcagcgc 1620

gtctccacga caaccaacca gaacaacaac agcaactttg cctggacggg agctgccaag 1680

tttaagctga acggccgaga ctctctaatg aatccgggcg tggcaatggc ttcccacaag 1740

gatgacgacg accgcttctt cccttcgagc ggggtcctga tttttggcaa gcaaggagcc 1800

gggaacgatg gagtggatta cagccaagtg ctgattacag atgaggaaga aatcaaggct 1860

accaaccccg tggccacaga agaatatgga gcagtggcca tcaacaacca ggccgccaat 1920

acgcaggcgc agaccggact cgtgcacaac caggggggtga ttcccggcat ggtgtggcag 1980

aatagagacg tgtacctgca gggtcccatc tgggccaaaa ttcctcacac ggacggcaac 2040

tttcacccgt ctcccctgat gggcggcttt ggactgaagc acccgcctcc tcaaattctc 2100

atcaagaaca caccggttcc agcggacccg ccgcttacct tcaaccaggc caagctgaac 2160

tctttcatca cgcagtacag caccggacag gtcagcgtgg aaatcgagtg ggagctgcag 2220

aaagaaaaca gcaaacgctg gaatccagag attcaataca cttccaacta ctacaaatct 2280

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acccgttacc tcacccgcaa cctgtaa 2367

<210> 962
<211> 2328
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 962
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatgtatacc 420

atctggatgc ccgagaaccc caggcccggt acccccctgcg acatcttcac caacagcagg 480

ggcaagcgag ccagcaacgg cggcggcggc ggcagcggcg gcggcggcag cgctcctgga 540

aagaaacgtc cggtagagca gtcgccacaa gagccagact cctcctcggg catcggcaag 600

acaggccagc agcccgctaa aaagagactc aattttggtc agactggcga ctcagagtca 660

gtccccgatc cacaacctct cggagaacct ccagcagccc cctcaggtct gggacctaat 720

acaatggctt caggcggtgg cgctccaatg gcagacaata acgaaggcgc cgacggagtg 780

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accagcaccc gaacctgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc 900

aacggcacct cgggaggaag caccaacgac aacacctatt ttggctacag cacccctgg 960

gggtattttg acttcaacag attccactgt cacttttcac cacgtgactg gcaacgactc 1020

atcaacaaca attggggatt ccggcccaaa agactcaact tcaagctgtt caacatccag 1080

gtcaaggaag tcacgacgaa cgaaggcacc aagaccatcg ccaataatct caccagcacc 1140

gtgcaggtct ttacggactc ggagtaccag ttaccgtacg tgctaggatc cgctcaccag 1200

ggatgtctgc ctccgttccc ggcggacgtc ttcatggttc ctcagtacgg ctatttaact 1260

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atttttggca agcaaggagc cgggaacgat ggagtggatt acagccaagt gctgattaca 1800

gatgaggaag aaatcaaggc taccaacccc gtggccacag aagaatatgg agcagtggcc 1860

atcaacaacc aggccgccaa tacgcaggcg cagaccggac tcgtgcacaa ccaggggggtg 1920

attcccggca tggtgtggca gaatagagac gtgtacctgc agggtcccat ctgggccaaa 1980

attcctcaca cggacggcaa ctttcacccg tctcccctga tgggcggctt tggactgaag 2040

cacccgcctc ctcaaattct catcaagaac acaccggttc cagcggaccc gccgcttacc 2100

ttcaaccagg ccaagctgaa ctctttcatc acgcagtaca gcaccggaca ggtcagcgtg 2160

gaaatcgagt gggagctgca gaaagaaaac agcaaacgct ggaatccaga gattcaatac 2220

acttccaact actacaaatc tacaaatgtg gactttgctg tcaacacgga gggggtttat 2280

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<210> 963
<211> 2298
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gatgaccttc 420

ttctacggcg gcagcagggg caagaggaac aacttcaaga ccgaggagta cggcggcggc 480

ggcagcggcg gcggcggcag cgctcctgga aagaaacgtc cggtagagca gtcgccacaa 540

gagccagact cctcctcggg catcggcaag acaggccagc agcccgctaa aaagagactc 600

aattttggtc agactggcga ctcagagtca gtccccgatc cacaacctct cggagaacct 660

ccagcagccc cctcaggtct gggacctaat acaatggctt caggcggtgg cgctccaatg 720

gcagacaata acgaaggcgc cgacggagtg ggtaattcct cgggaaattg gcattgcgat 780

tccacatggc tgggggacag agtcatcacc accagcaccc gaacctgggc cctgcccacc 840

tacaacaacc acctctacaa gcaaatctcc aacggcacct cgggaggaag caccaacgac 900

aacacctatt ttggctacag caccccctgg gggtattttg acttcaacag attccactgt 960

cacttttcac cacgtgactg gcaacgactc atcaacaaca attggggatt ccggcccaaa 1020

agactcaact tcaagctgtt caacatccag gtcaaggaag tcacgacgaa cgaaggcacc 1080

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acgactggaa ctggagggac gcagactctg gcattcagcc aagcgggtcc tagctcaatg 1500

gccaaccagg ctagaaattg ggtgcccgga ccttgctacc ggcagcagcg cgtctccacg 1560

acaaccaacc agaacaacaa cagcaacttt gcctggacgg gagctgccaa gtttaagctg 1620

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ggagtggatt acagccaagt gctgattaca gatgaggaag aaatcaaggc taccaacccc 1800

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cagaccggac tcgtgcacaa ccaggggggtg attcccggca tggtgtggca gaatagagac 1920

gtgtacctgc agggtcccat ctgggccaaa attcctcaca cggacggcaa ctttcacccg 1980

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agcaaacgct ggaatccaga gattcaatac acttccaact actacaaatc tacaaatgtg 2220

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ctcacccgca acctgtaa 2298

<210> 964
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 964

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa ggcggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

acgcttaatg atggaagcca ggccgtgggt cgttcgtcct tttactgcct ggaatatttc 1200

ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca actacgagtt tgagaacgta 1260

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gccataaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga 1800

atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc 1860

aaaattcctc acacggacgg caactttcac ccttctccgc tgatgggagg gtttggaatg 1920

aagcacccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 965
<211> 2277
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 965
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatgaacaac 420

cagaagatcg tgaacctgaa ggagaaggtg gcccagctgg aggccggcgg cggcggcagc 480

gctcctggaa agaagaggcc tgtagagcag tctcctcagg aaccggactc ctccgcgggt 540

attggcaaat cgggtgcaca gcccgctaaa aagagactca atttcggtca gactggcgac 600

acagagtcag tcccagaccc tcaaccaatc ggagaacctc ccgcagcccc ctcaggtgtg 660

ggatctctta caatggcttc aggtggtggc gcaccagtgg cagacaataa cgaaggtgcc 720

gatggagtgg gtagttcctc gggaaattgg cattgcgatt cccaatggct gggggacaga 780

gtcatcacca ccagcacccg aacctgggcc ctgcccacct acaacaatca cctctacaag 840

caaatctcca acagcacatc tggaggatct tcaaatgaca acgcctactt cggctacagc 900

acccccctggg ggtattttga cttcaacaga ttccactgcc acttctcacc acgtgactgg 960

cagcgactca tcaacaacaa ctggggattc cggcctaagc gactcaactt caagctcttc 1020

aacattcagg tcaaagaggt tacggacaac aatggagtca agaccatcgc caataacctt 1080

accagcacgg tccaggtctt cacggactca gactatcagc tcccgtacgt gctcgggtcg 1140

gctcacgagg gctgcctccc gccgttccca gcggacgttt tcatgattcc tcagtacggg 1200

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tatttcccgt cgcaaatgct aagaacgggt aacaacttcc agttcaacta cgagtttgag 1320

aacgtacctt tccatagcag ctacgctcac agccaaagcc tggaccgact aatgaatcca 1380

ctcatcgacc aatacttgta ctatctctca aagactatta acgattctgg acagaatcaa 1440

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agcgaatttg cttggcctgg agcttcttct tgggctctca atggacgtaa tagcttgatg 1620

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ggatctttaa tttttggcaa acaaggaact ggaagagaca acgtggatgc ggacgaagtc 1740

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caaggaatac ttccgggtat ggtttggcag gacagagatg tgtacctgca aggacccatt 1920

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atccagtaca cttccaacta ttacaagtct aataatgttg aatttgctgt taatactgaa 2220

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<210> 966
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 966
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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatgtatacc 420

atctggatgc ccgagaaccc caggcccggt acccccctgcg acatcttcac caacagcagg 480

ggcaagcgag ccagcaacgg cggcggcggc ggcagcgctc ctggaaagaa gaggcctgta 540

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gctaaaaaga gactcaattt cggtcagact ggcgacacag agtcagtccc agaccctcaa 660

ccaatcggag aacctcccgc agccccctca ggtgtgggat ctcttacaat ggcttcaggt 720

ggtggcgcac cagtggcaga caataacgaa ggtgccgatg gagtgggtag ttcctcggga 780

aattggcatt gcgattccca atggctgggg gacagagtca tcaccaccag cacccgaacc 840

tgggccctgc ccacctacaa caatcacctc tacaagcaaa tctccaacag cacatctgga 900

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ggattccggc ctaagcgact caacttcaag ctcttcaaca ttcaggtcaa agaggttacg 1080

gacaacaatg gagtcaagac catcgccaat aaccttacca gcacggtcca ggtcttcacg 1140

gactcagact atcagctccc gtacgtgctc gggtcggctc acgagggctg cctcccgccg 1200

ttcccagcgg acgttttcat gattcctcag tacgggtatc tgacgcttaa tgatggaagc 1260

caggccgtgg gtcgttcgtc cttttactgc ctggaatatt tcccgtcgca aatgctaaga 1320

acgggtaaca acttccagtt caactacgag tttgagaacg tacctttcca tagcagctac 1380

gctcacagcc aaagcctgga ccgactaatg aatccactca tcgaccaata cttgtactat 1440

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ggacccagca acatggctgt ccagggaaga aactacatac ctggacccag ctaccgacaa 1560

caacgtgtct caaccactgt gactcaaaac aacaacagcg aatttgcttg gcctggagct 1620

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cacaaagaag gagaggaccg tttctttcct ttgtctggat ctttaatttt tggcaaacaa 1740

ggaactggaa gagacaacgt ggatgcggac gaagtcatga taaccaacga agaagaaatt 1800

aaaactacta acccggtagc aacggagtcc tatggacaag tggccataaa ccaccagagt 1860

gcccaagcac aggcgcagac cggctgggtt caaaaccaag gaatacttcc gggtatggtt 1920

tggcaggaca gagatgtgta cctgcaagga cccatttggg ccaaaattcc tcacacggac 1980

ggcaactttc acccttctcc gctgatggga gggtttggaa tgaagcaccc gcctcctcag 2040

atcctcatca aaaacacacc tgtacctgcg gatcctccaa cggccttcaa caaggacaag 2100

ctgaactctt tcatcaccca gtattctact ggccaagtca gcgtggagat cgagtgggag 2160

ctgcagaagg aaaacagcaa gcgctggaac ccggagatcc agtacacttc caactattac 2220

aagtctaata atgttgaatt tgctgttaat actgaaggtg tatatagtga accccgcccc 2280

attggcacca gatacctgac tcgtaatctg taa 2313

<210> 967
<211> 2283
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 967

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatgaccttc 420

ttctacggcg gcagcagggg caagaggaac aacttcaaga ccgaggagta cggcggcggc 480

ggcagcgctc ctggaaagaa gaggcctgta gagcagtctc ctcaggaacc ggactcctcc 540

gcgggtattg gcaaatcggg tgcacagccc gctaaaaaga gactcaattt cggtcagact 600

ggcgacacag agtcagtccc agaccctcaa ccaatcggag aacctcccgc agcccctca 660

ggtgtgggat ctcttacaat ggcttcaggt ggtggcgcac cagtggcaga caataacgaa 720

ggtgccgatg gagtgggtag ttcctcggga aattggcatt gcgattccca atggctgggg 780

gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacctacaa caatcacctc 840

tacaagcaaa tctccaacag cacatctgga ggatcttcaa atgacaacgc ctacttcggc 900

tacagcaccc cctgggggta ttttgacttc aacagattcc actgccactt ctcaccacgt 960

gactggcagc gactcatcaa caacaactgg ggattccggc ctaagcgact caacttcaag 1020

ctcttcaaca ttcaggtcaa agaggttacg gacaacaatg gagtcaagac catcgccaat 1080

aaccttacca gcacggtcca ggtcttcacg gactcagact atcagctccc gtacgtgctc 1140

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tacgggtatc tgacgcttaa tgatggaagc caggccgtgg gtcgttcgtc cttttactgc 1260

ctggaatatt tcccgtcgca aatgctaaga acgggtaaca acttccagtt caactacgag 1320

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aatccactca tcgaccaata cttgtactat ctctcaaaga ctattaacga ttctggacag 1440

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aactacatac ctggacccag ctaccgacaa caacgtgtct caaccactgt gactcaaaac 1560

aacaacagcg aatttgcttg gcctggagct tcttcttggg ctctcaatgg acgtaatagc 1620

ttgatgaatc ctggacctgc tatggccagc cacaaagaag gagaggaccg tttctttcct 1680

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gaagtcatga taaccaacga agaagaaatt aaaactacta acccggtagc aacggagtcc 1800

tatggacaag tggccataaa ccaccagagt gcccaagcac aggcgcagac cggctgggtt 1860

caaaaccaag gaatacttcc gggtatggtt tggcaggaca gagatgtgta cctgcaagga 1920

cccatttggg ccaaaattcc tcacacggac ggcaactttc acccttctcc gctgatggga 1980

gggtttggaa tgaagcaccc gcctcctcag atcctcatca aaaacacacc tgtacctgcg 2040

gatcctccaa cggccttcaa caaggacaag ctgaactctt tcatcaccca gtattctact 2100

ggccaagtca gcgtggagat cgagtgggag ctgcagaagg aaaacagcaa gcgctggaac 2160

ccggagatcc agtacacttc caactattac aagtctaata atgttgaatt tgctgttaat 2220

actgaaggtg tatatagtga accccgcccc attggcacca gatacctgac tcgtaatctg 2280

taa 2283

<210> 968
<211> 2283
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 968
ctggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

gagtggtggg ctttgaaacc tggagcccct caacccaagg caaatcaaca acatcaagac 120

aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gatggcagct 420

gcggccgccg cggctgcagc ggctgcagcc gccgcagctg cggctgcagc gggcggcggc 480

ggcagcgctc ctggaaagaa gaggcctgta gagcagtctc ctcaggaacc ggactcctcc 540

gcgggtattg gcaaatcggg tgcacagccc gctaaaaaga gactcaattt cggtcagact 600

ggcgacacag agtcagtccc agaccctcaa ccaatcggag aacctcccgc agccccctca 660

ggtgtgggat ctcttacaat ggcttcaggt ggtggcgcac cagtggcaga caataacgaa 720

ggtgccgatg gagtgggtag ttcctcggga aattggcatt gcgattccca atggctgggg 780

gacagagtca tcaccaccag cacccgaacc tgggccctgc ccacctacaa caatcacctc 840

tacaagcaaa tctccaacag cacatctgga ggatcttcaa atgacaacgc ctacttcggc 900

tacagcaccc cctgggggta ttttgacttc aacagattcc actgccactt ctcaccacgt 960

gactggcagc gactcatcaa caacaactgg ggattccggc ctaagcgact caacttcaag 1020

ctcttcaaca ttcaggtcaa agaggttacg gacaacaatg gagtcaagac catcgccaat 1080

aaccttacca gcacggtcca ggtcttcacg gactcagact atcagctccc gtacgtgctc 1140

gggtcggctc acgagggctg cctcccgccg ttcccagcgg acgttttcat gattcctcag 1200

tacgggtatc tgacgcttaa tgatggaagc caggccgtgg gtcgttcgtc cttttactgc 1260

ctggaatatt tcccgtcgca aatgctaaga acgggtaaca acttccagtt caactacgag 1320

tttgagaacg tacctttcca tagcagctac gctcacagcc aaagcctgga ccgactaatg 1380

aatccactca tcgaccaata cttgtactat ctctcaaaga ctattaacga ttctggacag 1440

aatcaacaaa cgctaaaatt cagtgtggcc ggacccagca acatggctgt ccagggaaga 1500

aactacatac ctggacccag ctaccgacaa caacgtgtct caaccactgt gactcaaaac 1560

aacaacagcg aatttgcttg gcctggagct tcttcttggg ctctcaatgg acgtaatagc 1620

ttgatgaatc ctggacctgc tatggccagc cacaaagaag gagaggaccg tttctttcct 1680

ttgtctggat ctttaatttt tggcaaacaa ggaactggaa gagacaacgt ggatgcggac 1740

gaagtcatga taaccaacga agaagaaatt aaaactacta acccggtagc aacggagtcc 1800

tatggacaag tggccataaa ccaccagagt gcccaagcac aggcgcagac cggctgggtt 1860

caaaaccaag gaatacttcc gggtatggtt tggcaggaca gagatgtgta cctgcaagga 1920

cccatttggg ccaaaattcc tcacacggac ggcaactttc acccttctcc gctgatggga 1980

gggtttggaa tgaagcaccc gcctcctcag atcctcatca aaaacacacc tgtacctgcg 2040

gatcctccaa cggccttcaa caaggacaag ctgaactctt tcatcaccca gtattctact 2100

ggccaagtca gcgtggagat cgagtgggag ctgcagaagg aaaacagcaa gcgctggaac 2160

ccggagatcc agtacacttc caactattac aagtctaata atgttgaatt tgctgttaat 2220

actgaaggtg tatatagtga accccgcccc attggcacca gatacctgac tcgtaatctg 2280

taa 2283

<210> 969
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 969
Met Glu Val Gln Leu Gln Ala Ser Gly Gly Gly Leu Val Gln Ala Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Ile Thr His
20 25 30

Tyr Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
35 40 45

Val Ser Arg Ile Thr Trp Gly Gly Asp Asn Thr Phe Tyr Ser Asn Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Asp Tyr Tyr
85 90 95

```
Cys Ala Ala Gly Ser Thr Ser Thr Ala Thr Pro Leu Arg Val Asp Tyr
            100                 105                 110

Trp Gly Lys Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp
    130                 135                 140

Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg
145                 150                 155                 160

Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln
                165                 170                 175

Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr
            180                 185                 190

Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
225                 230                 235                 240

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly
                245                 250                 255

Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn
    290                 295                 300
```

```
Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly
305                 310                 315                 320

Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
                325                 330                 335

Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
            340                 345                 350

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe
    370                 375                 380

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
385                 390                 395                 400

Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr
                405                 410                 415

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
            420                 425                 430

Tyr Leu Tyr Tyr Leu Val Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr
        435                 440                 445

Gln Thr Leu Ala Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln
    450                 455                 460

Ala Arg Asn Trp Val Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
465                 470                 475                 480

Thr Thr Thr Asn Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala
                485                 490                 495

Ala Lys Phe Lys Leu Asn Gly Arg Asp Ser Leu Met Asn Pro Gly Val
            500                 505                 510
```

```
Ala Met Ala Ser His Lys Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser
        515                 520                 525

Gly Val Leu Ile Phe Gly Lys Gln Gly Ala Gly Asn Asp Gly Val Asp
    530                 535                 540

Tyr Ser Gln Val Leu Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn
545                 550                 555                 560

Pro Val Ala Thr Glu Glu Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala
                565                 570                 575

Ala Asn Thr Gln Ala Gln Thr Gly Leu Val His Asn Gln Gly Val Ile
            580                 585                 590

Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile
        595                 600                 605

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu
    610                 615                 620

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys
625                 630                 635                 640

Asn Thr Pro Val Pro Ala Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys
                645                 650                 655

Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
            660                 665                 670

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
        675                 680                 685

Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala
    690                 695                 700

Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg
705                 710                 715                 720
```

Tyr Leu Thr Arg Asn Leu
725

<210> 970
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 970
Met Glu Val Gln Leu Gln Ala Ser Gly Gly Gly Leu Val Gln Ala Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ser Ala Ser Val Arg Thr Phe Ser Ile
20 25 30

Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe
35 40 45

Val Ala Gly Ile Asn Arg Ser Gly Asp Val Thr Lys Tyr Ala Asp Phe
50 55 60

Val Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Met Val
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Leu Tyr Tyr
85 90 95

Cys Ala Ala Thr Trp Ala Tyr Asp Thr Val Gly Ala Leu Thr Ser Gly
100 105 110

Tyr Asn Phe Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly
115 120 125

Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln
130 135 140

```
Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala
145                 150                 155                 160


Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro
                165                 170                 175


Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser Gly Leu Gly
            180                 185                 190


Pro Asn Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn
        195                 200                 205


Glu Gly Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp
    210                 215                 220


Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp
225                 230                 235                 240


Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly
                245                 250                 255


Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr
            260                 265                 270


Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro
        275                 280                 285


Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys
    290                 295                 300


Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr
305                 310                 315                 320


Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln
                325                 330                 335


Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala
            340                 345                 350
```

```
His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro
        355                 360                 365

Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Leu Gly Arg
    370                 375                 380

Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His
                405                 410                 415

Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg Thr Gln Thr Thr Gly Thr
        435                 440                 445

Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln Ala Gly Pro Ser Ser Met
    450                 455                 460

Ala Asn Gln Ala Arg Asn Trp Val Pro Gly Pro Cys Tyr Arg Gln Gln
465                 470                 475                 480

Arg Val Ser Thr Thr Thr Asn Gln Asn Asn Asn Ser Asn Phe Ala Trp
                485                 490                 495

Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly Arg Asp Ser Leu Met Asn
            500                 505                 510

Pro Gly Val Ala Met Ala Ser His Lys Asp Asp Asp Asp Arg Phe Phe
        515                 520                 525

Pro Ser Ser Gly Val Leu Ile Phe Gly Lys Gln Gly Ala Gly Asn Asp
    530                 535                 540

Gly Val Asp Tyr Ser Gln Val Leu Ile Thr Asp Glu Glu Glu Ile Lys
545                 550                 555                 560
```

```
Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Ala Val Ala Ile Asn
                565                 570                 575


Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr Gly Leu Val His Asn Gln
            580                 585                 590


Gly Val Ile Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln
        595                 600                 605


Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
    610                 615                 620


Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
625                 630                 635                 640


Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Leu Thr Phe Asn
                645                 650                 655


Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
            660                 665                 670


Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
        675                 680                 685


Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Asn Val
    690                 695                 700


Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile
705                 710                 715                 720


Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725


<210> 971
<211> 651
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polypeptide"

<400> 971

```
Met Pro Ser Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr
1               5                  10                  15

Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys Leu Ala Thr Ala Leu Ser
            20                  25                  30

Leu Ser Asn Lys Phe Val Glu Gly Ser Pro Ser Gly Gly Gly Gly Ser
        35                  40                  45

Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser
    50                  55                  60

Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln
65                  70                  75                  80

Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser
                85                  90                  95

Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala Pro Ser Gly
            100                 105                 110

Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp
        115                 120                 125

Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His
    130                 135                 140

Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
145                 150                 155                 160

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
                165                 170                 175

Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr Phe Gly Tyr
            180                 185                 190

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
```

195 200 205

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
210 215 220

Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
225 230 235 240

Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
245 250 255

Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly
260 265 270

Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
275 280 285

Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Leu
290 295 300

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
305 310 315 320

Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro
325 330 335

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
340 345 350

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg Thr Gln Thr Thr
355 360 365

Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln Ala Gly Pro Ser
370 375 380

Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro Gly Pro Cys Tyr Arg
385 390 395 400

Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn Asn Asn Ser Asn Phe

405 410 415

Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly Arg Asp Ser Leu
420 425 430

Met Asn Pro Gly Val Ala Met Ala Ser His Lys Asp Asp Asp Asp Arg
435 440 445

Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly Lys Gln Gly Ala Gly
450 455 460

Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile Thr Asp Glu Glu Glu
465 470 475 480

Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Ala Val Ala
485 490 495

Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr Gly Leu Val His
500 505 510

Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr
515 520 525

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
530 535 540

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
545 550 555 560

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Leu Thr
565 570 575

Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly
580 585 590

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
595 600 605

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr

610 615 620

Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg
625 630 635 640

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
645 650

<210> 972
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 972
Met Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Pro Gly Thr Pro Cys
1 5 10 15

Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Asn Gly Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val
35 40 45

Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr
50 55 60

Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp
65 70 75 80

Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Ala
85 90 95

Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly Ala Pro
100 105 110

Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser Gly
115 120 125

```
Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr
    130                 135                 140

Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys
145                 150                 155                 160

Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn Thr Tyr
                165                 170                 175

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
            180                 185                 190

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
        195                 200                 205

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
    210                 215                 220

Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
225                 230                 235                 240

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
                245                 250                 255

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
            260                 265                 270

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
        275                 280                 285

Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
    290                 295                 300

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
305                 310                 315                 320

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
                325                 330                 335
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg Thr
            340                 345                 350

Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln Ala
        355                 360                 365

Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro Gly Pro
    370                 375                 380

Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn Asn Asn
385                 390                 395                 400

Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly Arg
                405                 410                 415

Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys Asp Asp
            420                 425                 430

Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly Lys Gln
        435                 440                 445

Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile Thr Asp
    450                 455                 460

Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly
465                 470                 475                 480

Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr Gly
                485                 490                 495

Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln Asn Arg
            500                 505                 510

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
        515                 520                 525

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
    530                 535                 540
```

```
Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
545                 550                 555                 560


Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln Tyr
                565                 570                 575


Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
            580                 585                 590


Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr
        595                 600                 605


Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser
    610                 615                 620


Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
625                 630                 635


<210> 973
<211> 628
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 973
Met Thr Phe Phe Tyr Gly Gly Ser Arg Gly Lys Arg Asn Asn Phe Lys
1               5                   10                  15


Thr Glu Glu Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro
            20                  25                  30


Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser
        35                  40                  45


Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn
    50                  55                  60
```

```
Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu
65                  70                  75                  80

Gly Glu Pro Pro Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala
                85                  90                  95

Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly
            100                 105                 110

Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly
        115                 120                 125

Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr
    130                 135                 140

Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser
145                 150                 155                 160

Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
                165                 170                 175

Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
            180                 185                 190

Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys
        195                 200                 205

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys
    210                 215                 220

Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser
225                 230                 235                 240

Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu
                245                 250                 255

Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu
            260                 265                 270
```

```
Thr Leu Asn Asn Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys
        275                 280                 285

Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln
    290                 295                 300

Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His
305                 310                 315                 320

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu
                325                 330                 335

Tyr Tyr Leu Val Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr
            340                 345                 350

Leu Ala Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg
        355                 360                 365

Asn Trp Val Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr
    370                 375                 380

Thr Asn Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys
385                 390                 395                 400

Phe Lys Leu Asn Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met
                405                 410                 415

Ala Ser His Lys Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val
            420                 425                 430

Leu Ile Phe Gly Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser
        435                 440                 445

Gln Val Leu Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val
    450                 455                 460

Ala Thr Glu Glu Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn
465                 470                 475                 480
```

```
Thr Gln Ala Gln Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly
                485                 490                 495


Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
            500                 505                 510


Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly
        515                 520                 525


Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr
    530                 535                 540


Pro Val Pro Ala Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn
545                 550                 555                 560


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu
                565                 570                 575


Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
            580                 585                 590


Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn
        595                 600                 605


Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu
    610                 615                 620


Thr Arg Asn Leu
625
```

<210> 974
<211> 621
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 974

```
Met Asn Asn Gln Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu
1               5                   10                  15

Glu Ala Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu
            20                  25                  30

Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys Ser Gly
        35                  40                  45

Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Thr
    50                  55                  60

Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Ala Pro
65                  70                  75                  80

Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala Pro Val
                85                  90                  95

Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn
            100                 105                 110

Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr Thr Ser
        115                 120                 125

Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln
    130                 135                 140

Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe
145                 150                 155                 160

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
                165                 170                 175

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
            180                 185                 190

Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys
        195                 200                 205
```

```
Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu Thr
    210                 215                 220

Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr Val
225                 230                 235                 240

Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
                245                 250                 255

Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln
            260                 265                 270

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
        275                 280                 285

Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe Glu Asn
    290                 295                 300

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
305                 310                 315                 320

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile
                325                 330                 335

Asn Asp Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly
            340                 345                 350

Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser
        355                 360                 365

Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser
    370                 375                 380

Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn
385                 390                 395                 400

Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu
                405                 410                 415
```

```
Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly
            420                 425                 430

Thr Gly Arg Asp Asn Val Asp Ala Asp Glu Val Met Ile Thr Asn Glu
        435                 440                 445

Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln
    450                 455                 460

Val Ala Ile Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp
465                 470                 475                 480

Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp
                485                 490                 495

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
            500                 505                 510

Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro
        515                 520                 525

Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro
    530                 535                 540

Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser
545                 550                 555                 560

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
                565                 570                 575

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys
            580                 585                 590

Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu
        595                 600                 605

Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
    610                 615                 620
```

<210> 975
<211> 633
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 975

```
Met Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Pro Gly Thr Pro Cys
1               5                  10                  15

Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Asn Gly Gly Gly
            20                  25                  30

Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln
        35                  40                  45

Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys Ser Gly Ala Gln Pro Ala
    50                  55                  60

Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Thr Glu Ser Val Pro
65                  70                  75                  80

Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Ala Pro Ser Gly Val Gly
                85                  90                  95

Ser Leu Thr Met Ala Ser Gly Gly Gly Ala Pro Val Ala Asp Asn Asn
            100                 105                 110

Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp
        115                 120                 125

Ser Gln Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp
    130                 135                 140

Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Ser
145                 150                 155                 160

Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr
```

```
                165                 170                 175

Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro
            180                 185                 190

Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys
        195                 200                 205

Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp
    210                 215                 220

Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln
225                 230                 235                 240

Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala
                245                 250                 255

His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro
            260                 265                 270

Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg
        275                 280                 285

Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
    290                 295                 300

Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe Glu Asn Val Pro Phe His
305                 310                 315                 320

Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
                325                 330                 335

Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Asp Ser Gly
            340                 345                 350

Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met
        355                 360                 365

Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln
```

```
    370                 375                 380

Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp
385                 390                 395                 400

Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn
                405                 410                 415

Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe
            420                 425                 430

Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp
        435                 440                 445

Asn Val Asp Ala Asp Glu Val Met Ile Thr Asn Glu Glu Glu Ile Lys
    450                 455                 460

Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Ile Asn
465                 470                 475                 480

His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln
                485                 490                 495

Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
            500                 505                 510

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
        515                 520                 525

Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile
    530                 535                 540

Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn
545                 550                 555                 560

Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
                565                 570                 575

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
```

580 585 590

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val
595 600 605

Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile
610 615 620

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
625 630

<210> 976
<211> 623
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 976
Met Thr Phe Phe Tyr Gly Gly Ser Arg Gly Lys Arg Asn Asn Phe Lys
1 5 10 15

Thr Glu Glu Tyr Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro
20 25 30

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys
35 40 45

Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly
50 55 60

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala
65 70 75 80

Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala
85 90 95

Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser
100 105 110

```
Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
        115                 120                 125

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
    130                 135                 140

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala
145                 150                 155                 160

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
                165                 170                 175

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
            180                 185                 190

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
        195                 200                 205

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
    210                 215                 220

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
225                 230                 235                 240

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
                245                 250                 255

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
            260                 265                 270

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
        275                 280                 285

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe
    290                 295                 300

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
305                 310                 315                 320
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
                325                 330                 335

Thr Ile Asn Asp Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
            340                 345                 350

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
        355                 360                 365

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
    370                 375                 380

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
385                 390                 395                 400

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
                405                 410                 415

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
            420                 425                 430

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Glu Val Met Ile Thr
        435                 440                 445

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
    450                 455                 460

Gly Gln Val Ala Ile Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
465                 470                 475                 480

Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
                485                 490                 495

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
            500                 505                 510

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
        515                 520                 525
```

```
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
    530                 535                 540

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln
545                 550                 555                 560

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
                565                 570                 575

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
            580                 585                 590

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
        595                 600                 605

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
    610                 615                 620


<210> 977
<211> 623
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 977
Met Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
1               5                   10                  15

Ala Ala Ala Ala Gly Gly Gly Gly Ser Ala Pro Gly Lys Lys Arg Pro
            20                  25                  30

Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys
        35                  40                  45

Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly
    50                  55                  60
```

```
Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala
65                  70                  75                  80

Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala
                85                  90                  95

Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser
            100                 105                 110

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
        115                 120                 125

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
    130                 135                 140

Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala
145                 150                 155                 160

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
                165                 170                 175

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
            180                 185                 190

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
        195                 200                 205

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
    210                 215                 220

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
225                 230                 235                 240

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
                245                 250                 255

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly
            260                 265                 270
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
        275                 280                 285

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Asn Tyr Glu Phe
    290                 295                 300

Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
305                 310                 315                 320

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Lys
                325                 330                 335

Thr Ile Asn Asp Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val
            340                 345                 350

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly
        355                 360                 365

Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn
    370                 375                 380

Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly
385                 390                 395                 400

Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu
                405                 410                 415

Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys
            420                 425                 430

Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Glu Val Met Ile Thr
        435                 440                 445

Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr
    450                 455                 460

Gly Gln Val Ala Ile Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr
465                 470                 475                 480
```

```
Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp
                485                 490                 495

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
            500                 505                 510

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys
        515                 520                 525

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
    530                 535                 540

Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln
545                 550                 555                 560

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
                565                 570                 575

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
            580                 585                 590

Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr
        595                 600                 605

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
    610                 615                 620


<210> 978
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<400> 978
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc       60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac      120
```

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgtcgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggca cctcgggagg aagcaccaac gacaacacct attttggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcca aaaagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 1020

acgattcagg tatttacgga ctcggaatac cagctgccat acgtcctcgg ctccgcgcac 1080

cagggctgcc tgcctccgtt cccggcggac gtcttcatga ttccccagta cggctacctt 1140

acactgaaca atggaagtca agccgtaggc cgttcctcct tctactgcct ggaatatttt 1200

ccttctcaaa tgctgagaac gggcaacaac tttgagttca gctaccagtt tgaggacgtg 1260

ccttttcaca gcagctacgc gcacagccaa agcctggacc ggctgatgaa ccccctcatc 1320

gaccagtacc tgtactacct gtctcggact cagtccacgg gaggtaccgc aagaactcag 1380

cagttgctat tttctcaggc cgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactctgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccatctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctacagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 979
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 979
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg acggcgctaa gacggctcct 420

ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaggac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa tcgagtggga gctgcagaaa gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca aatgtggact ttgctgtcaa cacggagggg 2160

gtttatagcg agcctcgccc cattggcacc cgttacctca cccgcaacct gtaa 2214

<210> 980
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (715)..(715)
<223> a, c, g, or t

<400> 980
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagagg ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagantcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atattttcca 1200

tctcaaatgc tgcgaactgg aaacaatttt gaattcagct acaccttcga ggacgtgcct 1260

ttccacagca gctacgcaca cagccagagc ttggaccgac tgatgaatcc tctcatcgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac gaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

accttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct acagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca attactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccgccccat tggcacgcgt ttcctcaccc gtaatctgta a 2211

<210> 981
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 981

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagagg ctcaattttg gccagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgtactagg atccgctcac 1080

cagggatgtc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatatttt 1200

ccatctcaga tgctgagaac gggcaataac tttaccttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctatgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

actctgggct tcagccaagg tgggcctaat acaatggcca atcaggcaaa gaactggctg 1440

ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacgaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctaatggg aggatttgga 1920

ctgaagcacc cacctcctca gatcctgatc aagaacacgc cggtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgtactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

caatacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccgccc cattggcacc cgttacctca cccgtaatct gtaa 2214

<210> 982
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 982
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Val Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Arg Thr Gln Gln Leu Leu Phe
    450                 455                 460

Ser Gln Ala Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495
```

```
Asn Asn Asn Ser Asn Ser Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700
```

```
Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 983
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 983
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Asp Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525
```

```
Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
```

Leu

<210> 984
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (239)..(239)
<223> Any naturally occurring amino acid

<400> 984
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Thr Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Phe Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 985
<211> 737

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 985

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175
```

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
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Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590
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Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Tyr Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
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<210> 986
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 986

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt cgacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag gttccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaaa agactcaact tcaagctgtt caacatccag 960

gtcaaggaag tcacgacgaa cgaaggcacc aagaccatcg ccaataatct caccagcacc 1020

gtgcaggtct ttacggactc ggagtaccag ttaccgtacg tgctaggatc cgctcaccag 1080

ggatgtctgc ctccgttccc ggcggacgtc ttcatggttc ctcagtacgg ctatttaact 1140

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cagtacctgt actacctggt cagaacgcaa acgactggaa ctggagggac gcagactctg 1380

gcattcagcc aagcgggtcc tagctcaatg gccaaccagg ctagaaattg ggtgcccgga 1440

ccttgctacc ggcagcagcg cgtctccacg acaaccaacc agaacaacaa cagcaacttt 1500

gcctggacgg gagctgccaa gtttaagctg aacggccgag actctctaat gaatccgggc 1560

gtggcaatgg cttcccacaa ggatgacgac gaccgcttct tcccttcgag cggggtcctg 1620

atttttggca agcaaggagc cgggaacgat ggagtggatt acagccaagt gctgattaca 1680

gatgaggaag aaatcaaggc taccaacccc gtggccacag aagaatatgg agcagtggcc 1740

atcaacaacc aggccgccaa tacgcaggcg cagaccggac tcgtgcacaa ccaggggggtg 1800

attcccggca tggtgtggca gaatagagac gtgtacctgc agggtcccat ctgggccaaa 1860

attcctcaca cggacggcaa ctttcacccg tctcccctga tgggcggctt tggactgaag 1920

cacccgcctc ctcaaattct catcaagaac acaccggttc cagcggaccc gccgcttacc 1980

ttcaaccagg ccaagctgaa ctctttcatc acgcagtaca gcaccggaca ggtcagcgtg 2040

gaaatcgagt gggagctgca gaaagaaaac agcaaacgct ggaatccaga gattcaatac 2100

acttccaact actacaaatc tacaaatgtg gactttgctg tcaacacgga gggggtttat 2160

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<210> 987
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<222> (337)..(337)
<223> a, c, g, or t

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gacagcaggg gtcttgtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcgaccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcnacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaga gaccagtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

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atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaattgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgctaataa ccttaccagc 1020

acggttcaag tcttctcgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

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gtgattcccg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtggacaa caatggactt 2160

tatactgagc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 988
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
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<222> (335)..(335)
<223> a, c, g, or t

<400> 988
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ggccggggtc tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag 180

ggggagcccg tcaacgcggc ggacgcagcg gccctcgagc acgacaaggc ctacgaccag 240

cagctcaaag cgggtgacaa tccgtacctg cggtataacc acgccgacgc cgagtttcag 300

gagcgtctgc aagaagatac gtcttttggg ggcancctcg ggcgagcagt cttccaggcc 360

aagaagcggg ttctcgaacc tctcggtctg gttgaggaag gcgctaagac ggctcctgga 420

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aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

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ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

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ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttaa accaggccaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa cccagagatt 2100

cagtacactt caaactacta caaatctaca aatgtggact ttgctgtcaa tacagaggga 2160

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<210> 989

<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
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<222> (338)..(338)
<223> a, c, g, or t

<400> 989
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gcccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcg aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcancc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccagtaga gcagtcaccc caagaaccag actcctcctc gggcatcggc 480

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aatacaatgg cttcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

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gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcact aagaccatcg ccaataacct taccagcacg 1020

attcaggtat ttacggactc ggaataccag ctgccgtacg tcctcggctc cgcgcaccag 1080

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gccttacctg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

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gccttcaaca aggacaagct gaactctttc atcacccagt attctactgg ccaagtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta 2160

tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 990
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220
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Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
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Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val Arg
        435                 440                 445

Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln Thr
            580                 585                 590

Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
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His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655


Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 991
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> MOD_RES
<222> (113)..(113)
<223> Any naturally occurring amino acid

<400> 991
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
```

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        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Thr Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Xaa Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
```

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                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
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    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Asp Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
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660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 992
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (112)..(112)
<223> Any naturally occurring amino acid

<400> 992
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Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

```
Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80


Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp
                85                  90                  95


Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Xaa
            100                 105                 110


Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125


Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140


Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270
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Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480
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Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Leu Asn Gln Ala Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685
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Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Phe Leu Thr Arg Asn
725 730 735

Leu

<210> 993
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (113)..(113)
<223> Any naturally occurring amino acid

<400> 993
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

```
Gln Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Xaa Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Arg Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
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His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser Gln Asn
                485                 490                 495
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Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Val Val Val Asp Asn Leu Gln Gln Thr Asn Thr Gly Pro Ile
            580                 585                 590

Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
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Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 994
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gagtggtggg ccctgaagcc cggcgccccc cagcccaagg ccaaccagca gcaccaggac 120

aacgcccgcg gcctggtgct gcccggctac aagtacctgg gccccggcaa cggcctggac 180

aagggcgagc ccgtgaacgc cgccgacgcc gccgccctgg agcacgacaa ggcctacgac 240

cagcagctga aggccggcga caacccctac ctgaagtaca accacgccga cgccgagttc 300

caggagcgcc tgaaggagga caccagcttc ggcggcaacc tgggccgcgc cgtgttccag 360

gccaagaagc gcctgctgga gcccctgggc ctggtggagg aggccgccaa gaccgccccc 420

ggcaagaagc gccccgtgga gcagagcccc caggagcccg acagcagcgc cggcatcggc 480

aagagcggcg cccagcccgc caagaagcgc ctgaacttcg gccagaccgg cgacaccgag 540

agcgtgcccg acccccagcc catcggcgag ccccccgccg cccccagcgg cgtgggcagc 600

ctgaccatgg ccagcggcgg cggcgccccc gtggccgaca acaacgaggg cgccgacggc 660

gtgggcagca gcagcggcaa ctggcactgc gacagccagt ggctgggcga ccgcgtgatc 720

accaccagca cccgcacctg ggccctgccc acctacaaca accacctgta caagcagatc 780

agcaacagca ccagcggcgg cagcagcaac gacaacgcct acttcggcta cagcaccccc 840

tggggctact tcgacttcaa ccgcttccac tgccacttca gcccccgcga ctggcagcgc 900

ctgatcaaca acaactgggg cttccgcccc aagcgcctga acttcaagct gttcaacatc 960

caggtgaagg aggtgaccga caacaacggc gtgaagacca tcgccaacaa cctgaccagc 1020

accgtgcagg tgttcaccga cagcgactac cagctgccct acgtgctggg cagcgcccac 1080

gagggctgcc tgcccccctt ccccgccgac gtgttcatga tcccccagta cggctacctg 1140

accctgaacg acggcagcca ggccgtgggc cgcagcagct tctactgcct ggagtacttc 1200

cccagccaga tgctgcgcac cggcaacaac ttccagttca gctacgagtt cgagaacgtg 1260

cccttccaca gcagctacgc ccacagccag agcctggacc gcctgatgaa ccccctgatc 1320

gaccagtacc tgtactacct gagcaagacc atcaacggca gcggccagaa ccagcagacc 1380

ctgaagttca gcgtggccgg ccccagcaac atggccgtgc agggccgcaa ctacatcccc 1440

ggccccagct accgccagca gcgcgtgagc accaccgtga cccagaacaa caacagcgag 1500

ttcgcctggc ccggcgccag cagctgggcc ctgaacggcc gcaacagcct gatgaacccc 1560

ggccccgcca tggccagcca caaggagggc gaggaccgct tcttcccccc gagcggcagc 1620

ctgatcttcg gcaagcaggg caccggccgc gacaacgtgg acgccgacaa ggtgatgatc 1680

accaacgagg aggagatcaa gaccaccaac cccgtggcca ccgagagcta cggccaggtg 1740

gccaccaacc accagagcgc ccaggcccag gcccagaccg gctgggtgca gaaccagggc 1800

atcctgcccg gcatggtgtg gcaggaccgc gacgtgtacc tgcagggccc catctgggcc 1860

aagatccccc acaccgacgg caacttccac cccagccccc tgatgggcgg cttcggcatg 1920

aagcaccccc ccccccagat cctgatcaag aacacccccg tgcccgccga ccccccccacc 1980

gccttcaaca aggacaagct gaacagcttc atcacccagt acagcaccgg ccaggtgagc 2040

gtggagatcg agtgggagct gcagaaggag aacagcaagc gctggaaccc cgagatccag 2100

tacaccagca actactacaa gagcaacaac gtggagttcg ccgtgaacac cgagggcgtg 2160

tacagcgagc cccgccccat cggcacccgc tacctgaccc gcaacctgta a 2211

<210> 995
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt taacattcaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

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ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 996
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

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ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa agccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtttg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

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tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

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<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 997
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa tacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

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ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

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cctggcatcg ctatggcctc acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

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ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

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ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

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accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacca ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 998
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 998

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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

attcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaaca 1140

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 999
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 999
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattcccaat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctataaca accacctcta caagcaaatc 780

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atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

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gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1000
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> modified_base
<222> (2241)..(2241)
<223> a, c, g, or t

<400> 1000
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

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accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

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accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

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tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

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aatcaataaa ccgtttaatt nttt 2244

<210> 1001
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1001
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

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cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaatcacct ctacaagcaa 780

atctccaaca gcacatctgg aggatcttca aatgacaacg cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caaccgcttc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa actcttcaac 960

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gttcctttcc acagcagcta cgctcacagc cagagtctgg accgtctcat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

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agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacaagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

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caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

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atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaacccca ccccattggc acccgttacc tcacccgtcc cctgtaa 2217

<210> 1002
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1002
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

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tccaacggga catcgggagg agccaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa ccttaccagc 1020

acgattcagg tctttacgga ttcggaatac cagctcccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcagta cggctaccta 1140

acgctcaaca atggtagcca ggcagtggga cggtcatcct tttactgcct ggaatatttc 1200

ccatcgcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggacgtt 1260

cctttccaca gcagctacgc tcacagccag agtctggacc gtctcatgaa tcctctgatt 1320

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cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1003
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1003
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg gtatctgacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caataacttt accttcagct acaccttcga ggacgtgcct 1260

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ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1004
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1004
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac atgggccttg cccacctata acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgatttcaa cagattccac tgccatttct caccacgtga ctggcagcga 900

ctcatcaaca acaatttggg atcccggccc aagagactca acttcaagct cttcatcatc 960

caagtcaagg aggtcacgac gaatgatggc gtcacgacca tcgctaataa ccttaccagc 1020

acggttcaag tcttctcgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

cagggctgcc tccctccgtt cccggcggac gtgttcatga ttccgcagta cggctaccta 1140

acgctcaaca atggcagcca ggcagtggga cggtcatcct tttactgcct ggaatatttc 1200

ccatcgcaga tgctgagaac gggcaataac tttaccttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctggacc ggctgatgaa tcctctcatc 1320

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gacttgctgt ttagccgggg gtctccagct ggcatgtctg ttcagcccaa aaactggcta 1440

cctggaccct gttaccggca gcagcgcgtt tctaaaacaa aaacagacaa caacaacagc 1500

aactttacct ggactggtgc ttcaaaatat aaccttaatg ggcgtgaatc tataatcaac 1560

cctggcactg ctatggcctc acacaaagac gacaaagaca agttctttcc catgagcggt 1620

gtcatgattt ttggaaagga gagcgccgga gcttcaaaca ctgcattgga caatgtcatg 1680

atcacagacg aagaggaaat caaagccact aaccccgtgg ccaccgaaag atttgggact 1740

gtggcagtca atctccagag cagcagcaca gaccctgcga ccggagatgt gcatgttatg 1800

ggagccttac ctggaatggt gtggcaagac agagacgtat acctgcaggg tcctatttgg 1860

gccaaaattc ctcacacgga tggacacttt cacccgtctc ctctcatggg cggctttgga 1920

cttaagcacc cgcctcctca gatcctcatc aaaaacacgc ctgttcctgc gaatcctccg 1980

gcagagtttt cggctacaaa gtttgcttca ttcatcaccc agtattccac aggacaagtg 2040

agcgtggaga ttgaatggga gctgcagaaa gaaaacagca aacgctggaa tcccgaagtg 2100

cagtatacat ctaactatgc aaaatctgcc aacgttgatt tcactgtgga caacaatgga 2160

ctttatactg agcctcgccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1005
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1005
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaactttg ggcagactgg cgactcagag 540

tcagtgcccg accctcaacc aatcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgatc cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1006
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1006
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca agagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

attcaggtct ttacggattc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccga gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1007
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1007
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcacca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaagctctt caacatccaa 960

gtcaaggagg tcacgacgaa tgatggcgtc acgaccatcg ctaataacct taccagcacg 1020

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ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctcatcgac 1320

cagtacctgt attacctgaa cagaactcag aatcagtccg gaagtgccca aaacaaggac 1380

ttgctgttta gccgggggtc tccagctggc atgtctgttc agcccaaaaa ctggctacct 1440

ggaccctgtt accggcagca gcgcgtttct aaaacaaaaa cagacaacaa caacagcaac 1500

tttacctgga caggtgcttc aaaatataac cttaatgggc gtgaatctat aatcaaccct 1560

ggcactgcta tggcctcaca caaagacgac aaagacaagt tctttcccat gagcggtgtc 1620

atgatttttg gaaaggagag cgccggagct tcaaacactg cattggacaa tgtcatgatc 1680

acagacgaag aggaaatcaa agccactaac cccgtggcca ccgaaagatt tgggactgtg 1740

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gccttacctg gaatggtgtg gcaagacaga gacgtatacc tgcagggtcc tatttgggcc 1860

aaaattcctc acacggatgg acactttcac ccgtctcctc tcatgggcgg ctttggactt 1920

aagcacccgc ctcctcagat cctcatcaaa aacacgcctg ttcctgcgaa tcctccggca 1980

gagttttcgg ctacaaagtt tgcttcattc atcacccagt attccacagg acaagtgagc 2040

gtggagattg aatgggagct gcagaaagaa aacagcaaac gctggaatcc cgaagtgcag 2100

tatacatcta actatgcaaa atctgccaac gttgatttca ctgtagacaa caatggactt 2160

tatactgtgc ctcgccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1008
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1008
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacgc ggcggacgcg gcggccctcg aacacgacaa ggcttacgac 240

cagcagctca aggcgggtga caacccctac ctgcggtata accacgccga cgccgagttc 300

caggagcggc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caagaaccgg actcctcctc gggtattggc 480

aaaacaggtg agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt tcacggactc agagtatcag ctgccgtacg tgctcgggtc ggctcaccag 1080

ggctgcctcc ctccgttccc agcggacgtg ttcatgattc ctcagtacgg gtatctgaca 1140

ctcaacaacg gcagtcaggc agtgggacgg tcatccttct actgcctgga atattttcca 1200

tcgcagatgc tgagaaccgg caacaacttt ccgttcagtt acaccttcga ggacgtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctgattgac 1320

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ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1009
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1009
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga acagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

gactgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggacgttcct 1260

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg gacaaaacaa caatagcaac 1500

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1010
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1010

atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcacca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga ctgagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatactc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1011
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1011
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtactt caacgggggc cagtaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

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ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1012
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1012
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cggcagctcg acagcggaga caacccgtac ctgcggtata accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

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ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaaca 1140

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ggcatcgcta tggcaacaca caaagacgac aggagcgttt ttttccagta ccgggatcct 1620

gattttggca aacaaaatgc tgccagagac aatgcggatt acagcgatgt catgctcacc 1680

agcgaggaag aaatcaaaac cactaaccct gtggctacag aggaatacgg tatcgtggca 1740

gataacttgc agcagcaaaa cacggctcct caaattggaa ctgtcaacag ccagggggcc 1800

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acctccaact actacaaatc tacaagtgtg gactttgctg ttaatacaga aggcgtgtac 2160

tctgaacccc accccattgg cacccgttac ctcacccgtc ccctgtaa 2208

<210> 1013
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1013
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccctac ctcaagtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccttgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgta 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1014
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1014
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

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accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

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gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

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gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

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accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

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tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

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<210> 1015
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

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gccttacccg gtatggtctg gcagaaccgg gatgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

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accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1016
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1016
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccgaccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaacgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

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cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

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cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

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ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

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accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcact cgttacctca cccgtcccct gtaa 2214

<210> 1017
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1017
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccctac ctcaagtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccttgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

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tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1018
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1018
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

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tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1019
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1019
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

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gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

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gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

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gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

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tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1020
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1020
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag cttccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

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accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1021

<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccttgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaatg gcagccaggc agtgggacgg tcatcctttt actgcctgga atatttccca 1200

tcgcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggacgttcct 1260

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cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggtttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcaa 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaacctg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1022
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1022
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc ctcgggcatc 480

ggcaagacag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg tggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattccc aatggctggg cgacagagtc 720

atcaccacca gcacccgaac atgggccttg cccacctata acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

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aactttgcct ggactgctgg gaccaaatac catctgaaag gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca aacgctggaa cccagagatt 2100

caatacactt ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1023
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
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<222> (676)..(676)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (697)..(697)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (715)..(715)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (748)..(748)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (750)..(750)
<223> a, c, g, or t

<220>

<221> modified_base
<222> (757)..(757)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (763)..(763)
<223> a, c, g, or t

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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

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accaccagca cccgaacctg ggccctgncn acctacnaca acnacctcta caagcaaatc 780

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tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

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ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ttggcagaac cgggacgtgt acctgcaggg tcctatctgg 1860

gccaagattc ctcacacgga cggaaacttt catccctcgc cgctgatggg aggctttgga 1920

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actaccttca gtcaagctaa gctggcgtcg ttcatcacgc aatacagcac aggacaagtg 2040

agtgtggaaa ttgaatggga gctgcagaaa gaaaacagca agcgctggaa tcccgaagtg 2100

cagtacacat ccaattatgc aaaatctgcc aacgttgatt ttactgtgga caacaatgga 2160

ctttatactg agcctcgccc cattggcacc cgttacctta cccgtcccct gtaa 2214

<210> 1024
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1024
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtgtggga 600

tctcttacaa tggcttcagg tggtggcgca ccagtggcag acaataacga aggtgccgat 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcacccgaac atgggccttg cccacctata acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgga caatgatgga gtcaagacca tcgccaataa ccttaccagc 1020

acgattcagg tctttacgga ctcggaatac cagttgccgt acgtcctcgg ctctgcgcac 1080

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aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

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ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

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accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1025
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1025
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1026
<211> 2211
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1026
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

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accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1027
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1027
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcaccagaac ctgggccctg cccacctaca acaatcacct ctacaagcaa 780

atctccaaca gcacatctgg aggatcttca aatgacaacg cctacttcgg ctacagcacc 840

ccctgggggt attttgactt caaccgcttc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

attcaggtca aagaggttac ggacaacaat ggagtcaaga ccatcgccaa taaccttacc 1020

agcacggtcc aggtctttac ggactcggag taccagttgc cgtacgtcct cggctctgcg 1080

caccagggct gcctccctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatat 1200

ttcccttctc agatgctgag aacgggcaac aactttacct tcagctacac ctttgaggac 1260

gttcctttcc acagcagcta cgctcacagc cagagtctgg accgtctcat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacaagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggcaaaga ttccacacac ggacggacat tttcacccct ctcccctcat gggtggattc 1920

ggacttaaac accctcctcc acagattctc atcaagaaca ccccggtacc tgcgaatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag cacaggacaa 2040

gtgagtgtgg aaattgaatg ggagctgcag aaagaaaaca gcaagcgctg gaatcccgaa 2100

gtgcagtaca catccaatta tgcaaaatct gccaacgttg attttactgt ggacaacaat 2160

ggactttata ctgagcctcg ccccattggc acccgttacc ttacccgtcc cctgtaa 2217

<210> 1028
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1028
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aaggggctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaactttg ggcagactgg cgactcagag 540

tcagtgcccg atcctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc catttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

attcaggtct ttacggattc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcattattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

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accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgccag tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1029
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1029
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gagtggtggg cgctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga gggttcttga acctttttggt ctggttgagg aagctgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtgcccg accctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

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gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

attcaggtct ttacggattc ggaataccag ctcccgtacg tcctcggctc tgcccaccag 1080

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1030
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1030
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc ccgtcaacga ggcggacgcg gcggccctcg aacacgacaa ggcttacgac 240

cagcagctca aggccggtga caacccctac ctgcggtaca accacgccga cgccgagttc 300

caggagcggc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcaggtg cacagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagtaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa cgatggagtc aagaccatcg ccaataacct taccagcacc 1020

attcaggtgt ttacggactc ggaataccag ctgccgtacg ttctcggctc cgcccaccag 1080

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1031
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1031
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttgggt ctggttgagg aaggggctaa gacggctcct 420

ggaaagaaaa ggccggtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aagacaggtg cacagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtg cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagtaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

atccaggtct ttacggactc ggagtaccag ctgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1032
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact ttggctacag cacccttgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1033
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1033
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccgaccc aagagactca acttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaacgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

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cctttccaca gcagctacgc gcacagccag agcttggacc ggctgatgaa tcctctgatt 1320

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cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1034
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1034
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggaa cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

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gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

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accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1035
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

agggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

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actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1036
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1036
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc aacagcccgc cagaaaaaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acttacaaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt taacattcaa 960

gtcaaagagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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ggcatcgcta tggcgacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1037
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1037
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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaggaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cggctcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaaactctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tctcagatgc tgagaacggg caacaacttt accttcagct acacctttga ggaagtgcct 1260

ttccacagca gctacgcgca cagccagagc ctggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcctcaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1038
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1038

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1039
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1039
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
```

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
```

```
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
```

```
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1040
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1040
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Asn Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Ser His
        515                 520                 525
```

```
Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Thr
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735
```

Leu

<210> 1041
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1041
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
```

```
Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1042
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
```

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1042
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1043
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1043

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
```

```
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1044
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1044
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp
            260                 265                 270

Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300
```

```
Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

Gly Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Pro Leu

<210> 1045
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1045
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Gln Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540
```

```
Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560


Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590


Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735


Leu
```

<210> 1046
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1046
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

```
Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1047
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1047

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
```

```
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Leu Gly Ser Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Ile Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
```

```
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn
        435                 440                 445

Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe
    450                 455                 460

Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp
                485                 490                 495

Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu
            500                 505                 510

Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe
    530                 535                 540

Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560

Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Arg Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro
            580                 585                 590

Ala Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
```

625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1048
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1048
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Asp Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1049
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1049
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Glu Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Phe Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

```
Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1050
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1050
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560
```

```
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Asn Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Val Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1051
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polypeptide"

<400> 1051

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Glu Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Pro Phe Ser Tyr Thr Phe
```

```
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1052
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1052
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Asp Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1053
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1053
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
```

```
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser Gln
    450                 455                 460

Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

```
Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys Asp
        515                 520                 525

Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Ile Leu Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln Ile
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
                645                 650                 655

Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1054
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1054
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Thr Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
```

```
Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590


Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1055
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polypeptide"

<400> 1055

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
```

```
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Arg Ser Val Phe Phe Gln Tyr Arg Asp Pro Asp Phe Gly Lys
    530                 535                 540

Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu Thr
545                 550                 555                 560

Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr
                565                 570                 575

Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln Ile
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

610 615 620

Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp
645 650 655

Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr
705 710 715 720

Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1056
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1056
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

```
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1057
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1057
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1058
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1058
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
```

```
Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590


Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1059
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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polypeptide"

<400> 1059

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
```

195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr

```
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
```

610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1060
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1060
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Asp
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1061
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1061
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Lys Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

```
Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1062
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1062
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335
```

```
Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Gly Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560


Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590


Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1063
<211> 736
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1063
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro

```
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
```

385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
435 440 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
450 455 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
500 505 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
515 520 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
530 535 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545 550 555 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln

595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1064
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1064
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Gln
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Leu Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1065
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1065
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Ser Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Val
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Ala Thr Gly Gln
                485                 490                 495
```

```
Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Lys Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700
```

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1066
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (226)..(226)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (233)..(233)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (239)..(239)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (250)..(250)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (253)..(253)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (255)..(255)

<223> Any naturally occurring amino acid

<400> 1066
```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Thr Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
```

195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Xaa Asn Trp His Cys Asp Ser Xaa Trp Leu Gly Asp Arg Xaa Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Xaa Thr Tyr Xaa Asn Xaa Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ala Thr Asn Asp Asn
260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr

```
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
```

610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly
705 710 715 720

Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1067
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1067
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asp Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445
```

```
Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
```

```
Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1068
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1068

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210> 1069
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1069
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1070
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1070
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln

```
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp
            260                 265                 270

Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
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    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
```

580 585 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asn Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr
690 695 700

Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn
705 710 715 720

Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Pro Leu

<210> 1071
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1071
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180   185   190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195   200   205

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp
            260                 265                 270

Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415
```

```
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620
```

```
Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asn Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn
705                 710                 715                 720


Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Pro Leu



<210> 1072
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1072
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Ile Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1073
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1073
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495
```

```
Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1074
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1074
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asp Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
```

```
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
```

545 550 555 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1075
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1075
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Thr Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1076
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1076
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30
```

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1077
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1077
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495
```

```
Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700
```

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1078
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1078
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asn Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn

325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
450 455 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465 470 475 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
485 490 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
500 505 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
515 520 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe

```
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1079
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1079
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Arg Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

```
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575
```

```
Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1080
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
```

<400> 1080

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ser Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Met Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
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Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1081
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1081
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
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```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Gly Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Ser His Lys
        515                 520                 525


Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540


Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560


Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590


Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
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Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1082
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1082
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gagtggtggg acttgaaacc tgcatccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc caaaaagaga ctcaatttcg gtcagactgg cggcacagag 540

tcagttccag accctcaacc tctcggagaa cctccagcag cgccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg atttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg atacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1083
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1083
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattcccaat ggctgggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg atttcaacag attccactgc catttctcac cacgtgactg gcagcgactc 900

atcaacaaca attggggatt ccggcccaag agactcaact tcaaactctt caacatccaa 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

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ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1084
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1084
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gagtggtggg acttggaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacaggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1085
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1085
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg tgctcgggtc ggctcacgag 1080

ggctgcctcc cgccgttccc agcggacgtt ttcatgattc ctcagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgattttcg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 1086
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1086
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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctg 2208

<210> 1087
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1087
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaaccg cttccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caaccatcca 960

ggtcaaggag gtcacgcaga atgaaggcac caagaccatc gccaataacc tcaccagcac 1020

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ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

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ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt gggtaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg 1980

gccttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1088
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1088
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaaca tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccaacggga cttcgggagg aagcaccaac gacaacacct acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaaact cttcaacatc 960

caagtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctccgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cggctaccta 1140

acactcaaca acggtagtca ggccgtggga cgctcctcct tctactgcct ggaatacttt 1200

ccttcgcaga tgctgagaac gggcaacaac tttaccttca gctacacctt tgaggacgtt 1260

cctttccaca gcagctacgc tcacagccag agtctggacc gtctcatgaa tcctctgatt 1320

gaccagtacc tgtactactt gtctcggact caaacaacag gaggcacggc aaatacgcag 1380

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aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg atccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1089
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1089
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggcttcagg cggtggcgca ccaatggcag acaataacga gggcgccgac 660

ggagtgggta attcctcggg aaattggcat tgcgattcca catggatggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgactttaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagagactca acttcaagct cttcaacatc 960

caagtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

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atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacac aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1090
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (676)..(676)
<223> a, c, g, or t

<400> 1090
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcangaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgcca cctataacaa ccacctctac aagcaaatct 780

ccagtgcttc aacgggggcg cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc agactatcag ctcccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacacagt actccacggg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1091
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (715)..(715)
<223> a, c, g, or t

<400> 1091
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctctgg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggctgggcga cagantcatc 720

accaccagca cccgaacctg ggccctgccc acctataaca accatctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

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tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact ttcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1092
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1092
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccctac ctcaagtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1093
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1093
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cagcagctcc aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc ttcaaggaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg acttcaaccg cttccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcagct tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

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gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1094
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1094
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgctaaaaag agactcaatt ttggtcagac tggcgactca 540

gagtcagtcc ccgacccaca acctctcgga gaacctccag caacccccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta atgcctcagg aaattggcat tgcgattcca catggctggg ggacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacttcggg aggaagcacc aacgacaaca cctacttcgg ctgcgtcacg 840

ccctgggggt attttgactt taacaaattc cactgccact tttcaccgga tgactggcaa 900

cgactcatca acaacggctg gggattccgg actaagcgac tcaacttcaa gctcttcagc 960

atgaaagtca aaaagggtac ggacaacact ggaatcaaga ccatcgcgaa taaccttacc 1020

aacacggtcc atgtcttcgc ggactcggag taccagttgc cgtacgtcct cggctctgcg 1080

caccagggct gcctccctcc gttcccggcg gacgtgttca tgattccgca gtacggctac 1140

ctaacgctca acaatggcag ccaggcagtg ggacggtcat ccttttactg cctggaatat 1200

ttcccatcgc agatgctgag aacgggcaac aactttacct tcagctacac ctttgaggac 1260

gttccttttcc acagcagcta cgctcacagc cagagtctgg accgtctcat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacaagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggaaaaca gcaagcgctg gaacccggag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaacccca ccccattggc acccgttacc tcacccgtcc cctgtaa 2217

<210> 1095
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1095
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgat 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg ggacagagtc 720

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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

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ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acctgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

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atgaagcacc cgcctcctcc gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgccgaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggt 2160

gtgtactatg aaccccaccc cattggcacc cgttacctca cccctcccct gtaa 2214

<210> 1096
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1096
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gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aagggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgctctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

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cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

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tgggggtatt ttgatttcaa cagattccac tgccactttt caccacgtga ctggcagcga 900

ctcatcacaa caattggggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcggagtac cagttgccgt acgtcctcgg ctctgcgcac 1080

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atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacgc aatacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa ccccgagatc 2100

cagtacacct ccaactacta caaatctaca agtgtggact ttgctgttaa tacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1097
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1097
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagaaaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttttcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc cgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgatcc cccagtacgg ctacctaaca 1140

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ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

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aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg cttcggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1098
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1098
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctca gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgcccgc tgctgtggga 600

cctactacaa tggcttcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattccc aatggctggg ggacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccagtg cttcaacggg ggccagcaac gacaaccact acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccactttt caccacgtga ctggcaaaga 900

ctcatcaaca acaactgggg attccggccc aagagactca gcttcaagct cttcaacatc 960

caggtcaagg aggtcacgca gaatgaaggc accaagacca tcgccaataa cctcaccagc 1020

accatccagg tgtttacgga ctcggagtac cagctgccgt acgttctcgg ctctgcccac 1080

cagggctgcc tgcctccgtt cccggcggac gtgttcatga ttccccagta cgggtacctg 1140

actctgaaca atggcagtca ggccgtgggc cgttcctcct tctactgcct ggagtacttt 1200

ccttctcaaa tgctgagaac cggcaacaac ttccagttta cttacacctt cgaggacgtg 1260

cctttccaca gcagctacgc ccacagccag agcttggacc ggctgatgaa tcctctgatt 1320

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ccaggaccct gttaccgcca acaacgcgtc tcaacgacaa ccgggcaaaa caacaatagc 1500

aactttgcct ggactgctgg gaccaaatac catctgaatg gaagaaattc attggctaat 1560

cctggcatcg ctatggcaac acacaaagac gacaaggagc gttttttttcc cagtaacggg 1620

atcctgattt ttggcaaaca aaatgctgcc agagacaatg cggattacag cgatgtcatg 1680

ctcaccagcg aggaagaaat caaaaccact aaccctgtgg ctacagagga atacggtatc 1740

gtggcagata acttgcagca gcaaaacacg gctcctcaaa ttggaactgt caacagccag 1800

ggggccttac ccggtatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga cggcaacttc cacccgtctc cgctgatggg cggctttggc 1920

ctgaaacatc ctccgcctca gatcctgatc aagaacacgc ctgtacctgc ggatcctccg 1980

accaccttca accagtcaaa gctgaactct ttcatcacac agtactccac gggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaag gaaaacagca agcgctggaa cccggagatc 2100

cagtacactt ccaactacta caaatctaca aatgtggact ttgctgttaa cacagaaggc 2160

gtgtactctg aaccccaccc cattggcacc cgttacctca cccgtcccct gtaa 2214

<210> 1099
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1099
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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggacct 600

aatacaatgg ctgcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattccacat ggatgggtga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctaaca 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctca acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacacagt actccacggg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacttcaccc gtcccctgta a 2211

<210> 1100
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1100
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaaaaga ctcaattttg gtcagactgg cgactcagag 540

tcagttccag accctcaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggtgg tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag cacccctgg 840

gggtattttg acttcaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcctaag cgactcaact tcaagctctt caacattcag 960

gtcaaagagg ttacggacaa caatggagtc aagaccatcg ccaataacct taccagcacg 1020

gtccaggtct tcacggactc ggagtaccag ttgccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctcc ctccgttccc ggcggacgtg ttcatgattc cgcagtacgg ctacctaacg 1140

ctcaacaacg gtagtcaggc cgtgggacgc tcctccttct actgcctgga atactttcct 1200

tcgcagatgc tgagaaccgg caacaacttc cagtttactt acaccttcga ggacgtgcct 1260

ttccacagca gctacgccca cagccagagc ttggaccggc tgatgaatcc tctgattgac 1320

cagtacctgt actacttgtc tcggactcaa acaacaggag gcacggcaaa tacgcagact 1380

ctgggcttca gccaaggtgg gcctaataca atggccaatc aggcaaagaa ctggctgcca 1440

ggaccctgtt accgccaaca acgcgtctcg acgacaaccg ggcaaaacaa caatagcaac 1500

tttgcctgga ctgctgggac caaataccat ctgaatggaa gaaattcatt ggctaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgctgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtatcgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtttg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtctccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacacagt actccacggg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc ggagatccag 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgttaacac agaaggcgtg 2160

tactctgaac cccaccccat tggcacccgt tacctcaccc gtcccctgta a 2211

<210> 1101
<211> 2211

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1101
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcacca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcggaca ataacgaagg cgccgatgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caacgggggc cagcaacgac aaccactact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgcagaa tgaaggcacc aagaccatcg ccaataacct caccagcacc 1020

atccaggtgt ttacggactc ggagtaccag ctgccgtacg ttctcggctc tgcccaccag 1080

ggctgcctgc ctccgttccc ggcggacgtg ttcatgattc cccagtacgg ctacctgact 1140

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tttgcctgga ctgctgggac caaataccat atgaatggaa gaaattcatt ggttaatcct 1560

ggcatcgcta tggcaacaca caaagacgac aaggagcgtt tttttcccag taacgggatc 1620

ctgatttttg gcaaacaaaa tgttgccaga gacaatgcgg attacagcga tgtcatgctc 1680

accagcgagg aagaaatcaa aaccactaac cctgtggcta cagaggaata cggtattgtg 1740

gcagataact tgcagcagca aaacacggct cctcaaattg gaactgtcaa cagccagggg 1800

gccttacccg gtatggtctg gcagaaccgg gacgtgtacc tgcagggtcc catctgggcc 1860

aagattcctc acacggacgg caacttccac ccgtcgccgc tgatgggcgg ctttggcctg 1920

aaacatcctc cgcctcagat cctgatcaag aacacgcctg tacctgcgga tcctccgacc 1980

accttcaacc agtcaaagct gaactctttc atcacgcaat acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaggaa aacagcaagc gctggaaccc cgagatccag 2100

tacacctcca actactacaa atctacaagt gtggactttg ctgttaatac agaaggcgtg 2160

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<210> 1102
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1102
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro

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        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Arg Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
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    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
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660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1103
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1103
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Ala Ser Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Gly Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
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Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
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Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1104
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1104
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
```

```
Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1105
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
```

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1105
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Glu Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400
```

```
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

```
Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1106
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1106

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
```

```
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1107
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1107
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720
```

```
Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1108
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1108
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn His Pro
305                 310                 315                 320

Gly Gln Gly Gly His Ala Glu Arg His Gln Asp His Arg Gln Pro His
                325                 330                 335

Gln His Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350
```

```
Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365


Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380


Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400


Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe Glu Asp
                405                 410                 415


Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430


Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln
        435                 440                 445


Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser Gln Gly
    450                 455                 460


Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480


Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn Asn Asn
                485                 490                 495


Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn Gly Arg
            500                 505                 510


Asn Ser Leu Gly Asn Pro Gly Ile Ala Met Ala Thr His Lys Asp Asp
        515                 520                 525


Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly Lys Gln
    530                 535                 540


Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu Thr Ser
545                 550                 555                 560
```

```
Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly
               565                 570                 575

Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln Ile Gly
            580                 585                 590

Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro
               645                 650                 655

Pro Thr Ala Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr
    690                 695                 700

Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val Tyr Ser
705                 710                 715                 720

Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
               725                 730
```

<210> 1109
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1109
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys His Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400
```

```
Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605
```

```
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Asp Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1110
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1110

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
```

```
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val
```

225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
260 265 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser

```
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
```

645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1111
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (226)..(226)
<223> Any naturally occurring amino acid

<400> 1111
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

```
Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Xaa Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Pro Ile Thr Thr Thr Ser
                245                 250                 255

Thr Ser Lys Ser Pro Val Leu Gln Arg Gly Arg Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445
```

```
Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655
```

```
Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1112
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"


<220>
<221> MOD_RES
<222> (239)..(239)
<223> Any naturally occurring amino acid

<400> 1112
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Xaa Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Phe Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735

<210> 1113
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1113
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320
```

```
Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525
```

```
Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1114
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1114
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
```

```
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
```

580 585 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1115
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1115
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
```

```
Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Cys Val Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Lys Phe His Cys His Phe Ser Pro Asp Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Gly Trp Gly Phe Arg Thr Lys Arg Leu Asn Phe Lys Leu Phe Ser
305                 310                 315                 320

Met Lys Val Lys Lys Gly Thr Asp Asn Thr Gly Ile Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Asn Thr Val His Val Phe Ala Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Pro Leu

<210> 1116
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1116
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255
```

```
Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460
```

```
Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Leu
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Met Lys His Pro Pro Pro Pro Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670
```

```
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Pro Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720


Val Tyr Tyr Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Pro Pro
                725                 730                 735


Leu



<210> 1117
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1117
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80
```

```
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Ala Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Thr Thr
    290                 295                 300

Ile Gly Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495
```

```
Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590

Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700
```

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
725 730 735

Leu

<210> 1118
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1118
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
```

```
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn His Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
```

```
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 1119

<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1119
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Gln Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Ala Gln Thr Leu Gly Phe
    450                 455                 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe
    530                 535                 540

Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met
545                 550                 555                 560

Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro
            580                 585                 590
```

```
Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
                725                 730                 735

Leu
```

<210> 1120
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1120

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205
```

```
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620
```

```
Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Phe Thr Arg Pro Leu
                725                 730                 735


<210> 1121
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1121
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45
```

```
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
```

```
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460
```

```
Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480


Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495


Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510


Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525


Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540


Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560


Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590


Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670
```

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1122
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1122
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
```

305 310 315 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Gln Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
435 440 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
450 455 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Met Asn
500 505 510

Gly Arg Asn Ser Leu Val Asn Pro Gly Ile Ala Met Ala Thr His Lys

```
        515                 520                 525

Asp Asp Lys Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Val Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro His Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
```

725 730 735

<210> 1123
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1123
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtttggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1124
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1124
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415


Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1125
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1125
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
```

```
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
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465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
```

675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1126
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1126
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320
```

```
Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Leu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Arg Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525
```

```
Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Phe Arg Asp Leu Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Ser Thr Pro Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1127
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1127
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365
```

```
Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Tyr Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Leu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575
```

```
Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1128
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1128

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205
```

```
Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415
```

```
Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Gly Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Ile Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Leu Tyr Asp Ala Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Leu Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1129
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1129
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
```

```
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
```

```
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Thr Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Thr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Gly Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Arg Val Asp Thr Ser Ala Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Tyr Thr Asn Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
```

675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1130
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1130
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320
```

```
Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ser Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Phe Ala Thr Ala Gly
        515                 520                 525
```

```
Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Asp Tyr Asp Ser Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Asp Thr Thr Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1131
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1131
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365
```

```
Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ser Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Trp Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Cys Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575
```

```
Gly Asn Leu Pro Gln Gly Asp Ser Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590


Asp Arg Met Thr Val Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605


Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685


Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700


Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720


Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735


<210> 1132
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1132
```

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205
```

```
Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415
```

```
Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Cys Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Arg Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Leu Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Tyr Lys Asp Ser Ser Arg Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Glu Thr Ser Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1133
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1133
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
```

```
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
```

```
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ile Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Tyr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Arg Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Trp Ile Asp Asn Ser Arg Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Pro Thr Ser Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Lys Asn Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Thr Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
```

675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1134
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1134
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320
```

```
Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Gly Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Ile Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Arg Ala Thr Ala Gly
        515                 520                 525
```

```
Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1135
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1135
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365
```

```
Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Val Ile Pro Ala
                485                 490                 495

Thr Glu Ser Asp Ser Leu Ile Tyr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Tyr Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575
```

```
Gly Asn Leu Pro Pro Arg Asp Asp Ser Thr Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Lys Thr Tyr Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1136
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1136

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205
```

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Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415
```

```
Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Tyr Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Ile Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Ile Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ser Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Thr Asp Asp Asp Ser Arg Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Met Thr Leu Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1137
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1137
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
```

```
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
```

```
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr His Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Tyr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Ser Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Arg Arg Asp Ser Ser Val Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Tyr Thr Asp Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
```

675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1138
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1138
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320
```

```
Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ser Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Ser Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Arg Ala Thr Ala Gly
        515                 520                 525
```

```
Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Arg His Asp Ser Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Asn Thr Gly Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1139
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1139
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365
```

```
Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Phe Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Arg Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Leu Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575
```

```
Gly Asn Leu Pro Val Ile Asp Phe Ser Lys Ser Asn Leu Pro Thr Val
            580                 585                 590


Asp Arg Leu Thr His Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605


Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620


Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640


His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685


Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700


Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720


Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735


<210> 1140
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1140
```

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205
```

```
Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415
```

```
Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Val Arg Asp Phe Ser Leu Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Thr Thr Lys Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1141
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1141
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
```

```
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
```

465 470 475 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Phe Ile Pro Ala
485 490 495

Thr Gly Ser Asp Ser Leu Ile Gln Tyr Glu Thr His Ser Thr Leu Asp
500 505 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
515 520 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
530 535 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545 550 555 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
565 570 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val
580 585 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
595 600 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys

675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1142
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1142
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320
```

```
Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Met Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Ile Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Phe Ala Thr Ala Gly
        515                 520                 525
```

```
Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Val Trp
                565                 570                 575

Gly Asn Leu Pro Ser Gly Asp His Ser Gln Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Pro Thr Met Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ile Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val His Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asp Tyr
    690                 695                 700

Gly Gln His Ser Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Thr Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
```

<210> 1143
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1143
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

```
Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365
```

```
Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Asp Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575
```

```
Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 1144
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1144

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205
```

```
Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415
```

```
Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Ile Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Thr Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Val Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Phe Asn Asp Asp Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Ser Thr Phe Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620
```

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1145
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1145
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Ser Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
```

```
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
```

```
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
```

675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 1146
<211> 742
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1146
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Lys Gln Leu Glu Gln Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Ala Thr Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Lys Thr Pro Asn Arg Pro Thr Asn Pro Asp Ser Gly Lys
145                 150                 155                 160

Ala Pro Ala Lys Lys Lys Gln Lys Asp Gly Glu Pro Ala Asp Ser Ala
                165                 170                 175

Arg Arg Thr Leu Asp Phe Glu Asp Ser Gly Ala Gly Asp Gly Pro Pro
            180                 185                 190

Glu Gly Ser Ser Ser Gly Glu Met Ser His Asp Ala Glu Met Arg Ala
        195                 200                 205

Ala Pro Gly Gly Asn Ala Val Glu Ala Gly Gln Gly Ala Asp Gly Val
    210                 215                 220

Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly
225                 230                 235                 240

Arg Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr Asn
                245                 250                 255

Asn His Leu Tyr Leu Arg Ile Gly Thr Thr Ala Asn Ser Asn Thr Tyr
            260                 265                 270

Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Leu Arg Pro Lys Ser Met Arg Val Lys Ile Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro Tyr
            340                 345                 350

Val Met Asp Ala Gly Gln Glu Gly Ser Phe Pro Pro Phe Pro Asn Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Val Val Thr Gly Lys
    370                 375                 380

Asn Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Val Ser Tyr Gln
                405                 410                 415

Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Met Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp His Leu Gln
        435                 440                 445

Ser Thr Thr Thr Gly Asn Ser Leu Asn Gln Gly Thr Ala Thr Thr Thr
    450                 455                 460

Tyr Gly Lys Ile Thr Thr Gly Asp Phe Ala Tyr Tyr Arg Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Ala Cys Ile Lys Gln Gln Lys Phe Ser Lys Asn Ala Asn
                485                 490                 495

Gln Asn Tyr Lys Ile Pro Ala Ser Gly Gly Asp Ala Leu Leu Lys Tyr
            500                 505                 510

Asp Thr His Thr Thr Leu Asn Gly Arg Trp Ser Asn Met Ala Pro Gly
        515                 520                 525
```

```
Pro Pro Met Ala Thr Ala Gly Ala Gly Asp Ser Asp Phe Ser Asn Ser
    530                 535                 540

Gln Leu Ile Phe Ala Gly Pro Asn Pro Ser Gly Asn Thr Thr Thr Ser
545                 550                 555                 560

Ser Asn Asn Leu Leu Phe Thr Ser Glu Glu Glu Ile Ala Thr Thr Asn
                565                 570                 575

Pro Arg Asp Thr Asp Met Phe Gly Gln Ile Ala Asp Asn Asn Gln Asn
            580                 585                 590

Ala Thr Thr Ala Pro His Ile Ala Asn Leu Asp Ala Met Gly Ile Val
        595                 600                 605

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
    610                 615                 620

Trp Ala Lys Val Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
625                 630                 635                 640

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
                645                 650                 655

Asn Thr Pro Val Pro Ala Asn Pro Asn Thr Thr Phe Ser Ala Ala Arg
            660                 665                 670

Ile Asn Ser Phe Leu Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Gln
        675                 680                 685

Ile Asp Trp Glu Ile Gln Lys Glu His Ser Lys Arg Trp Asn Pro Glu
    690                 695                 700

Val Gln Phe Thr Ser Asn Tyr Gly Thr Gln Asn Ser Met Leu Trp Ala
705                 710                 715                 720

Pro Asp Asn Ala Gly Asn Tyr His Glu Leu Arg Ala Ile Gly Ser Arg
                725                 730                 735
```

Phe Leu Thr His His Leu
740

<210> 1147
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1147
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350
```

```
Leu Ser Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Gly Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala Tyr Ser Gln Ser Pro Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Leu Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560
```

```
Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730
```

<210> 1148
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1148
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Leu
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe His Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145 150 155 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
165 170 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
180 185 190

```
Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400
```

```
Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Gly Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605
```

```
Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620


His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640


Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655


Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670


Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685


Ser Lys Arg Arg Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
    690                 695                 700


Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705                 710                 715                 720


Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725                 730


<210> 1149
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1149
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
```

```
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Thr Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Gly Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
```

```
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Tyr Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
```

660 665 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Cys Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 1150
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1150
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300
```

```
Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510
```

```
Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Thr Val
            580                 585                 590

Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720
```

```
Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735


<210> 1151
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1151
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350
```

```
Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560
```

```
Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Val Val
            580                 585                 590

Arg Gly Leu Arg Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735


<210> 1152
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
```

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1152
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145 150 155 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
165 170 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
180 185 190

```
Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400
```

```
Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Val Val
            580                 585                 590

Asn Arg Leu Ser Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605
```

```
Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
        675                 680                 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
    690                 695                 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705                 710                 715                 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
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<210> 1153
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1153

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
```

```
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
```

```
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Ser Ser Asn Leu Pro Pro Val
            580                 585                 590

Met Gly Leu Gly Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn
        595                 600                 605

Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln
```

660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys
675 680 685

Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr
690 695 700

Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr
705 710 715 720

Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730 735

<210> 1154
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1154
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300
```

```
Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350

Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510
```

```
Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560

Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Arg Val Asp Arg Leu Pro Thr
            580                 585                 590

Val Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys
705                 710                 715                 720
```

```
Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735


<210> 1155
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1155
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu
                165                 170                 175

Thr Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met
            180                 185                 190

Ser Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu
        195                 200                 205

Gly Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His
    210                 215                 220

Cys Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg
225                 230                 235                 240

Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly
                245                 250                 255

Glu Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly
            260                 265                 270

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
        275                 280                 285

Gln Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg
    290                 295                 300

Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly
305                 310                 315                 320

Glu Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala
                325                 330                 335

Asp Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly
            340                 345                 350
```

```
Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly
        355                 360                 365

Tyr Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg
    370                 375                 380

Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr
385                 390                 395                 400

Gly Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His
                405                 410                 415

Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu
            420                 425                 430

Ile Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr
        435                 440                 445

Leu Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr
    450                 455                 460

Asn Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys
465                 470                 475                 480

Gln Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Glu Ile Pro Ala
                485                 490                 495

Thr Gly Ser Asp Ser Leu Ile Glu Tyr Glu Thr His Ser Thr Leu Asp
            500                 505                 510

Gly Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly
        515                 520                 525

Pro Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro
    530                 535                 540

Lys Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr
545                 550                 555                 560
```

```
Ser Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp
                565                 570                 575

Gly Asn Leu Pro Gly Gly Asp Gln Ser Arg Ala Leu Arg Leu Pro Thr
            580                 585                 590

Val Asp Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln
        675                 680                 685

Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690                 695                 700

Tyr Gly Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys
705                 710                 715                 720

Tyr Thr Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730                 735
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<210> 1156
<211> 1172
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1156
cttaattagg ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg 60

ggcgaccttt ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtggccaa 120

ctccatcact aggggttcct tgtagttaat gattaacccg ccatgctact tatctaccag 180

ggtaatgggg atcctctaga actatagcta gtcgacattg attattgact agttattaat 240

agtaatcaat tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac 300

ttacggtaaa tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa 360

tgacgtatgt tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact 420

atttacggta aactgcccac ttggcagtac atcaagtgta tcatatgcca agtacgcccc 480

ctattgacgt caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat 540

gggactttcc tacttggcag tacatctacg tattagtcat cgctattacc atgtcgaggc 600

cacgttctgc ttcactctcc ccatctcccc cccctcccca cccccaattt tgtatttatt 660

tatttttaa ttattttgtg cagcgatggg ggcgggggggg gggggcgcgc gccaggcggg 720

gcggggcggg gcgaggggcg gggcggggcg aggcggagag gtgcggcggc agccaatcag 780

agcggcgcgc tccgaaagtt tccttttatg gcgaggcggc ggcggcggcg gccctataaa 840

aagcgaagcg cgcggcgggc gggagcaagc tttattgcgg tagtttatca cagttaaatt 900

gctaacgcag tcagtgcttc tgacacaaca gtctcgaact taagctgcag aagttggtcg 960

tgaggcactg ggcaggtaag tatcaaggtt acaagacagg tttaaggaga ccaatagaaa 1020

ctgggcttgt cgagacagag aagactcttg cgtttctgat aggcacctat tggtcttact 1080

gacatccact ttgcctttct ctccacaggt gtccactccc agttcaatta cagctcttaa 1140

ggctagagta cttaatacga ctcsactata gg 1172

<210> 1157
<211> 3231
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1157
taagaattca cgcgtggtac ctctagagtc gacccgggcg gcctcgagga cggggtgaac 60

tacgcctgag gatccgatct ttttccctct gccaaaaatt atggggacat catgaagccc 120

cttgagcatc tgacttctgg ctaataaagg aaatttattt tcattgcaat agtgtgttgg 180

aatttttgt gtctctcact cggaagcaat tcgttgatct gaatttcgac cacccataat 240

acccattacc ctggtagata agtagcatgg cgggttaatc attaactaca aggaacccct 300

agtgatggag ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc 360

aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag 420

ccttaattaa cctaattcac tggccgtcgt tttacaacgt cgtgactggg aaaaccctgg 480

cgttacccaa cttaatcgcc ttgcagcaca tccccctttc gccagctggc gtaatagcga 540

agaggcccgc accgatcgcc cttcccaaca gttgcgcagc ctgaatggcg aatgggacgc 600

gccctgtagc ggcgcattaa gcgcggcggg tgtggtggtt acgcgcagcg tgaccgctac 660

acttgccagc gccctagcgc ccgctccttt cgctttcttc ccttcctttc tcgccacgtt 720

cgccggcttt ccccgtcaag ctctaaatcg ggggctccct ttagggttcc gatttagtgc 780

tttacggcac ctcgacccca aaaaacttga ttagggtgat ggttcacgta gtgggccatc 840

gccctgatag acggtttttc gccctttgac gttggagtcc acgttcttta atagtggact 900

cttgttccaa actggaacaa cactcaaccc tatctcggtc tattcttttg atttataagg 960

gattttgccg atttcggcct attggttaaa aaatgagctg atttaacaaa aatttaacgc 1020

gaattttaac aaaatattaa cgcttacaat ttaggtggca cttttcgggg aaatgtgcgc 1080

ggaaccccta tttgtttatt tttctaaata cattcaaata tgtatccgct catgagacaa 1140

taaccctgat aaatgcttca ataatattga aaaaggaaga gtatgagtat tcaacatttc 1200

cgtgtcgccc ttattccctt ttttgcggca ttttgccttc ctgtttttgc tcacccagaa 1260

acgctggtga aagtaaaaga tgctgaagat cagttgggtg cacgagtggg ttacatcgaa 1320

ctggatctca acagcggtaa gatccttgag agttttcgcc ccgaagaacg ttttccaatg 1380

atgagcactt ttaaagttct gctatgtggc gcggtattat cccgtattga cgccgggcaa 1440

gagcaactcg gtcgccgcat acactattct cagaatgact tggttgagta ctcaccagtc 1500

acagaaaagc atcttacgga tggcatgaca gtaagagaat tatgcagtgc tgccataacc 1560

atgagtgata acactgcggc caacttactt ctgacaacga tcggaggacc gaaggagcta 1620

accgcttttt tgcacaacat gggggatcat gtaactcgcc ttgatcgttg ggaaccggag 1680

ctgaatgaag ccataccaaa cgacgagcgt gacaccacga tgcctgtagc aatggcaaca 1740

acgttgcgca aactattaac tggcgaacta cttactctag cttcccggca acaattaata 1800

gactggatgg aggcggataa agttgcagga ccacttctgc gctcggccct tccggctggc 1860

tggtttattg ctgataaatc tggagccggt gagcgtgggt ctcgcggtat cattgcagca 1920

ctggggccag atggtaagcc ctcccgtatc gtagttatct acacgacggg gagtcaggca 1980

actatggatg aacgaaatag acagatcgct gagataggtg cctcactgat taagcattgg 2040

taactgtcag accaagttta ctcatatata ctttagattg atttaaaact tcatttttaa 2100

tttaaaagga tctaggtgaa gatccttttt gataatctca tgaccaaaat cccttaacgt 2160

gagttttcgt tccactgagc gtcagacccc gtagaaaaga tcaaaggatc ttcttgagat 2220

cctttttttc tgcgcgtaat ctgctgcttg caaacaaaaa aaccaccgct accagcggtg 2280

gtttgtttgc cggatcaaga gctaccaact ctttttccga aggtaactgg cttcagcaga 2340

gcgcagatac caaatactgt tcttctagtg tagccgtagt taggccacca cttcaagaac 2400

tctgtagcac cgcctacata cctcgctctg ctaatcctgt taccagtggc tgctgccagt 2460

ggcgataagt cgtgtcttac cgggttggac tcaagacgat agttaccgga taaggcgcag 2520

cggtcgggct gaacgggggg ttcgtgcaca cagcccagct tggagcgaac gacctacacc 2580

gaactgagat acctacagcg tgagctatga gaaagcgcca cgcttcccga agggagaaag 2640

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gggggaaacg cctggtatct ttatagtcct gtcgggtttc gccacctctg acttgagcgt 2760

cgatttttgt gatgctcgtc agggggggcgg agcctatgga aaaacgccag caacgcggcc 2820

tttttacggt tcctggcctt ttgctggcct tttgctcaca tgttctttcc tgcgttatcc 2880

cctgattctg tggataaccg tattaccgcc tttgagtgag ctgataccgc tcgccgcagc 2940

cgaacgaccg agcgcagcga gtcagtgagc gaggaagcgg aagagcgccc aatacgcaaa 3000

ccgcctctcc ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac 3060

tggaaagcgg gcagtgagcg caacgcaatt aatgtgagtt agctcactca ttaggcaccc 3120

caggctttac actttatgct tccggctcgt atgttgtgtg gaattgtgag cggataacaa 3180

tttcacacag gaaacagcta tgaccatgat tacgccagat ttaattaagg c 3231

<210> 1158
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> MOD_RES
<222> (264)..(264)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (266)..(266)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (268)..(268)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (448)..(448)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (459)..(460)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (467)..(467)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES

<222> (470)..(471)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (474)..(474)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (495)..(495)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (516)..(516)
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<223> Any naturally occurring amino acid

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<223> Any naturally occurring amino acid

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<223> Any naturally occurring amino acid

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<223> Any naturally occurring amino acid

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<222> (710)..(710)
<223> Any naturally occurring amino acid

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<222> (717)..(719)
<223> Any naturally occurring amino acid

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<222> (723)..(723)
<223> Any naturally occurring amino acid

<400> 1158
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

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            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
```

225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Xaa Ser Xaa Gly Xaa Thr Asn Asp Asn
260 265 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa

```
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Xaa Xaa Glu Leu Leu Phe
    450                 455                 460

Ser Gln Xaa Gly Pro Xaa Xaa Met Ser Xaa Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Xaa Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Xaa Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Xaa Gly Ala Gly Xaa Asn Asn Thr Xaa Leu Xaa Asn Val Met
545                 550                 555                 560

Xaa Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Xaa Tyr Gly Val Val Ala Xaa Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Xaa Thr Gly Xaa Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
```

645 650 655

Ala Asn Pro Pro Xaa Xaa Phe Xaa Xaa Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Xaa Asn Val Asp Phe Ala Val Xaa Xaa Xaa Gly
705 710 715 720

Val Tyr Xaa Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1159
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1159
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270
```

```
His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480
```

```
Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Ala Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Glu Gly Ala Gly Ala Asn Asn Thr Ala Leu Glu Asn Val Met
545                 550                 555                 560

Leu Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Ala Thr Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Thr Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685
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Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Asn Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1160
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1160
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Ser Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510
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```
Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Ala Asn Asn Thr Thr Leu Asp Asn Val Met
545                 550                 555                 560

Met Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Ala Val Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu Gly
705                 710                 715                 720
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Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu



<210> 1161
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1161
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Ala Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Thr Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540
```

```
Gly Lys Gln Gly Ala Gly Ala Asn Asn Thr Ala Leu Asp Asn Val Met
545                 550                 555                 560


Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590


Ala Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605


Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620


His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640


Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655


Ala Asn Pro Pro Thr Val Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670


Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685


Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700


Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Ser Glu Gly
705                 710                 715                 720


Val Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735


Leu
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<210> 1162
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<222> (264)..(264)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (448)..(448)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (459)..(459)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (470)..(470)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (495)..(495)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (533)..(533)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (547)..(547)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (555)..(555)
<223> Any naturally occurring amino acid

<220>

<221> MOD_RES
<222> (557)..(557)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (561)..(561)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (563)..(563)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (593)..(593)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (596)..(596)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (661)..(662)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (664)..(664)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (718)..(718)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (723)..(723)
<223> Any naturally occurring amino acid

<400> 1162
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Xaa Ser Ser Gly Ser Thr Asn Asp Asn
            260                 265                 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa
        435                 440                 445
```

```
Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Xaa Arg Glu Leu Leu Phe
    450                 455                 460

Ser Gln Gly Gly Pro Xaa Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Xaa Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Xaa Gly Ala Gly Ala Asn Asn Thr Xaa Leu Xaa Asn Val Met
545                 550                 555                 560

Xaa Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
            580                 585                 590

Xaa Thr Gly Xaa Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655
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Ala Asn Pro Pro Xaa Xaa Phe Xaa Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Xaa Glu Gly
705 710 715 720

Val Tyr Xaa Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1163
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (264)..(264)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (448)..(448)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (470)..(470)
<223> Any naturally occurring amino acid

<220>

<221> MOD_RES
<222> (533)..(533)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (547)..(547)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (555)..(555)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (557)..(557)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (561)..(561)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (563)..(563)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (593)..(593)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (596)..(596)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (662)..(662)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (664)..(664)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (718)..(718)

<223> Any naturally occurring amino acid

<400> 1163
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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
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195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Ser Xaa Ser Ser Gly Ser Thr Asn Asp Asn
260 265 270

His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr

405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa
435 440 445

Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Leu Phe
450 455 460

Ser Gln Gly Gly Pro Xaa Asn Met Ser Ala Gln Ala Lys Asn Trp Leu
465 470 475 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Ser Gln
485 490 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
500 505 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
515 520 525

Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
530 535 540

Gly Lys Xaa Gly Ala Gly Ala Asn Asn Thr Xaa Leu Xaa Asn Val Met
545 550 555 560

Xaa Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
565 570 575

Gln Tyr Gly Val Val Ala Ser Asn Leu Gln Ser Ser Asn Thr Ala Pro
580 585 590

Xaa Thr Gly Xaa Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro

610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Ala Xaa Phe Xaa Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Ala Lys Ser Thr Asn Val Asp Phe Ala Val Asn Xaa Glu Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 1164
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1164
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca 540

gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

cctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac 1140

ctaacactca acaacggtag tcaggccgtg ggacgctcct ccttctactg cctggaatac 1200

tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac 1260

gtgcctttcc acagcagcta cgcccacagc cagagcttgg accggctgat gaatcctctg 1320

attgaccagt acctgtacta cttgtctcgg actcaaacaa caggaggcac ggcaaatacg 1380

cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg 1440

ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat 1500

agcaactttg cctggactgc tgggaccaaa taccatctga atggaagaaa ttcattggct 1560

aatcctggca tcgctatggc aacacacaaa gacgacgagg agcgtttttt tcccagtaac 1620

gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc 1680

atgctcacca gcgaggaaga aatcaaaacc actaaccctg tggctacaga ggaatacggt 1740

atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc 1800

caggggggcct tacccggtat ggtctggcag aaccgggacg tgtacctgca gggtcccatc 1860

tgggccaaga ttcctcacac ggacggcaac ttccacccgt ctccgctgat gggcggcttt 1920

ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct 1980

ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag 2040

gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgctg gaaccccgag 2100

atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa 2160

ggcgtgtact ctgaaccccg ccccattggc acccgttacc tcacccgtaa tctgtaa 2217

<210> 1165
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1165
Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

```
Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Val Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
                165                 170                 175

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
            180                 185                 190

Ala Pro Ser Gly Val Gly Ser Thr Thr Met Ala Ser Gly Gly Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300
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```
Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320


Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335


Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350


Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365


Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380


Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400


Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415


Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430


Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln
        435                 440                 445


Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala Gly
    450                 455                 460


Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
465                 470                 475                 480


Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn Ser
                485                 490                 495


Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
            500                 505                 510
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```
Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp Lys
        515                 520                 525

Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu Gly
    530                 535                 540

Thr Asn Ala Asn Asn Ala Asp Leu Glu Asn Val Met Ile Thr Asp Glu
545                 550                 555                 560

Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Thr
                565                 570                 575

Val Ser Asn Asn Leu Gln Asn Ser Asn Ala Gly Pro Thr Thr Gly Thr
            580                 585                 590

Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg Asp
        595                 600                 605

Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro
                645                 650                 655

Thr Asn Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys
    690                 695                 700

Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu
705                 710                 715                 720
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Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730

<210> 1166
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1166
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcaggtggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1167
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1167
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

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Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220
```

```
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430
```

```
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Val Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640
```

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1168
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1168
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cggtcaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1169
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1169
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

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Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350
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Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560
```

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Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Val Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720

Thr Arg Pro Leu
```

<210> 1170
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1170
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacac ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1171
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1171
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val

```
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
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            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
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465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Thr Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
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675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1172
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1172
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cggtcaacac ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgacccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1173
<211> 724
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1173

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Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175
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Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400


Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415


Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430


Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445


Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460


Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Val Asn Thr Gln Glu Ile Val Pro
            580                 585                 590
```

```
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu
```

<210> 1174
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1174
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggccgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1175
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1175
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

```
Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300
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```
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510
```

```
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Ala Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
```

Thr Arg Pro Leu

<210> 1176
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1176
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttatggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1177
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1177
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

```
Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220
```

```
Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Met Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430
```

```
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640
```

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1178
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1178
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtcgatgtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1179
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1179
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile

```
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Asp Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
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            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
```

545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1180
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1180
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggacccag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1181
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1181
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

```
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255
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```
Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Gln Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460
```

```
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480


Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495


Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510


Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525


Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540


Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560


Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575


Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590


Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670
```

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 1182
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1182
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccagtcgg cgaacccggg caccaccgcc 1620

acgtacctcg agggcaacat gctcatcacc agcgagagcg agacgcagcc ggtgaaccgc 1680

gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1183
<211> 724

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1183

```
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1               5                  10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175
```

```
Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380
```

```
Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Ser Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590
```

```
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605


Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620


Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640


Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655


Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670


Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685


Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700


Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720


Thr Arg Pro Leu
```

<210> 1184
<211> 2203
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1184
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcaac agccaggggg cgaacccggg caccaccgcc 1620

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gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgccccc 1740

gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac 1800

gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc 1860

tctccggcca tgggcggatt cggactcaaa cacccaccgc ccatgatgct catcaagaac 1920

acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc 1980

cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc 2040

aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac 2100

tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt 2160

acccgacccc tttaacccat tcatgtcgca taccctcaat aaa 2203

<210> 1185
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1185
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

```
Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300
```

```
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510
```

```
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Gly Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
            660                 665                 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
        675                 680                 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
    690                 695                 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705                 710                 715                 720
```

Thr Arg Pro Leu

<210> 1186
<211> 2194
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1186
atgtcttttg ttgatcaccc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag 60

tttttgggcc ttgaagcggg cccaccgaaa ccaaaaccca atcagcagca tcaagatcaa 120

gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga 180

ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240

cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300

gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360

aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420

ggaaagcgga tagacgacca ctttccaaaa agaaagaagg ctcggaccga agaggactcc 480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc 540

ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600

ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660

gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720

agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780

aacgcctact ttggatacag cacccctgg gggtactttg actttaaccg cttccacagc 840

cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg 900

tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc 960

accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020

ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080

tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140

gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200

aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctgt tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc 1320

acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc 1380

tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg 1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg 1500

agttaccagg tgcccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc 1560

tatgccctgg agaacactat gatcttcggg aagcaaggct cagagaaaac aaatgtggac 1620

attgaaaagg tcatgatcac cagcgagagc gagacgcagc cggtgaaccg cgtggcgtac 1680

aacgtcggcg ggcagatggc caccaacaac cagagctcca ccactgcccc cgcgaccggc 1740

acgtacaacc tccaggaaat cgtgcccggc agcgtgtgga tggagaggga cgtgtacctc 1800

caaggaccca tctgggccaa gatcccagag acgggggcgc actttcaccc ctctccggcc 1860

atgggcggat tcggactcaa acacccaccg cccatgatgc tcatcaagaa cacgcctgtg 1920

cccggaaata tcaccagctt ctcggacgtg cccgtcagca gcttcatcac ccagtacagc 1980

accgggcagg tcaccgtgga gatggagtgg gagctcaaga aggaaaactc caagaggtgg 2040

aacccagaga tccagtacac aaacaactac aacgaccccc agtttgtgga ctttgccccg 2100

gacagcaccg gggaatacag aaccaccaga cctatcggaa cccgatacct tacccgaccc 2160

ctttaaccca ttcatgtcgc ataccctcaa taaa 2194

<210> 1187
<211> 721
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1187
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu

```
1               5                   10                  15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20                  25                  30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35                  40                  45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
```

210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp

```
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val
    530                 535                 540

Met Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg Val Ala Tyr
545                 550                 555                 560

Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser Thr Thr Ala
                565                 570                 575

Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro Gly Ser Val
            580                 585                 590

Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
        595                 600                 605

Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met Gly Gly Phe
    610                 615                 620

Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val
```

625 630 635 640

Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile
645 650 655

Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu
660 665 670

Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn
675 680 685

Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp Ser Thr Gly
690 695 700

Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro
705 710 715 720

Leu

<210> 1188
<211> 519
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1188
Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp
1 5 10 15

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
20 25 30

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly
35 40 45

Gly Ala Thr Asn Asp Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
50 55 60

```
Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
65                  70                  75                  80

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser
                85                  90                  95

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly
            100                 105                 110

Thr Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr
        115                 120                 125

Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
    130                 135                 140

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly
145                 150                 155                 160

Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe
                165                 170                 175

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
            180                 185                 190

Phe Gln Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr
        195                 200                 205

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
    210                 215                 220

Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn
225                 230                 235                 240

Thr Gln Thr Leu Gly Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn
                245                 250                 255

Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val
            260                 265                 270
```

```
Ser Thr Thr Thr Gly Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala
        275                 280                 285

Gly Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly
    290                 295                 300

Ile Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser
305                 310                 315                 320

Asn Gly Ile Leu Ile Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala
                325                 330                 335

Asp Tyr Ser Asp Val Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr
            340                 345                 350

Asn Pro Val Ala Thr Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln
        355                 360                 365

Gln Gln Asn Thr Ala Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala
    370                 375                 380

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro
385                 390                 395                 400

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
                405                 410                 415

Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile
            420                 425                 430

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser
        435                 440                 445

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
    450                 455                 460

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
465                 470                 475                 480
```

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe
485 490 495

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
500 505 510

Arg Tyr Leu Thr Arg Asn Leu
515

<210> 1189
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1189
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525
```

```
His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735
```

Asn Leu

<210> 1190
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1190
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Thr Gly Lys Arg
130 135 140

```
Ile Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp
145                 150                 155                 160


Ser Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser
                165                 170                 175


Gln Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp
            180                 185                 190


Thr Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly
        195                 200                 205


Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr
    210                 215                 220


Trp Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu
225                 230                 235                 240


Pro Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val
                245                 250                 255


Asp Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
            260                 265                 270


Tyr Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp
        275                 280                 285


Gln Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg
    290                 295                 300


Val Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser
305                 310                 315                 320


Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr
                325                 330                 335


Asp Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly
            340                 345                 350
```

```
Cys Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly
        355                 360                 365

Tyr Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser
    370                 375                 380

Ser Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser
                405                 410                 415

Ser Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val
            420                 425                 430

Asp Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val
        435                 440                 445

Gln Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn
    450                 455                 460

Trp Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser
465                 470                 475                 480

Gly Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met
                485                 490                 495

Glu Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met
            500                 505                 510

Thr Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met
        515                 520                 525

Ile Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu
    530                 535                 540

Glu Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn
545                 550                 555                 560
```

```
Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser
                565                 570                 575


Ser Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val
            580                 585                 590


Pro Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile
        595                 600                 605


Trp Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala
    610                 615                 620


Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys
625                 630                 635                 640


Asn Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val
                645                 650                 655


Ser Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met
            660                 665                 670


Glu Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
        675                 680                 685


Gln Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro
    690                 695                 700


Asp Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr
705                 710                 715                 720


Leu Thr Arg Pro Leu
                725


<210> 1191
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polypeptide"

<400> 1191

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
```

405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
450 455 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
485 490 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
530 535 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
580 585 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His

610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1192
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1192
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

```
Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50                  55                  60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly Lys
145                 150                 155                 160

Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
                165                 170                 175

Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala
            180                 185                 190

Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly Ala
        195                 200                 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
    210                 215                 220

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
225                 230                 235                 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
                245                 250                 255
```

```
Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr Phe
            260                 265                 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys
        275                 280                 285

His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly
    290                 295                 300

Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val Lys
305                 310                 315                 320

Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr
                325                 330                 335

Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val
            340                 345                 350

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
        355                 360                 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
    370                 375                 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
385                 390                 395                 400

Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp
                405                 410                 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
            420                 425                 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln
        435                 440                 445

Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly Lys
    530                 535                 540

Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr Thr
            580                 585                 590

Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

```
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1193
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1193
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95
```

```
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300
```

```
Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590

Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720
```

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1194
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1194
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190


Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
            260                 265                 270


Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285


His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300


Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320


Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn Asn
                325                 330                 335


Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
```

```
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly Phe Ser
    450                 455                 460

Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile Phe Gly
    530                 535                 540

Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val Met Leu
545                 550                 555                 560
```

```
Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575


Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala Pro Gln
            580                 585                 590


Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1195
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
```

polypeptide"

<400> 1195

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
```

```
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
```

```
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Ser Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1196
<211> 3695
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1196
ctctttgcgc ttgcgttttc ccttgtccag atagcccagt agctgacatt catccggggt 60

cagcaccgtt tctgcggact ggctttctac gtgaaaagga tctaggtgaa gatccttttt 120

gataatctca tgcctgacat ttatattccc cagaacatca ggttaatggc gtttttgatg 180

tcattttcgc ggtggctgag atcagccact tcttccccga taacggagac cggcacactg 240

gccatatcgg tggtcatcat gcgccagctt tcatccccga tatgcaccac cgggtaaagt 300

tcacgggaga ctttatctga cagcagacgt gcactggcca gggggatcac catccgtcgc 360

cccggcgtgt caataatatc actctgtaca tccacaaaca gacgataacg gctctctctt 420

ttataggtgt aaaccttaaa ctgccgtacg tataggctgc gcaactgttg ggaagggcga 480

tcggtgcggg cctcttcgct attacgccag ctggcgaaag ggggatgtgc tgcaaggcga 540

ttaagttggg taacgccagg gttttcccag tcacgacgtt gtaaaacgac ggccagtgaa 600

ttgtaatacg actcactata gggcgaattg aatttagcgg ccgcgaattc gcccttatga 660

tatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca aggccattct 720

cggcggcagc aaagtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga tcgatcccac 780

tcccgtcatt gtcacctcca acaccaacat gtgcgccgtg attgacggga acagcaccac 840

cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactta cccgccgtct 900

ggagcatgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc gctgggcgca 960

ggatcacgtg accgaggtgg cgcatgagtt ccacgtcaga aagggtggag ccaacaagag 1020

acccgccccc gatgacgctg ataaaagcga gcccaagcgg gcctgcccct cagtcgcaga 1080

tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt accaaaacaa 1140

atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaagacat gcgagagaat 1200

gaatcagaat ttcaacattt gcttcacgca cgggaccagg gactgttcgg agtgcttccc 1260

cggcgtgtca gaatctcaac cggtcgtcag aaaaaggacg tatcggaaac tctgtgccat 1320

tcatcatctg ctggggaggg ctcccgagat tgcttgctcg gcctgcgatc tggtcaacgt 1380

ggacctggat gactgtgtct ctgagcaata aatgacttaa accaggtatg gctgccgatg 1440

gttatcttcc agattggctc gaggacaacc tctctgaggg cattcgcgag tggtgggact 1500

tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacgac ggccggggtc 1560

tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag ggggagcccg 1620

tcaacgcggc ggacgcagcg gccctcgagc acgacaaggc ctacgaccag cagctcaaag 1680

cgggtgacaa tccgtacctg cggtataacc acgccgacgc cgagtttcag gagcgtctgc 1740

aagaagatac gtcttttggg ggcaacctcg ggcgagcagt cttccaggcc aagaagcggg 1800

ttctcgaacc tctcggtctg gttgaggaag gcgctaagac ggctcctgga aagaagagac 1860

cggtagagca gtcaccccaa gaaccagact cctcatcggg catcggcaag acaggccagc 1920

agcccgctaa aaagagactc aattttggtc agactggcga cacagagtca gtccccgacc 1980

cacaacctct cggagaacct ccagcagccc cctcaggtct gggacctaat acaatggctt 2040

caggcggtgg cgctccaatg gcagacaata acgaaggcgc cgacggagtg ggtaattcct 2100

cgggaaattg gcattgcgat tccacatggc tgggggacag agtcatcacc accagcaccc 2160

gaacctgggc cctgcccacc tacaacaacc acctctacaa gcaaatctcc aacggcacct 2220

cgggaggaag caccaacgac aacacctact ttggctacag cacccctgg gggtattttg 2280

acttcaacag attccactgc cacttttcac cacgtgactg gcagcgactc atcaacaaca 2340

attggggatt ccggcccaag agactcaact tcaagctctt caacatccag gtcaaggaag 2400

tcacgacgaa cgaaggcacc aagaccatcg ccaataatct caccagcacc gtgcaggtct 2460

ttacggactc ggagtaccag ctaccgtacg tgctaggatc agctcaccag ggatgtctgc 2520

ctccgttccc ggcggacgtc ttcatggttc ctcagtacgg ttatctaact ctgaacaatg 2580

gcagccaggc cctgggacgt tcctccttct actgcctgga gtatttccca tcgcagatgc 2640

tgagaaccgg caacaacttt cagttcagct acaccttcga ggacgtgcct ttccacagca 2700

gctacgcgca cagccaaagc ctggacaggc tgatgaatcc cctcatcgac cagtacctgt 2760

attacctggt cagaacgcag acaaccggga ctggagggac gcagactctg gcattcagcc 2820

aagcaggccc tagctcaatg gccagccagg ctagaaactg ggtgcccgga ccgagctacc 2880

ggcagcagcg cgtctccacg acaaccaacc agaacaacaa cagcaacttt gcctggacgg 2940

gagctgccaa atttaaactg aacggccgag actctctaat gaaccccggc gtggccatgg 3000

cttcacacaa ggatgacgag gaccgcttct tcccttctag cggggtcctg attttcggca 3060

agcaaggagc cgggaatgat ggagtggatt acagccaagt gctgattaca gatgaggaag 3120

aaatcaaggc taccaacccc gtggcaacag aggaatatgg agcagtggcc atcaacaacc 3180

aggccgctaa tacgcaggcg cagaccggac tcgtgcacaa ccaggggggtg attcccggca 3240

tggtgtggca gaacagagac gtgtacctgc agggtcccat ctgggccaaa attcctcaca 3300

cggacggcaa ctttcacccg tctcccctga tgggcggctt tggactgaag cacccgcctc 3360

ctcaaattct catcaagaac acaccggttc cagcggaccc gccgcttacc ttcaaccagg 3420

ccaagctgaa ctctttcatc acgcagtaca gcaccggaca ggtcagcgtg gaaatcgagt 3480

gggagctgca gaaagaaaac agcaaacgct ggaatccaga gattcagtac acttccaact 3540

actacaaatc tacaaatgtg gactttgctg tcaacacgga aggagtgtat agcgagcctc 3600

gccccattgg cacccgttac ctcacccgca acctgtaatt gcctgttaat caataaaccg 3660

gttaattcgt ttcagtaagg aagaattcgt ttaaa 3695

<210> 1197
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1197
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540
```

```
Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590

Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1198
<211> 736

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1198
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Pro Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380
```

```
Gly Ser Gln Ala Leu Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Val
        435                 440                 445

Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr Gln Thr Leu Ala Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Asn Met Ala Ser Gln Ala Arg Asn Trp Val Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Ala Lys Phe Lys Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Asp Gly Val Asp Tyr Ser Gln Val Leu Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala Ala Asn Thr Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Leu Val His Asn Gln Gly Val Ile Pro Gly Met Val Trp Gln
        595                 600                 605


Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Leu Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1199
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1199
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220
```

```
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350


Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365


Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380


Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400


Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415


Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
```

```
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
```

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1200
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1200
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro

```
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
```

```
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
```

```
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
```

675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 1201
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1201
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320
```

```
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Val Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
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Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Val Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
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Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

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Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Xaa Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Xaa Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350
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Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Xaa Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Xaa Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560
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Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Xaa
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Xaa Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Xaa Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


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<223> a, c, g, or t

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<223> a, c, g, or t

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

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ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctcttc gggcatcggc 480

aagaaaggcc agcagcccgc gnnnaagaga ctcaactttg ggcagacagg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgn nngcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaacg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccagccaat cgggannnag caccaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag nnnctcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcacc acgaccatcg ccaataacct taccagcacg 1020

gttcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

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cagtacctgt actacctgtc tcggactcag accacgagtg gtaccgcagg aaatcggnnn 1380

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ggtcccgcta tggcaaccca caaggacgac gaagacaaat tttttccgat gagcggagtc 1620

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gccttacctg gcatggtctg gcagnnncgg gacgtgtacc tgcagggtcc tatctgggcc 1860

aagattcctc acacggacgg acactttcat ccctcgccgc tgatgggagg ctttggactg 1920

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accttcagtc cagctaagtt tgcgtcgttc atcacgcagt acagcaccgg acaggtcagc 2040

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tacacttcca actacaacaa atctacaaat gtggactttg ctgttgacac aaatggcgtt 2160

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            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Xaa Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
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Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Xaa Xaa Gln Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
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            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Asn Xaa Xaa Leu Gln Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540

Gly Lys Gln Gly Ala Gly Asn Xaa Asn Val Asp Xaa Xaa Asn Val Met
545                 550                 555                 560

Ile Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Xaa Val Ala Thr Asn Leu Gln Ser Xaa Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
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625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Thr Thr Phe Xaa Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Glu Gly
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Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
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<223> a, c, g, or t

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<223> a, c, g, or t

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gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

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acggttcagg tctttacgga ctcggaatac cagctcccgt acgtcctcgg ctctgcgcac 1080

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actaccttcn nnccagctaa gtttgcgtcg ttcatcacgc agtacagcac cggacaggtc 2040

agcgtggaaa ttgaatggga gctgcagaaa gaaaacagca aacgctggaa cccagagatt 2100

caatacactt ccaactacaa caaatctaca aatgtggact ttgctgttga cacagaaggc 2160

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<211> 738
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<213> Artificial Sequence

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polypeptide"

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Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Xaa Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220
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Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430
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Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Ile Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Val Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala
            580                 585                 590

Pro Gln Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640
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Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
               645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
               725                 730                 735


Asn Leu
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<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
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polynucleotide"

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<223> a, c, g, or t

<220>
<221> modified_base
<222> (505)..(507)
<223> a, c, g, or t

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<222> (1690)..(1692)
<223> a, c, g, or t

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cnnnggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctctcgga gaacctccag cagcgccctc tggtgtggga 600

tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta attcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aagaggtcac gacgaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccgtcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

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gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

cagacgttgc agttttctca ggccgggcct agcagcatgg cgaatcaggc caaaaactgg 1440

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aatccgggcg tcgccatggc aacccacaag gacgacgagg accgcttctt cccatccagc 1620

ggcgtcctca tatttggcaa gcagggagct ggaaatgaca acgtggacta tagcaacgtg 1680

atgataaccn nngaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggcta ctaacctaca gtcggcaaac accgctcctc aaacggggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

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<212> PRT
<213> Artificial Sequence

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Arg Glu Pro Asp Ser Ser Xaa Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Xaa Phe Lys Leu Phe Asn

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305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Gly Thr Gln Thr Leu Gln
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Xaa Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
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515 520 525

His Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Xaa Leu Ile
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Glu Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
580 585 590

Pro Gln Xaa Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
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Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg

725 730 735

Asn Leu

<210> 1209
<211> 2214
<212> DNA
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<223> a, c, g, or t

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<223> a, c, g, or t

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<223> a, c, g, or t

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<223> a, c, g, or t

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<222> (1414)..(1416)
<223> a, c, g, or t

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<222> (1600)..(1602)
<223> a, c, g, or t

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<222> (1624)..(1626)
<223> a, c, g, or t

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<222> (1783)..(1785)
<223> a, c, g, or t

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcagtcacca cagcgtgagc ccgactcctc cnnnggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

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tctaatacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcnnnttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

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gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagacta cgggaggcac agcgggaacc 1380

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agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagn nncgcttctt cccatccagc 1620

ggcnnnctca tatttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga agagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctcctc aannngggac cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

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polypeptide"

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<223> Any naturally occurring amino acid

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<223> Any naturally occurring amino acid

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<400> 1210

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            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
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Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Xaa Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
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Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Xaa Arg Phe Phe Pro Ser Ser Gly Xaa Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590
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Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 1211
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<223> a, c, g, or t

<220>
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<222> (943)..(945)
<223> a, c, g, or t

<220>
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<222> (1600)..(1602)
<223> a, c, g, or t

<220>
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<222> (1624)..(1626)
<223> a, c, g, or t

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gagtggtggg acctgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccgtcacca cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

gagtcagtcc ccgaccctca acctatcgga gaacctccag cagcgccctc tggtgtggga 600

tctggtacaa tggctgcagg cggtggcgca ccaatggcag acaataacga aggtgccgac 660

ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctg cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacctcggg aggcagcacc aacgacaaca cctactttgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcnnnttcaa gctcttcaac 960

atccaggtca aagaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc 1020

agcaccatcc aggtgtttac ggactcggaa taccagctgc cgtacgtcct cggctctgcc 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacggctac 1140

ctgactctca acaacggtag tcaggccgtg ggacgttcct ccttctactg cctggagtac 1200

ttcccctctc agatgctgag aacgggcaac aactttgagt tcagctacac tttcgaggac 1260

gtgcctttcc acagcagcta cgcgcacagc cagagtttgg acaggctgat gaatcctctc 1320

atcgaccagt acctgtacta cctgtcaaga acccagtcta cgggaggcac agcgggaacc 1380

cagcagttgc tgttttctca ggccgggcct agcaacatgt cggctcaggc caaaaactgg 1440

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agcaactttg cctggactgg tgccaccaag tatcatctga acggcagaga ctctctggtg 1560

aatccgggcg tcgccatggc aacccacaag gacgacgagn nncgcttctt cccatccagc 1620

ggcnnnctca tgtttggcaa gcagggagct ggaaaagaca acgtggacta tagcaacgtg 1680

atgctaacca gcgaggaaga aatcaagacc accaaccccg tggccacaga acagtatggc 1740

gtggtggctg ataacctaca gcagcaaaac accgctccta ttgtgggggc cgtcaacagc 1800

cagggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatt 1860

tgggccaaga ttcctcacac agatggcaac tttcacccgt ctcctttaat gggcggcttt 1920

ggacttaaac atccgcctcc tcagatcctc atcaaaaaca ctcctgttcc tgcggatcct 1980

ccaacaacgt tcaaccaggc caagctgaat tctttcatca cgcagtacag caccggacaa 2040

gtcagcgtgg agatcgagtg ggagctgcag aaggagaaca gcaagcgctg gaacccagag 2100

attcagtata cttccaacta ctacaaatct acaaatgtgg actttgctgt taatactgag 2160

ggtgtttact ctgagcctcg ccccattggc actcgttacc tcacccgtaa tctg 2214

<210> 1212
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (471)..(471)
<223> Any naturally occurring amino acid

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
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Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

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Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
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Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Xaa Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590
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Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 1213
<211> 2214
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<223> a, c, g, or t

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gccatcaccc cagcgttctc cagactcctc tacgggcatc 480

ggcaagaaag gccagcagcc cgcgaaaaag agactcaact ttgggcagac tggcgactca 540

gagtcagtgc ccgaccctca accaatcgga gaacccccg caggcccctc tggtctggga 600

tctggtacaa tggctgcagg cggtggcgct ccaatggcag acaataacga aggcgccgac 660

ggagtgggta gttcctcagg aaattggcat tgcgattcca catggctggg cgacagagtc 720

atcaccacca gcacccgaac ctgggccctc cccacctaca acaaccacct ctacaagcaa 780

atctccaacg ggacttcggg aggaagcacc aacgacaaca cctacttcgg ctacagcacc 840

ccctgggggt attttgactt taacagattc cactgccact tctcaccacg tgactggcag 900

cgactcatca acaacaactg gggattccgg cccaagagac tcaacttcaa gctcttcaac 960

atccaggtca aggaggtcac gcagaatgaa ggcaccaaga ccatcgccaa taaccttacc 1020

agcacgattc aggtctttac ggactcggaa taccagctcc cgtacgtcct cggctctgcg 1080

caccagggct gcctgcctcc gttcccggcg gacgtcttca tgattcctca gtacgggtac 1140

ctgactctga acaatggcag tcaggccgtg ggccgttcct ccttctactg cctggagtac 1200

tttccttctc aaatgctgag aacgggcaac aactttgagt tcagctacac gtttgaggac 1260

gtgcctttc acagcagcta cgcgcacagc caaagcctgg accggctgat gaaccccctc 1320

atcgaccagt acctgtacta cctgtctcgg actcagtcca cgggaggtac cgcaggaact 1380

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agcaactttg cctggaccgg tgccaccaag tatcatctga atggcagaga ctctctggta 1560

aatcccggtg tcgctatggc aacccacaag gacgacgaag agcgattttt tccgtccagc 1620

ggagtcttaa tgtttgggaa acagggagct ggaaaagaca acgtggacta tagcagcgtt 1680

atgctaacca gtgaggaaga aattaaaacc accaacccag tggccacaga acagtacggc 1740

gtggtggccg ataacctgca acagcaaaac accgctccta ttgtaggggc cgtcaacagt 1800

caaggagcct tacctggcat ggtctggcag aaccgggacg tgtacctgca gggtcctatc 1860

tgggccaaga ttcctcacac ggacggaaac tttcatccct cgccgctgat gggaggcttt 1920

ggactgaaac acccgcctcc tcagatcctg attaagaata cacctgttcc cgcggatcct 1980

ccaactacct tcagtcaagc taagctggcg tcgttcatca cgcagtacag caccggacag 2040

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attcaataca cttccaacta ctacaaatct acaaatgtgg actttgctgt taacacagaa 2160

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<210> 1214
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<222> (148)..(148)
<223> Any naturally occurring amino acid

<220>
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<222> (169)..(169)
<223> Any naturally occurring amino acid

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<221> MOD_RES
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<223> Any naturally occurring amino acid

<220>
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<222> (466)..(466)
<223> Any naturally occurring amino acid

<220>
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<222> (563)..(563)
<223> Any naturally occurring amino acid

<220>
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<222> (580)..(580)
<223> Any naturally occurring amino acid

<220>
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<222> (588)..(588)
<223> Any naturally occurring amino acid

<400> 1214

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Xaa Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Xaa Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
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Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Thr Thr Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Xaa Gln Ala Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
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His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Xaa Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Xaa Val Ser Ser Asn Leu Gln Ser Xaa Asn Thr Ala Pro
            580                 585                 590

Gln Thr Gln Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Asp Lys Ser Thr Asn Val Asp Phe Ala Val Asp Ser Glu Gly
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
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Leu

<210> 1215
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<223> a, c, g, or t

<220>
<221> modified_base
<222> (505)..(507)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (940)..(942)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1396)..(1398)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1687)..(1689)
<223> a, c, g, or t

<220>
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<222> (1738)..(1740)
<223> a, c, g, or t

<220>
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<222> (1762)..(1764)
<223> a, c, g, or t

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gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtcattt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gnnntcacct cagcgttccc ccgactcctc cacgggcatc 480

ggcaagaaag gccagcagcc cgccnnnaag agactcaatt tcggtcagac tggcgactca 540

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tgggggtatt ttgactttaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggccc aagaagctgn nnttcaagct cttcaacatc 960

caggtcaagg aggtcacgac gaatgacggc gttacgacca tcgctaataa ccttaccagc 1020

acggttcagg tattctcgga ctcggaatac cagctgccgt acgtcctcgg ctctgcgcac 1080

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agcaactttg cttggactgg tgccaccaaa tatcacctga acggcagaaa ctcgttggtt 1560

aatcccggcg tcgccatggc aactcacaag gacgacgagg accgcttttt cccatccagc 1620

ggagtcctga tttttggaaa aactggagca gctaacaaaa ctacattgga aaatgtgtta 1680

atgacannng aagaagaaat taaaactact aatcctgtag ccacggaaga atacgggnnn 1740

gtcagcagca acttacaatc gnnnaatact gcaccccaga cacaaactgt caacagccag 1800

ggagccttac ctggcatggt ctggcagaac cgggacgtgt acctgcaggg tcccatctgg 1860

gccaagattc ctcacacgga tggcaacttt cacccgtctc ctttgatggg cggctttgga 1920

cttaaacatc cgcctcctca gatcctgatc aagaacactc ccgttcccgc taatcctccg 1980

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agcgtggaaa tcgagtggga gctgcagaag gaaaacagca agcgctggaa cccggagatt 2100

cagtacacct ccaactatga taagtcgact aatgtggact ttgccgttga cagcgagggt 2160

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<210> 1216
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> MOD_RES
<222> (162)..(162)
<223> Any naturally occurring amino acid

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

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Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Xaa Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Xaa
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
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Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Ala Gln Asn Arg Glu Leu Xaa Phe Ser Gln
    450                 455                 460

Ala Gly Pro Ser Ser Met Xaa Asn Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
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Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ala Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Xaa Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
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Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1217
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<223> a, c, g, or t

<220>
<221> modified_base
<222> (502)..(504)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (670)..(672)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (928)..(930)
<223> a, c, g, or t

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<222> (1228)..(1230)
<223> a, c, g, or t

<220>
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<222> (1336)..(1338)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1381)..(1383)
<223> a, c, g, or t

<220>
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<222> (1411)..(1413)
<223> a, c, g, or t

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<222> (2122)..(2124)
<223> a, c, g, or t

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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctcttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagnnnggcc agcagcccgc tnnnaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcag ccccctctgg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatn nntcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtcaat caggggccag caacgacaac cactacttcg gctacagcac cccctggggg 840

tattttgatt tcaacagatt ccactgccat ttctcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagnnn ctcaacttca agctcttcaa catccaagtc 960

aaggaggtca cgacgaatga tggcaccacg accatcgcta ataaccttac cagcacggtt 1020

caagtcttca cggactcgga gtaccagttg ccgtacgtcc tcggctctgc gcaccagggc 1080

tgcctccctc cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc 1140

aacaatggca gccaggcagt gggacggtca tccttttact gcctggaata tttcccatcg 1200

cagatgctga gaacgggcaa taactttnnn ttcagctaca ccttcgagga cgtgcctttc 1260

cacagcagct acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag 1320

tacctgtatt acctgnnnag aactcagact acgtccggaa ctgcccaaaa cagggagttg 1380

nnntttagcc aggcgggtcc atctagcatg nnnaatcagg ccaaaaactg gctacctgga 1440

ccctgttacc ggcagcagcg cgtttctaaa acagcaaatg acaacaacaa cagcaacttt 1500

gcctggactg gtgctacaaa atatcacctt aatgggcgtg attctttagt caaccctggc 1560

cctgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcttg 1620

atttttggaa agcagggcgc cggagcttca aacgttgatt tggacaatgt catgatcaca 1680

gacgaagagg aaatcaaaac cactaacccc gtggccaccg aacaatatgg gactgtggca 1740

accaatctcc agagcagcaa cacagcccct gcgaccggaa ctgtgaattc tcagggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

attcctcaca cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag 1920

cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccgacaacg 1980

ttttcgcctg caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga aatacagtat 2100

acatctaact ataataaatc tnnnaacgtt gatttcactg tggacaccaa tggagtttat 2160

agtgagcctc gccccattgg cacccgttac ctcacccgta acctg 2205

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<211> 735
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> Any naturally occurring amino acid

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<222> (410)..(410)
<223> Any naturally occurring amino acid

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<222> (446)..(446)
<223> Any naturally occurring amino acid

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<223> Any naturally occurring amino acid

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<223> Any naturally occurring amino acid

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<222> (504)..(504)
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asp Xaa Arg Gly Leu Val Leu Pro
        35   40   45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Xaa Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Xaa Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Xaa Arg Thr
        435                 440                 445

Gln Thr Thr Ser Gly Thr Thr Gln Gln Ser Arg Leu Xaa Phe Ser Gln
    450                 455                 460
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Ala Gly Pro Ser Ser Met Xaa Gln Gln Ala Xaa Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Ala Trp Thr Xaa Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Xaa Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Gly Ala Ser Asn Val Asp Leu Asp Asn Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala Thr
            580                 585                 590

Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
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Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


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<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> modified_base
<222> (502)..(504)
<223> a, c, g, or t

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<222> (928)..(930)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1228)..(1230)
<223> a, c, g, or t

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<221> modified_base
<222> (1336)..(1338)
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<223> a, c, g, or t

<220>
<221> modified_base
<222> (1381)..(1383)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1411)..(1413)
<223> a, c, g, or t

<220>
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<222> (1423)..(1425)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1510)..(1512)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1615)..(1617)
<223> a, c, g, or t

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gagtggtggg atctgaaacc tggagcccct caacccaaag cgaaccaaca acaccaggac 120

gacnnncggg gtcttgtgct tccgggttac aaatacctcg gacccttaa cggactcgac 180

aaaggagagc cggtcaacga ggcggacgcg gcagccctcg aacacgacaa agcttacgac 240

cagcagctca aggccggtga caacccgtac ctcaagtaca accacgccga cgccgagttt 300

caggagcgtc ttcaagaaga tacgtctttt gggggcaacc ttggcagagc agtcttccag 360

gccaaaaaga gggtccttga gcctcttggt ctggttgagg aagcagctaa aacggctcct 420

ggaaagaaga ggcctgtaga acagtctcct caggaaccgg actcatcatc tggtattggc 480

aaatcgggcc aacagcctgc cnnnaaaaga ctaaatttcg gtcagactgg agactcagag 540

tcagtcccag accctcaacc tctcggagaa ccaccagcag ccccctcagg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaggg tgccgatgga 660

gtgggtaatt cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 780

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 840

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 900

aacaacaact ggggattccg gcccaagnnn ctcaacttca agctcttcaa catccaagtt 960

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cagatgctaa ggactggaaa taacttcnnn ttcagctata ccttcgagga tgtacctttt 1260

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 1320

tatctgtact acctgnnnag aacgcaaaca acctctggaa caacccaaca atcacggctg 1380

nnntttagcc aggctgggcc ttcgtctatg nnncagcagg ccnnnaattg gctacctggg 1440

ccctgctacc ggcaacagag agtttcaaag actgctaacg acaacaacaa cagtaacttt 1500

gcttggacan nngccaccaa atatcatctc aatggccgcg actcgctggt gaatccagga 1560

ccagctatgg ccagtcacaa ggacgatgaa gaaaaatttt tccctatgca cggcnnncta 1620

atatttggca aacaagggac aggggcaagt aacgtagatt tagataatgt aatgattacg 1680

gatgaagaag agattcgtac caccaatcct gtggcaacag agcagtatgg aactgtggca 1740

actaacttgc agagctcaaa tacagctccc gcgactggaa ctgtcaatag tcaggggggcc 1800

ttacctggca tggtgtggca agatcgtgac gtgtaccttc aaggacctat ctgggcaaag 1860

attcctcaca cggatggaca ctttcatcct tctcctctga tgggaggctt tggactgaaa 1920

catccgcctc ctcaaatctt gatcaaaaat actccggtac cggcaaatcc tccgacgact 1980

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gaaattgagt gggagctaca gaaagaaaac agcaaacgtt ggaatccaga gattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tagacactaa tggtgtttat 2160

agtgaacctc gccctattgg aacccggtat ctcacacgaa acttg 2205

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<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
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Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590
```

```
Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1221
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1221
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1222
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1222
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1223
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1223
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
```

```
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
```

```
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1224

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1224
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

```
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380
```

```
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590
```

```
Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1225
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1225
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430
```

```
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640
```

```
Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1226
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1226
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160


Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190


Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270
```

```
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
        435                 440                 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
    450                 455                 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465                 470                 475                 480
```

```
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Asn Gln Asn
                485                 490                 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ser Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1227
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1227
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
```

325 330 335

Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
435 440 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe Ser
450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly

```
    530                 535                 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Thr Asn Leu Gln Ser Ala Asn Thr Ala Pro Ala
            580                 585                 590

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1228

<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1228
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga gaccggtaga gcaatcaccc caggaaccag actcctcttc gggcatcggc 480

aagaaaggcc agcagcccgc gaaaaagaga ctcaactttg ggcagacagg cgactcagag 540

tcagtgcccg accctcaacc actcggagaa ccccccgcag ccccctctgg tgtgggatct 600

aatacaatgg ctgcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaacg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctcccc acctacaaca accacctcta caagcaaatc 780

tccagccaat cgggagcaag caccaacgac aacacctact tcggctacag caccccctgg 840

gggtattttg actttaacag attccactgc cacttctcac cacgtgactg gcagcgactc 900

atcaacaaca actggggatt ccggcccaag agactcaact tcaagctctt caacatccag 960

gtcaaggagg tcacgacgaa tgatggcacc acgaccatcg ccaataacct taccagcacg 1020

gttcaggtct ttacggactc ggaataccag ctcccgtacg tcctcggctc tgcgcaccag 1080

ggctgcctgc ctccgttccc ggcggacgtc ttcatgattc ctcagtacgg gtacctgact 1140

ctgaacaatg gcagtcaggc cgtgggccgt tcctccttct actgcctgga gtactttcct 1200

tctcaaatgc tgagaacggg caacaacttt gagttcagct acacgtttga ggacgtgcct 1260

tttcacagca gctacgcgca cagccaaagc ctggaccggc tgatgaaccc cctcatcgac 1320

cagtacctgt actacctgtc tcggactcag accacgagtg gtaccgcagg aaatcggacg 1380

ttgcaatttt ctcaggccgg gcctagtagc atggcgaatc aggccaaaaa ctggctaccc 1440

gggccctgct accggcagca acgcgtctcc aagacagcga atcaaaataa caacagcaac 1500

tttgcctgga ccggtgccac caagtatcat ctgaatggca gagactctct ggtaaatccc 1560

ggtcccgcta tggcaaccca caaggacgac gaagacaaat tttttccgat gagcggagtc 1620

ttaatatttg ggaaacaggg agctggaaat agcaacgtgg accttgacaa cgttatgata 1680

accagtgagg aagaaattaa aaccaccaac ccagtggcca cagaacagta cggcacggtg 1740

gccactaacc tgcaatcgtc aaacaccgct cctgctacag ggaccgtcaa cagtcaagga 1800

gccttacctg gcatggtctg gcagaaccgg gacgtgtacc tgcagggtcc tatctgggcc 1860

aagattcctc acacggacgg acactttcat ccctcgccgc tgatgggagg ctttggactg 1920

aaacacccgc ctcctcagat cctgattaag aatacacctg ttcccgcgaa tcctccaact 1980

accttcagtc cagctaagtt tgcgtcgttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaattg aatgggagct gcagaaagaa aacagcaaac gctggaaccc agagattcaa 2100

tacacttcca actacaacaa atctacaaat gtggactttg ctgttgacac aaatggcgtt 2160

tattctgagc ctcgccccat cggcacccgt tacctcaccc gtaatctgta a 2211

<210> 1229
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1229
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

```
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240
```

```
Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445
```

```
Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655
```

```
Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720


Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
```

<210> 1230
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1230

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
```

```
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
```

```
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
```

485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr

690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 1231
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (157)..(157)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (169)..(169)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (457)..(457)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (463)..(463)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (508)..(508)
<223> Any naturally occurring amino acid

<220>

<221> MOD_RES
<222> (510)..(511)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (558)..(558)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (585)..(585)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (587)..(587)
<223> Any naturally occurring amino acid

<400> 1231

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Xaa Leu Gly Ile
145                 150                 155                 160

Gly Lys Thr Gly Gln Gln Pro Ala Xaa Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ser Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Thr Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335
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Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Thr Xaa Gly Thr Gln Thr Leu Xaa Phe
    450                 455                 460

Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Arg Asn Trp Val
465                 470                 475                 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Asn Gln
                485                 490                 495

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Xaa Lys Xaa Xaa Leu
            500                 505                 510

Asn Gly Arg Asp Ser Leu Met Asn Pro Gly Val Ala Met Ala Ser His
        515                 520                 525

Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    530                 535                 540
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Gly Lys Gln Gly Ala Gly Asn Asp Asn Val Asp Tyr Ser Xaa Val Met
545                 550                 555                 560


Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu
                565                 570                 575


Glu Tyr Gly Ala Val Ala Thr Asn Xaa Gln Xaa Leu Ala Asn Thr Gln
            580                 585                 590


Ala Gln Thr Gly Leu Val His Asn Gln Gly Val Leu Pro Gly Met Val
        595                 600                 605


Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640


Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655


Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700


Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu
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<210> 1232
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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<223> a, c, g, or t

<220>
<221> modified_base
<222> (502)..(504)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1366)..(1368)
<223> a, c, g, or t

<220>
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<222> (1384)..(1386)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1519)..(1521)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1525)..(1530)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1669)..(1671)
<223> a, c, g, or t

<220>
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<222> (1750)..(1752)
<223> a, c, g, or t

<220>

<221> modified_base
<222> (1756)..(1758)
<223> a, c, g, or t

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gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa agcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata atcacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaga ggccggtaga gcagtcgcca caagagccag actcctccnn nggcatcggc 480

aagacaggcc agcagcccgc tnnnaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcag ccccctcagg tgtgggatct 600

aatacaatgg cttcaggcgg tggcgctcca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggctggggga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caagcaaatc 780

tccaacggca cctcgggagg aagcaccaac gacaacacct attttggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgtcactttt caccacgtga ctggcaacga 900

ctcatcaaca acaattgggg attccggccc aaaagactca acttcaagct gttcaacatc 960

caggtcaagg aagtcacgac gaacgaaggc accaagacca tcgccaataa tctcaccagc 1020

accgtgcagg tctttacgga ctcggagtac cagttaccgt acgtgctagg atccgctcac 1080

cagggatgtc tgcctccgtt cccggcggac gtcttcatga ttcctcagta cggctattta 1140

actttaaaca atggaagcca agccgtggga cgttcctcct tctactgtct ggagtatttc 1200

ccatcgcaga tgctgagaac cggcaacaac tttcagttca gctacacctt cgaggacgtg 1260

cctttccaca gcagctacgc gcacagccag agcctggaca ggctgatgaa tcccctcatc 1320

gaccagtacc tgtactacct gtccagaacg caaacgactg gaactnnngg gacgcagact 1380

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ggaccttgct accggcagca gcgcgtctcc acgacaacca accagaacaa caacagcaac 1500

tttgcctgga cgggagctnn naagnnnnnn ctgaacggcc gagactctct aatgaatccg 1560

ggcgtggcaa tggcttccca caaggatgac gaggaccgct tcttcccttc gagcggggtc 1620

ctgatttttg gcaagcaagg agccgggaac gataatgtgg attacagcnn ngtgatgatt 1680

acaaatgagg aagaaatcaa gactaccaac cccgtggcca cagaagaata tggagcagtg 1740

gccaccaacn nncagnnngc caatacgcag gcgcagaccg gactcgtgca caaccagggg 1800

gtgcttcccg gcatggtgtg gcagaataga gacgtgtacc tgcagggtcc catctgggcc 1860

aaaattcctc acacggacgg caactttcac ccgtctcccc tgatgggcgg ctttggactg 1920

aagcacccgc ctcctcaaat tctcatcaag aacacaccgg ttccagcgga cccgccgact 1980

accttcaacc aggccaagct gaactctttc atcacgcagt acagcaccgg acaggtcagc 2040

gtggaaatcg agtgggagct gcagaaagaa aacagcaaac gctggaatcc agagattcaa 2100

tacacttcca actactacaa atctacaaat gtggactttg ctgtcaacac ggagggggtt 2160

tatagcgagc ctcgccccat tggcacccgt tacctcaccc gcaacctgta a 2211

<210> 1233
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

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    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
```

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            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Met Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
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465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
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675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
725 730

<210> 1234
<211> 4472
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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attacgtcat aggggagtgg tcctgtatta gctgtcacgt gagtgctttt gcgacatttt 120

gcgacaccac gtggccattc atggtatata tggccgagtg agcgagcagg atctccattt 180

tgaccgcgaa atttgaacga gcagcagcca tgccgggctt ctacgagatc gtgcttaagg 240

tgccgagcga cctggacgag cacctgccgg gcatttctga ctcgtttgtg aactgggtgg 300

cagagaagga atgggagctg cccccggatt ctgacatgga tcggaatctg attgagcagg 360

caccctgac cgtggccgag aagctacagc gcgacttcct ggtccaatgg cgccgcgtga 420

gtaaggcccc ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc 480

tccatattct ggtagagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc 540

agattcggga caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact 600

ggttcgcggt gacaaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt 660

gctacatccc caactacctg ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta 720

acatggagga gtatataagc gcgtgcttga acctggccga gcgcaaacgg ctcgtggcgc 780

agcacctgac ccacgtcagc cagacccagg agcagaacaa ggagaatctg aacccgaatt 840

ctgacgcgcc tgtcatccgg tcaaaaacct ccgcgcgcta catggagctg gtcgggtggc 900

tggtggaccg gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca 960

tctccttcaa cgccgcctcc aactcgcggt ctcagatcaa ggccgcgctg gacaatgccg 1020

gcaagatcat ggcgctgacc aaatccgcgc ccgactacct ggtaggcccc gctctgcccg 1080

cggacattaa atccaaccgc atctaccgca tcctggagct gaatggctac gaccctgcct 1140

acgccggttc cgtctttctc ggctgggccc agaaaaagtt tggcaaaagg aacaccatct 1200

ggctgtttgg gccggccacc acgggcaaga ccaacatcgc ggaagccatc gcccacgccg 1260

tgcccttcta cggctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg 1320

acaagatggt gatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca 1380

aggccattct cggcggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga 1440

tcgatcccac ccccgtgatc gtcacctcca acaccaacat gtgcgccgtg attgacggga 1500

acagcaccac cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactta 1560

cccgccgtct ggagcacgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc 1620

gctgggcgca ggatcacgtg accgaggtgg cgcatgagtt ctacgtcaga aagggtggag 1680

ctaacaaaag acccgccccc gatgacgcgg atataagcga gcccaagcgg gcctgcccct 1740

cagtcgcgga tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt 1800

accaaaacaa atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaaaacat 1860

gcgagagaat gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag 1920

aatgtttccc tggcgtgtca gaatctcaac cggtcgtcag aaaaaagacg tatcggaaac 1980

tctgtgcgat tcatcatctg ctggggcggg cacccgagat tgcttgctcg gcctgcgacc 2040

tggtcaacgt ggacctggat gactgtgttt ctgagcaata aatgacttaa accaggtatg 2100

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accaccagca cccgcacctg ggccctgccc acctacaaca accacctcta caagcaaatc 2880

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gaccagtact tgtactacct gtcccggact caaagcacgg gcggtactgc aggaactcag 3480

cagttgctat tttctcaggc cgggcctaac aacatgtcgg ctcaggccaa gaactggcta 3540

cccggtccct gctaccggca gcaacgcgtc tccacgacac tgtcgcagaa caacaacagc 3600

aactttgcct ggacgggtgc caccaagtat catctgaatg gcagagactc tctggtgaat 3660

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gtcttaatgt ttgggaaaca gggagctgga aaagacaacg tggactatag cagcgtgatg 3780

ctaaccagcg aggaagaaat aaagaccacc aacccagtgg ccacagaaca gtacggcgtg 3840

gtggccgata acctgcaaca gcaaaacgcc gctcctattg taggggccgt caatagtcaa 3900

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accaccttca ctaaggccaa gctggcttct ttcatcacgc agtacagtac cggccaggtc 4140

agcgtggaga tcgagtggga gctgcagaag gagaacagca aacgctggaa cccagagatt 4200

cagtacactt ccaactacta caaatctaca aatgtggact ttgctgtcaa tactgagggt 4260

acttattccg agcctcgccc cattggcacc cgttacctca cccgtaatct gtaattacat 4320

gttaatcaat aaaccggtta attcgtttca gttgaacttt ggtctcctgt ccttcttatc 4380

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acttacgtca tcgggttacc cctagtgatg ga 4472

<210> 1235
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gaaggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aataccatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg tgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

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cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaatac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggctatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
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Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
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Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Lys Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

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Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
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Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
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Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
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Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
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Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
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Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
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Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
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Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
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Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
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Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
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Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
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Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
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Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
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Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
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Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
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Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
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Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
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Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
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Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
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Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
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Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
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Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
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Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
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Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
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Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
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<400> 1239
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1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly

```
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Xaa Xaa Gly Ala Xaa Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
```

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            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Xaa Xaa Xaa Xaa Gly Thr Xaa Xaa Xaa Xaa Xaa Leu Xaa Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Xaa Xaa Xaa Xaa Xaa Asn
                485                 490                 495

Asn Asn Ser Xaa Phe Pro Trp Xaa Ala Ala Ser Xaa Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Xaa
        515                 520                 525

Asp Asp Xaa Xaa Xaa Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Met Ile
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545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Xaa Xaa Xaa Xaa Xaa Pro Thr
580 585 590

Xaa Xaa Xaa Val Xaa His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
610 615 620

<210> 1240
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1240
accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 60

tccagccaat caggagcttc aaacgacaac cactactttg gctacagcac cccttggggg 120

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 180

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 240

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 300

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 360

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 420

aacaacggaa gtcaagcggt gggacgctca tcctttttact gcctggagta cttcccttcg 480

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 540

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 600

tatctgtact acctgaacag aacgcaagga acaacctctg gaacaaccaa ccaatcacgg 660

ctgcttttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 720

gggccctgct accggcaaca gagactttca aagactgcta acgacaacaa caacagtaac 780

tttccttgga cagcggccag caaatatcat ctcaatggcc gcgactcgct ggtgaatcca 840

ggaccagcta tggccagtca caaggacgat gaagaaaaat ttttccctat gcacggcaat 900

ctaatatttg gcaaagaagg gacaacggca agtaacgcag aattagataa tgtaatgatt 960

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1020

gcaaataact tgcagagctc aaatacagct cccacgactg gaactgtcaa tcatcagggg 1080

gccttacctg gcatggtgtg gcaagatcgt gacgtctacc ttcaaggacc tatctgggca 1140

aagattcctc acacggatgg acactttcat ccttctcctc tgatgggagg ctttggactg 1200

aaacatccgc ctcctcaaat catgatcaaa aatactccgg taccggcaaa tcctccgacg 1260

actttcagcc cggccaagtt tgcttcattt atcactcagt actccactgg acaggtcagc 1320

gtggaaattg agtgggagct acagaaagaa aacagcaaac gttggaatcc agagattcag 1380

tacacttcca actacaacaa gtctgttaat gtggacttta ctgtagacac taatggtgtt 1440

tatagtgaac ctcgccctat tggaacccgg tatctcacac gaaacttgtg a 1491

<210> 1241
<211> 482
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1241
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
1 5 10 15

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
20 25 30

Phe Gly Tyr Ser Thr Pro Trp Tyr Phe Asp Phe Asn Arg Phe His Cys
35 40 45

```
His Phe Ser Pro Arg Asp Trp Gln Arg Leu Asn Asn Asn Trp Gly Phe
    50                  55                  60

Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Arg Gly Val
65                  70                  75                  80

Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr
                85                  90                  95

Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser
            100                 105                 110

Ala His Gln Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro
        115                 120                 125

Gln Tyr Gly Tyr Leu Thr Asn Asn Gly Ser Gln Ala Val Gly Arg Ser
    130                 135                 140

Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Gln Met Leu Arg Thr Gly Asn
145                 150                 155                 160

Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro His Ser Ser Tyr
                165                 170                 175

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Tyr
            180                 185                 190

Leu Tyr Tyr Leu Asn Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn
        195                 200                 205

Gln Ser Leu Leu Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln
    210                 215                 220

Ala Arg Asn Trp Leu Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys
225                 230                 235                 240

Thr Ala Asn Asp Asn Asn Asn Ser Phe Pro Trp Thr Ala Ala Ser Lys
                245                 250                 255
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Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Gly Pro Ala Met Ala
            260                 265                 270

Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Leu Ile
        275                 280                 285

Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val
    290                 295                 300

Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr
305                 310                 315                 320

Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala
                325                 330                 335

Pro Thr Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val
            340                 345                 350

Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
        355                 360                 365

Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe
    370                 375                 380

Gly Leu Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val
385                 390                 395                 400

Pro Ala Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe
                405                 410                 415

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
            420                 425                 430

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
        435                 440                 445

Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn
    450                 455                 460
```

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
465 470 475 480

Asn Leu

<210> 1242
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> modified_base
<222> (636)..(636)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (665)..(665)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (1064)..(1064)
<223> a, c, g, or t

<400> 1242
accaccagca ccagaacctg ggccctgccc acttacaaca accatctcta caagcaaatc 60

tccagcvvmd caggagctas caacgacaac cactactttg gctacagcac cccttggggg 120

tattttgact ttaacagatt ccactgccac ttctcaccac gtgactggca gcgactcatt 180

aacaacaact ggggattccg gcccaagaaa ctcagcttca agctcttcaa catccaagtt 240

agaggggtca cgcagaacga tggcacgacg actattgcca ataaccttac cagcacggtt 300

caagtgttta cggactcgga gtatcagctc ccgtacgtgc tcgggtcggc gcaccaaggc 360

tgtctcccgc cgtttccagc ggacgtcttc atggtccctc agtatggata cctcaccctg 420

aacaacggaa gtcaagcggt gggacgctca tccttttact gcctggagta cttcccttcg 480

cagatgctaa ggactggaaa taacttccaa ttcagctata ccttcgagga tgtacctttt 540

cacagcagct acgctcacag ccagagtttg gatcgcttga tgaatcctct tattgatcag 600

tatctgtact acctgaacag aacgcaargc amcvcnrgcg gaacarccrv cmhsmrsvvs 660

ctgvngttta gccaggctgg gcctcagtct atgtctttgc aggccagaaa ttggctacct 720

gggccctgct accggcaaca gagactttca amarycbmcr vcsrsaacaa caacagtras 780

tttccttggm cagcggccag camatatcat ctcaatggcc gcgactcgct ggtgaatcca 840

ggaccagcta tggccagtca crrggacgat rmsgrsarat ttttccctat gcacggcaat 900

ctaatatttg gcaaasaarr crscrvsrva rvcratrycg msdwcgrsvr sgtaatgatt 960

acggatgaag aagagattcg taccaccaat cctgtggcaa cagagcagta tggaactgtg 1020

gcaaataact tgcagrvsvv smrsrvcvvs cccacgdhtv vsrnsgtcvm scatcagggg 1080

gccttacctg gcatggtgtg gcaagatcgt gacgtctacc ttcaaggacc tatctgggca 1140

<210> 1243
<211> 620
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> MOD_RES
<222> (263)..(264)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (267)..(267)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (450)..(453)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (456)..(460)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (462)..(462)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (491)..(495)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (500)..(500)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (504)..(504)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (508)..(508)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (528)..(528)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (531)..(533)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (546)..(557)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (586)..(590)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (593)..(595)
<223> Any naturally occurring amino acid

<220>

<221> MOD_RES
<222> (597)..(597)
<223> Any naturally occurring amino acid

<400> 1243

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Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Xaa Xaa Gly Ala Xaa Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400
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```
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Xaa Xaa Xaa Xaa Gly Thr Xaa Xaa Xaa Xaa Xaa Leu Xaa Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Xaa Xaa Xaa Xaa Xaa Asn
                485                 490                 495

Asn Asn Ser Xaa Phe Pro Trp Xaa Ala Ala Ser Xaa Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Xaa
        515                 520                 525

Asp Asp Xaa Xaa Xaa Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Xaa Xaa Xaa Xaa Xaa Pro Thr
            580                 585                 590

Xaa Xaa Xaa Val Xaa His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605
```

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala
610 615 620

<210> 1244
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1244
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190


Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205


Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220


Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240


Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255


Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270


Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285


Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300


Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320


Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335


Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
```

```
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

```
Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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<210> 1245
<211> 2258
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1245
tcgaggacaa cctctctgag ggcattcgcg agtggtggga cttgaaacct ggagccccga 60

aacccaaagc caaccagcaa aagcaggacg acggccgggg tctggtgctt cctggctaca 120

agtacctcgg acccttcaac ggactcgaca agggggagcc cgtcaacgcg gcggacgcag 180

cggccctcga gcacgacaag gcctacgacc agcagctcaa agcgggtgac aatccgtacc 240

tgcggtataa ccacgccgac gccgagtttc aggagcgtct gcaagaagat acgtcttttg 300

ggggcaacct cgggcgagca gtcttccagg ccaagaagcg ggttctcgaa cctctcggtc 360

tggttgagga aggcgctaag acggctcctg gaaagaagag accggtagag ccatcacccc 420

agcgttctcc agactcctct acgggcatcg gcaagaaagg ccagcagccc gcgaaaaaga 480

gactcaactt tgggcagact ggcgactcag agtcagtgcc cgaccctcaa ccaatcggag 540

aacccccgc aggcccctct ggtctgggat ctggtacaat ggctgcaggc ggtggcgctc 600

caatggcaga caataacgaa ggcgccgacg gagtgggtag ttcctcagga aattggcatt 660

gcgattccac atggctgggc gacagagtca tcaccaccag cacccgaacc tgggccctcc 720

ccacctacaa caaccacctc tacaagcaaa tctccaacgg gacttcggga ggaagcacca 780

acgacaacac ctacttcggc tacagcaccc cctgggggta ttttgacttt aacagattcc 840

actgccactt ctcaccacgt gactggcagc gactcatcaa caacaactgg ggattccggc 900

ccaagagact caacttcaag ctcttcaaca tccaggtcaa ggaggtcacg cagaatgaag 960

gcaccaagac catcgccaat aaccttacca gcacgattca ggtctttacg gactcggaat 1020

accagctccc gtacgtcctc ggctctgcgc accagggctg cctgcctccg ttcccggcgg 1080

acgtcttcat gattcctcag tacgggtacc tgactctgaa caatggcagt caggccgtgg 1140

gccgttcctc cttctactgc ctggagtact ttccttctca aatgctgaga acgggcaaca 1200

actttgagtt cagctaccag tttgaggacg tgccttttca cagcagctac gcgcacagcc 1260

aaagcctgga ccggctgatg aacccctca tcgaccagta cctgtactac ctgtctcgga 1320

ctcagtccac gggaggtacc gcaggaactc agcagttgct attttctcag gccgggccta 1380

ataacatgtc ggctcaggcc aaaaactggc tacccgggcc ctgctaccgg cagcaacgcg 1440

tctccacgac actgtcgcaa aataacaaca gcaactttgc ctggaccggt gccaccaagt 1500

atcatctgaa tggcagagac tctctggtaa atcccggtgt cgctatggca acccacaagg 1560

acgacgaaga gcgatttttt ccgtccagcg gagtcttaat gtttgggaaa cagggagctg 1620

gaaaagacaa cgtggactat agcagcgtta tgctaaccag tgaggaagaa attaaaacca 1680

ccaacccagt ggccacagaa cagtacggcg tggtggccga taacctgcaa cagcaaaacg 1740

ccgctcctat tgtaggggcc gtcaacagtc aaggagcctt acctggcatg gtctggcaga 1800

accgggacgt gtacctgcag ggtcctatct gggccaagat tcctcacacg gacggaaact 1860

ttcatccctc gccgctgatg ggaggctttg gactgaaaca cccgcctcct cagatcctga 1920

ttaagaatac acctgttccc gcggatcctc caactacctt cagtcaagct aagctggcgt 1980

cgttcatcac gcagtacagc accggacagg tcagcgtgga aattgaatgg gagctgcaga 2040

aagaaaacag caaacgctgg aacccagaga ttcaatacac ttccaactac tacaaatcta 2100

caaatgtgga ctttgctgtt aacacagatg gcacttattc tgagcctcgc cccatcggca 2160

cccgttacct cacccgtaat ctgtaattgc ttgttaatca ataaaccggt tgattcgttt 2220

cagttgaact ttggtctctg cgaagggcga attcgttt 2258

<210> 1246
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1246
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt tcttaagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaattc 1500

tcgtggaccg gtgctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagaggcaa cagacaagca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg taccagattc ctgactcgta atctgtaa 2208

<210> 1247
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1247
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

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Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320
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Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525
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His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Trp Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala Pro
            580                 585                 590

Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu Gly
705                 710                 715                 720

Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735
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Leu

<210> 1248
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1248
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cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagcgctt caacgggagc ctcgaacgac aatcactact ttggctacag cacccttgg 840

gggtattttg acttcaacag attccactgc cacttttcac cacgtgactg gcaaagactc 900

atcaacaaca actggggatt ccgacccaag agactcaact tcaagctctt taacattcaa 960

gtcaaagagg tcacgcagaa tgacggtacg acgacgattg ccaataacct taccagcacg 1020

gttcaggtgt ttactgactc ggagtaccag ctcccgtacg tcctcggctc ggcgcatcaa 1080

ggatgcctcc cgccgttccc agcagacgtc ttcatggtgc cacagtatgg atacctcacc 1140

ctgaacaacg ggagtcaggc agtaggacgc tcttcatttt actgcctgga gtactttcct 1200

tctcagatgc tgcgtaccgg aaacaacttt accttcagct acacttttga ggacgttcct 1260

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cttcagtttt ctcaggccgg agcgagtgac attcgggacc agtctaggaa ctggcttcct 1440

ggaccctgtt accgccagca gcgagtatca aagacatctg cggataacaa caacagtgaa 1500

tactcgtgga ctggagctac caagtaccac ctcaatggca gagactctct ggtgaatccg 1560

ggcccggcca tggcaagcca caaggacgat gaagaaaagt tttttcctca gagcggggtt 1620

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tctaccaacc tccagagagg caacagacaa gcagctaccg cagatgtcaa cacacaaggc 1800

gttcttccag gcatggtctg gcaggacaga gatgtgtacc ttcaggggcc catctgggca 1860

aagattccac acacggacgg acattttcac ccctctcccc tcatgggtgg attcggactt 1920

aaacaccctc ctccacagat tctcatcaag aacaccccgg tacctgcgaa tccttcgacc 1980

accttcagtg cggcaaagtt tgcttccttc atcacacagt actccacggg acaggtcagc 2040

gtggagatcg agtgggagct gcagaaggaa aacagcaaac gctggaatcc cgaaattcag 2100

tacacttcca actacgccaa gtctgtcaat gtggacttta ctgtggacaa taatggcgtg 2160

tattcagagc ctcgccccat tggcaccaga tacctgactc gtaatctgta a 2211

<210> 1249
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1249
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gagtggtggg acttgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaagc gggttctcga acctctcggt ctggttgagg aaggcgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcatcggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg atccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgcacctg ggccttgccc acctacaata accacctcta caagcaaatc 780

tccagtgctt caggggccag caacgacaac cactacttcg gctacagcac cccctggggg 840

tattttgatt tcaacagatt ccactgccac ttttcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcaacttca aactcttcaa catccaagtc 960

aaggaggtca cgacgaatga tggcgtcaca accatcgcta ataaccttac cagcacggtt 1020

caagtcttct cggactcgga gtaccagctt ccgtacgtcc tcggctctgc gcaccagggc 1080

tgcctccctc cgttcccggc ggacgtgttc atgattccgc aatacggcta cctgacgctc 1140

aacaatggca gccaagccgt gggacgttca tccttttact gcctggaata tttcccttct 1200

cagatgctga gaacgggcaa caactttacc ttcagctaca cctttgagga agtgcctttc 1260

cacagcagct acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccaa 1320

tacctgtatt acctgaacag aactcaaaat cagtccggaa gtgcccaaaa caaggacttg 1380

ctgtttagcc gtgggtctcc agctggcatg tctgttcagc ccaaaaactg gctacctgga 1440

ccctgttatc ggcagcagcg cgtttctaaa acaaaaacag acaacaacaa cagcaatttt 1500

acctggactg gtgcttcaaa atataacctc aatgggcgtg aatccatcat caaccctggc 1560

actgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcatg 1620

attttggaa aagagagcgc cggagcttca aacactgcat tggacaatgt catgattaca 1680

gacgaagagg aaattaaagc cactaaccct gtggccaccg aaagatttgg gaccgtggca 1740

gtcaatttcc agagcagcag cacagaccct gcgaccggag atgtgcatgc tatgggagca 1800

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acatccaatt atgcaaaatc tgccaacgtt gattttactg tggacaacaa tggactttat 2160

actgagcctc gccccattgg cacccgttac cttacccgtc ccctgtaa 2208

<210> 1250
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1250
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agtggtggga cttgaaacct ggagccccga aacccaaagc caaccagcaa aagcaggacg 120

acggccgggg tdggtgcttc ctggctacaa gtacctcgga cccttcaacg gactcgacaa 180

gggggagccc gtcaacgcgg cggatgcagc ggccctcgag cacgacaagg cctacgacca 240

gcagctcaaa gcgggtgaca atccgtacct gcggtataac cacgccgacg ccgagtttca 300

ggagcgtctg caagaagata cgtcttttgg gggcaacctc gggcgagcag tcttccaggc 360

caagaagagg gttctcgaac cttttggtdg gttgaggaag gtgctaagac ggctcctgga 420

aagaaacgtc cggtagagca gtcgccacaa gagccagact cctcctcggg cattggcaag 480

acaggccagc agcccgctaa aaagagactc aattttggtc agactggcga ctcagagtca 540

gtccccgacc cacaacctct cggagaacct ccagcaaccc ccgctgctgt gggacctact 600

acaatggctt caggcggtgg cgcaccaatg gcagacaata acgaaggcgc cgacggagtg 660

ggtaatgcct caggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc 720

accagcaccc gaacatgggc cttgcccacc tataacaacc acctctacaa gcaaatctcc 780

agtgcttcag gggccagcaa cgacaaccac tacttcggct acagcacccc ctgggggtat 840

tttgatttca acagattcca ctgccatttc tcaccacgtg actggcagcg actcatcaac 900

aacaattggg gattccggcc caagagactc aacttcaagc tcttcaacat ccaagtcaag 960

gaggtcacga cgaatgatgg cgtcacgacc atcgctaata accttaccag cacggttcaa 1020

gtcttctcgg actcggagta ccagttgccg tacgtcctcg gctctgcgca ccagggctgc 1080

ctccctccgt tcccggcgga cgtgttcatg attccgcagt acggctacct aacgctcaac 1140

aatggcagcc aggcagtggg acggtcatcc ttttactgcc tggaatattt cccatcgcag 1200

atgctgagaa cgggcaataa ctttaccttc agctacacct tcgaggacgt gcctttccac 1260

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ctgtattacc tgaacagaac tcagaatcag tccggaagtg cccaaaacaa ggacttgctg 1380

tttagccggg ggtctccagc tggcatgtct gttcagccca aaaactggct acctggaccc 1440

tgttaccggc agcagcgcgt ttctaaaaca aaaacagaca acaacaacag caactttacc 1500

tggactggtg cttcaaaata taaccttaat gggcgtgaat ctataatcaa ccctggcact 1560

gctatggcct cacacaaaga cgacaaagac aagttctttc ccatgagcgg tgtcatgatt 1620

tttggaaagg agagcgccgg agcttcaaac actgcattgg acaatgtcat gatcacagac 1680

gaagaggaaa tcaaagccac taaccccgtg gccaccgaaa gatttgggac tgtggcagtc 1740

aatctccaga gcagcagcac agaccctgcg accggagatg tgcatgttat gggagcctta 1800

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cctcacacgg atggacactt tcacccgtct cctctcatgg gcggctttgg acttaagcac 1920

ccgcctcctc agatcctcat caaaaacacg cctgttcctg cgaatcctcc ggcagagttt 1980

tcggctacaa agtttgcttc attcatcacc cagtattcca caggacaagt gagcgtggag 2040

attgaatggg agctgcagaa agaaaacagc aaacgctgga atcccgaagt gcagtataca 2100

tctaactatg caaaatctgc caacgttgat ttcactgtgg acaacaatgg actttatact 2160

gagcctcgcc ccattggcac ccgttacctc acccgtcccc tgtaa 2205

<210> 1251
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1251
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc 60

gagtggtggg acttgaaacc tggagccccg aaacccaaag ccaaccagca aaagcaggac 120

gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac 180

aaggggggagc ccgtcaacgc ggcggatgca gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aagcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt 300

caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaagaaga gggttctcga acctttttggt ctggttgagg aaggtgctaa gacggctcct 420

ggaaagaaac gtccggtaga gcagtcgcca caagagccag actcctcctc gggcattggc 480

aagacaggcc agcagcccgc taaaaagaga ctcaattttg gtcagactgg cgactcagag 540

tcagtccccg acccacaacc tctcggagaa cctccagcaa cccccgctgc tgtgggacct 600

actacaatgg cttcaggcgg tggcgcacca atggcagaca ataacgaagg cgccgacgga 660

gtgggtaatg cctcaggaaa ttggcattgc gattccacat ggctgggcga cagagtcatc 720

accaccagca cccgaacatg ggccttgccc acctataaca accacctcta caagcaaatc 780

tccagtgctt caggggccag caacgacaac cactacttcg gctacagcac cccctggggg 840

tattttgatt tcaacagatt ccactgccat ttctcaccac gtgactggca gcgactcatc 900

aacaacaatt ggggattccg gcccaagaga ctcaacttca agctcttcaa catccaagtc 960

aaggaggtca cgacgaatga tggcgtcacg accatcgcta ataaccttac cagcacggtt 1020

caagtcttct cggactcgga gtaccagttg ccgtacgtcc tcggctctgc gcaccagggc 1080

tgcctccctc cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc 1140

aacaatggca gccaggcagt gggacggtca tccttttact gcctggaata tttcccatcg 1200

cagatgctga gaacgggcaa taactttacc ttcagctaca ccttcgagga cgtgcctttc 1260

cacagcagct acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag 1320

tacctgtatt acctgaacag aactcagaat cagtccggaa gtgcccaaaa caaggacttg 1380

ctgtttagcc gggggtctcc agctggcatg tctgttcagc ccaaaaactg gctacctgga 1440

ccctgttacc ggcagcagcg cgtttctaaa acaaaaacag acaacaacaa cagcaacttt 1500

acctggactg gtgcttcaaa atataacctt aatgggcgtg aatctataat caaccctggc 1560

actgctatgg cctcacacaa agacgacgaa gacaagttct ttcccatgag cggtgtcatg 1620

atttttggaa aggagagcgc cggagcttca aacactgcat tggacaatgt catgatcaca 1680

gacgaagagg aaatcaaagc cactaacccc gtggccaccg aaagatttgg gactgtggca 1740

gtcaatctcc agagcagcag cacagaccct gcgaccggag atgtgcatgt tatgggagcc 1800

ttacctggaa tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa 1860

attcctcaca cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag 1920

cacccgcctc ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag 1980

ttttcggcta caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg 2040

gagattgaat gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat 2100

acatctaact atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat 2160

actgagcctc gccccattgg cacccgttac ctcacccgtc ccctgtaa 2208

<210> 1252
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1252
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga gggttcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gtggagccag actcctcctc gggaaccgga 480

aaggcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg ctacaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgca gtcaaggctt 1380

cagttttctg tggccggacc cagtaacatg gctgtccagg gaaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acatctgcgg ataacaacaa cagtgaattt 1500

gcttggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtttt ttcctcagag cggggttctc 1620

atctttggga agcaaggctc agagaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agcaacagaa cacagcacca gctaccgcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 1253
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1253
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

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Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300
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Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Val
    450                 455                 460

Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510
```

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Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Gln Gln Asn Thr Ala Pro Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720
```

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 1254
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1254
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aagtcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcagcttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgat gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtatt ttcctcagag cggggttctc 1620

atctttggga agcaagactc aggaaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

attccacaca cggacggaca ttttcacccc tctcccctca tgggtggatt cggacttaaa 1920

caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 1255
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1255
atggctgccg atggttatct tccagattgg ctcgaggaca ctctctctga aggaataaga 60

cagtggtgga agctcaaacc tggcccacca ccaccaaagc ccgcagagcg gcataaggac 120

gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gacccttcaa cggactcgac 180

aagggagagc cggtcaacga ggcagacgcc gcggccctcg agcacgacaa agcctacgac 240

cggcagctcg acagcggaga caacccgtac ctcaagtaca accacgccga cgcggagttt 300

caggagcgcc ttaaagaaga tacgtctttt gggggcaacc tcggacgagc agtcttccag 360

gcgaaaaaga ggattcttga acctctgggc ctggttgagg aacctgttaa gacggctccg 420

ggaaaaaaga ggccggtaga gcactctcct gcggagccag actcctcctc gggaaccgga 480

aagtcgggcc agcagcctgc aagaaaaaga ttgaattttg gtcagactgg agacgcagac 540

tcagtacctg acccccagcc tctcggacag ccaccagcag ccccctctgg tctgggaact 600

aatacgatgg cttcaggcag tggcgcacca atggcagaca ataacgaggg cgccgacgga 660

gtgggtaatt cctcgggaaa ttggcattgc gattccacat ggatgggcga cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca accacctcta caaacaaatt 780

tccagccaat caggagcctc gaacgacaat cactactttg gctacagcac cccttggggg 840

tattttgact tcaacagatt ccactgccac ttttcaccac gtgactggca aagactcatc 900

aacaacaact ggggattccg acccaagaga ctcaacttca agctctttaa cattcaagtc 960

aaagaggtca cgcagaatga cggtacgacg acgattgcca ataaccttac cagcacggtt 1020

caggtgttta ctgactcgga gtaccagctc ccgtacgtcc tcggctcggc gcatcaagga 1080

tgcctcccgc cgttcccagc agacgtcttc atggtgccac agtatggata cctcaccctg 1140

aacaacggga gtcaggcagt aggacgctct tcattttact gcctggagta ctttccttct 1200

cagatgctgc gtaccggaaa caactttacc ttcagctaca cttttgagga cgttcctttc 1260

cacagcagct acgctcacag ccagagtctg gaccgtctca tgaatcctct catcgaccag 1320

tacctgtatt acttgagcag aacaaacact ccaagtggaa ccaccacgat gtcaaggctt 1380

cagttttctc aggccggagc gagtgacatt cgggaccagt ctaggaactg gcttcctgga 1440

ccctgttacc gccagcagcg agtatcaaag acagctgcgg ataacaacaa cagtgattac 1500

tcgtggactg gagctaccaa gtaccacctc aatggcagag actctctggt gaatccgggc 1560

ccggccatgg caagccacaa ggacgatgaa gaaaagtatt ttcctcagag cggggttctc 1620

atctttggga agcaagactc aggaaaaaca aatgtggaca ttgaaaaggt catgattaca 1680

gacgaagagg aaatcaggac aaccaatccc gtggctacgg agcagtatgg ttctgtatct 1740

accaacctcc agagcggcaa cacacaagca gctacctcag atgtcaacac acaaggcgtt 1800

cttccaggca tggtctggca ggacagagat gtgtaccttc aggggcccat ctgggcaaag 1860

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caccctcctc cacagattct catcaagaac accccggtac ctgcgaatcc ttcgaccacc 1980

ttcagtgcgg caaagtttgc ttccttcatc acacagtact ccacgggaca ggtcagcgtg 2040

gagatcgagt gggagctgca gaaggaaaac agcaaacgct ggaatcccga aattcagtac 2100

acttccaact acaacaagtc tgttaatgtg gactttactg tggacactaa tggcgtgtat 2160

tcagagcctc gccccattgg caccagatac ctgactcgta atctgtaa 2208

<210> 1256
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1256
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

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Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
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Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495
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Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700
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Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1257
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 1257
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125
```

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Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335
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```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Phe Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540
```

```
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560


Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575


Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590


Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720


Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735


<210> 1258
<211> 747
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1258
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro

```
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
```

385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Ala Ala Ala Gly Ser
580 585 590

Thr Pro Pro Pro Met Ala Ala Arg Gln Ala Ala Thr Ala Asp Val Asn

595 600 605

Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
610 615 620

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe
625 630 635 640

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
645 650 655

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr
660 665 670

Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
675 680 685

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
690 695 700

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val
705 710 715 720

Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg
725 730 735

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 1259
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1259
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220
```

```
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430
```

```
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Ala Ala Ala Gly Glu
            580                 585                 590

Thr Arg Ala Pro Leu Ala Ala Arg Gln Ala Ala Thr Ala Asp Val Asn
        595                 600                 605

Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
    610                 615                 620

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe
625                 630                 635                 640
```

His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro
645 650 655

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr
660 665 670

Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly
675 680 685

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
690 695 700

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val
705 710 715 720

Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg
725 730 735

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 1260
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1260
Thr Leu Ala Val Pro Phe Lys
1 5

<210> 1261
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1261
Lys Phe Pro Val Ala Leu Thr
1 5

<210> 1262
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1262
Leu Ala Val Pro Phe Lys
1 5

<210> 1263
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1263
Ala Val Pro Phe Lys
1 5

<210> 1264
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1264
Val Pro Phe Lys
1

<210> 1265
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1265
Thr Leu Ala Val Pro Phe
1   5

<210> 1266
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1266
Thr Leu Ala Val Pro
1   5

<210> 1267
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1267
Thr Leu Ala Val
1

<210> 1268
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1268
Ser Val Ser Lys Pro Phe Leu
1 5

<210> 1269
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1269
Phe Thr Leu Thr Thr Pro Lys
1 5

<210> 1270
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1270
Met Asn Ala Thr Lys Asn Val
1 5

<210> 1271
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1271
Gln Ser Ser Gln Thr Pro Arg
1 5

<210> 1272
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1272
Ile Leu Gly Thr Gly Thr Ser
1 5

<210> 1273
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1273
Thr Arg Thr Asn Pro Glu Ala
1 5

<210> 1274
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1274
Asn Gly Gly Thr Ser Ser Ser
1 5

<210> 1275
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1275
Tyr Thr Leu Ser Gln Gly Trp
1 5

<210> 1276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 1276
aagtttcctg tggcgttgac t 21

<210> 1277
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 1277
actttggcgg tgcctttaa g 21

<210> 1278
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 1278
agtgtgagta agccttttt g 21

<210> 1279
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1279
tttacgttga cgacgcctaa g 21

<210> 1280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1280
atgaatgcta cgaagaatgt g 21

<210> 1281
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1281
cagtcgtcgc agacgcctag g 21

<210> 1282
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1282
attctgggga ctggtacttc g 21

<210> 1283
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1283
acgcggacta atcctgaggc t 21

<210> 1284
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1284
aatgggggga ctagtagttc t 21

<210> 1285
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1285
tatactttgt cgcagggttg g 21

<210> 1286
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1286
Ala Gln Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1287
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1287
Ala Gln Ser Val Ser Lys Pro Phe Leu Ala Gln
1 5 10

<210> 1288
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1288
Ala Gln Phe Thr Leu Thr Thr Pro Lys Ala Gln
1 5 10

<210> 1289
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1289
Asp Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1290
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1290
Glu Ser Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1291
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1291
Gly Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

<210> 1292
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1292
Ala Gln Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1293
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1293
Ala Thr Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1294
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1294
Asp Gly Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1295
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1295
Gly Gly Thr Leu Ala Thr Pro Phe Lys Ala Gln
1 5 10

<210> 1296
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1296
Ser Gly Ser Leu Ala Val Pro Phe Lys Ala Gln

1 5 10

<210> 1297
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1297
Ala Gln Thr Leu Ala Gln Pro Phe Lys Ala Gln
1 5 10

<210> 1298
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1298
Ala Gln Thr Leu Gln Gln Pro Phe Lys Ala Gln
1 5 10

<210> 1299
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1299
Ala Gln Thr Leu Ser Asn Pro Phe Lys Ala Gln
1 5 10

<210> 1300
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1300
Ala Gln Thr Leu Ala Val Pro Phe Ser Asn Pro
1   5   10

<210> 1301
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1301
Gln Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1   5   10

<210> 1302
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1302
Asn Gln Thr Leu Ala Val Pro Phe Lys Ala Gln
1   5   10

<210> 1303
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1303

Glu Gly Ser Leu Ala Val Pro Phe Lys Ala Gln
1   5   10

<210> 1304
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1304
Ser Gly Asn Leu Ala Val Pro Phe Lys Ala Gln
1   5   10

<210> 1305
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1305
Glu Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
1   5   10

<210> 1306
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<210> 1307
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Ala Val Thr Leu Ala Val Pro Phe Lys Ala Gln
1 5 10

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Ala Gln Thr Leu Ser Thr Pro Phe Lys Ala Gln
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<210> 1309
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<400> 1309
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1 5 10

<210> 1310
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Ala Gln Thr Leu Ser Gln Pro Phe Lys Ala Gln
1   5   10

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<210> 1312
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<400> 1312
Ala Gln Thr Leu Thr Met Pro Phe Lys Ala Gln
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<210> 1313
<211> 11
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<400> 1313
Ala Gln Thr Leu Thr Thr Pro Phe Lys Ala Gln
1   5   10

<210> 1314
<211> 11

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<400> 1314
Ala Gln Tyr Thr Leu Ser Gln Gly Trp Ala Gln
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<400> 1315
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<210> 1316
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<400> 1316
Ala Gln Val Ser Gly Gly His His Ser Ala Gln
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<210> 1317
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<400> 1317
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1   5   10

<210> 1318
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<400> 1318
Ala Gln Thr Leu Ser Lys Pro Phe Lys Ala Gln
1   5   10

<210> 1319
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<400> 1319
Gln Ala Val Arg Thr Ser Leu
1   5

<210> 1320
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1   5

<210> 1321

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<400> 1321
Met Asn Ser Thr Lys Asn Val
1   5

<210> 1322
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<400> 1322
Val Ser Gly Gly His His Ser
1   5

<210> 1323
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<400> 1323
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1   5   10

<210> 1324
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peptide"

<220>
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1   5   10

<210> 1325
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<220>
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<400> 1325
Ser Ala Gln Xaa Xaa Xaa Val Pro Phe Lys Ala Gln Ala Gln
1   5   10

<210> 1326
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<220>
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1 5 10

<210> 1327
<211> 14
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<220>
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Ser Ala Gln Thr Leu Ala Val Pro Phe Xaa Xaa Xaa Ala Gln
1 5 10

<210> 1329
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<223> /note="Description of Artificial Sequence: Synthetic
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<400> 1329
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<210> 1330
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<400> 1330
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1   5

<210> 1331
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<400> 1331
Asp Gly Thr Leu Ala Thr Pro Phe Lys
1   5

<210> 1332
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<400> 1332
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<210> 1333
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<400> 1333
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<210> 1334
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<400> 1334
Val Pro Phe Lys Ala Gln
1   5

<210> 1335
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<400> 1335
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<210> 1336
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<400> 1336
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1 5

<210> 1337
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<400> 1337
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<400> 1338
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<400> 1341
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<400> 1342
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1 5

<210> 1343
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<400> 1343
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1 5

<210> 1344
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<400> 1344
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<210> 1345
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<400> 1345
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<210> 1346
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<210> 1347
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<210> 1348
<211> 33
<212> DNA
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<400> 1348
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<210> 1349
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<400> 1349
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<400> 1350
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<210> 1351
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<210> 1352
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<210> 1353
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<210> 1354
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<210> 1355
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<223> a, c, g, or t

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<223> a, c, g, or t

<400> 1356
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nttgggcact ctggtggttt gtc 83

<210> 1357
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<223> a, c, g, or t

<400> 1357
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tttg 64

<210> 1358
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tttgggcact 70

<210> 1359
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tttgggcact ctggtgg 77

<210> 1360
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<222> (60)..(61)
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<400> 1360
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nttgggcact ctggtggttt gtg 83

<210> 1361
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 1361
cttgcgaagg agcggctttc g 21

<210> 1362
<211> 10
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<400> 1362
Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
1 5 10

<210> 1363
<211> 14
<212> PRT
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<400> 1363
Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp
1 5 10

<210> 1364
<211> 11
<212> PRT
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<221> source
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<400> 1364
Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser
1 5 10

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<400> 1365
Glu Lys Gln Arg Asn Gly Thr Leu Thr
1 5

<210> 1366
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<212> PRT
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<400> 1366
Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala Leu Met
1 5 10 15

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<210> 1367
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Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly
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<210> 1368
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<400> 1368
Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg
1 5 10

<210> 1369
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Thr Ile Thr Cys Leu Trp Asp Leu Ala Pro Ser Lys
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<210> 1370
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Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
1 5 10

<210> 1371
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<400> 1371
Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser
1 5 10

<210> 1372
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<400> 1372
Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala
1 5 10 15

Leu Met Arg Ser Thr Thr Lys
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<210> 1373
<211> 8
<212> PRT
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<400> 1373
Leu Pro Arg Ala Leu Met Arg Ser
1 5

<210> 1374
<211> 8
<212> PRT

<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
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<400> 1374
Ile Asn His Arg Gly Tyr Trp Val
1 5

<210> 1375
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peptide"

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Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp
1 5 10

<210> 1376
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<220>
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peptide"

<400> 1376
Ala Lys Ala Val Ser Asn Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln
1 5 10 15

Ser

<210> 1377
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<400> 1377
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1 5 10

<210> 1378
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<400> 1378
Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp
1 5 10

<210> 1379
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<212> PRT
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<220>
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<400> 1379
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<210> 1380
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Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr Ala
1 5 10

<210> 1382
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<400> 1382
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1 5 10 15

Ser

<210> 1383
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<400> 1383
Ser Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr
1 5 10

<210> 1384

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<223> /note="Description of Artificial Sequence: Synthetic
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<400> 1384
Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp
1 5 10

<210> 1385
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Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly
1 5 10

<210> 1386
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Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr Ala Ser Tyr Leu
1 5 10 15

<210> 1387
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<400> 1387
Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr Ala
1   5   10

<210> 1388
<211> 11
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peptide"

<400> 1388
Asp Gln Ser Ile Asp Phe Glu Ile Asp Ser Ala
1   5   10

<210> 1389
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1389
Lys Asn Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu
1   5   10   15

Leu Gly Asp Ser
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<210> 1390
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1390

Lys Asn Val Ser Glu Asp Leu Pro Leu Pro Thr
1   5   10

<210> 1391
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1391
Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp
1   5   10

<210> 1392
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1392
Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
1   5   10

<210> 1393
<211> 9
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1393
Asp Ala Glu Phe Arg His Asp Ser Gly
1   5

<210> 1394
<211> 16
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1394
His Tyr Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu
1 5 10 15

<210> 1395
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1395
Tyr Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln
1 5 10

<210> 1396
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1396
Arg Ser Gln Lys Glu Gly Leu His Tyr Thr
1 5 10

<210> 1397
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1397
Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Trp Ala Asn Pro
1   5   10   15

Gln Ala Glu

<210> 1398
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1398
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Trp Ala Asn Pro
1   5   10   15

<210> 1399
<211> 9
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1399
Ser Ser Arg Thr Pro Ser Asp Lys Pro
1   5

<210> 1400
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1400
Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro
1   5   10

<210> 1401
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1401
Asp Gly Asn Val Asp Tyr His Met Asn Ser Val
1 5 10

<210> 1402
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1402
Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln
1 5 10 15

<210> 1403
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1403
Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
1 5 10

<210> 1404
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1404
Gln Met Trp Ala Pro Gln Trp Gly Pro Asp
1 5 10

<210> 1405
<211> 6
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1405
Arg Gly Asn Arg Gln Ala
1 5

<210> 1406
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1406
Ser Ser Ser Thr Asp Pro
1 5

<210> 1407
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1407
Ser Ser Asn Thr Ala Pro

1 5

<210> 1408
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1408
Ser Asn Ser Asn Leu Pro
1 5

<210> 1409
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1409
Ser Ser Thr Thr Ala Pro
1 5

<210> 1410
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1410
Ala Ala Asn Thr Ala Ala
1 5

<210> 1411
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1411
Gln Gln Asn Thr Ala Pro
1 5

<210> 1412
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1412
Ser Ala Gln Ala Gln Ala
1 5

<210> 1413
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1413
Gln Ala Asn Thr Gly Pro
1 5

<210> 1414
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1414

Asn Ala Thr Thr Ala Pro
1   5

<210> 1415
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1415
Ser Ser Thr Ala Gly Pro
1   5

<210> 1416
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1416
Gln Gln Asn Thr Ala Ala
1   5

<210> 1417
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1417
Pro Ser Thr Ala Gly Pro
1   5

<210> 1418
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1418
Asn Gln Asn Thr Ala Pro
1 5

<210> 1419
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1419
Gln Ala Ala Asn Ala Pro
1 5

<210> 1420
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1420
Ser Ile Val Gly Leu Pro
1 5

<210> 1421
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1421
Ala Ala Ser Thr Ala Ala
1 5

<210> 1422
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1422
Ser Gln Asn Thr Thr Ala
1 5

<210> 1423
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1423
Gln Gln Asp Thr Ala Pro
1 5

<210> 1424
<211> 6
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1424
Gln Thr Asn Thr Gly Pro
1 5

<210> 1425
<211> 6

<212> PRT
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<220>
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peptide"

<400> 1425
Gln Thr Asn Gly Ala Pro
1 5

<210> 1426
<211> 6
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1426
Gln Gln Asn Ala Ala Pro
1 5

<210> 1427
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1427
Ala Ala Asn Thr Gln Ala
1 5

<210> 1428
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1428
Asn Gly Arg Ala His Ala
1   5

<210> 1429
<211> 7
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1429
Gln Pro Glu His Ser Ser Thr
1   5

<210> 1430
<211> 7
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1430
Val Asn Thr Ala Asn Ser Thr
1   5

<210> 1431
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1431
His Gly Pro Met Gln Lys Ser
1   5

<210> 1432

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1432
Pro His Lys Pro Pro Leu Ala
1 5

<210> 1433
<211> 7
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1433
Ile Lys Asn Asn Glu Met Trp
1 5

<210> 1434
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1434
Arg Asn Leu Asp Thr Pro Met
1 5

<210> 1435
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 1435
Val Asp Ser His Arg Gln Ser
1 5

<210> 1436
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1436
Tyr Asp Ser Lys Thr Lys Thr
1 5

<210> 1437
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1437
Ser Gln Leu Pro His Gln Lys
1 5

<210> 1438
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1438
Ser Thr Met Gln Gln Asn Thr
1 5

<210> 1439
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1439
Thr Glu Arg Tyr Met Thr Gln
1 5

<210> 1440
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1440
Asp Ala Ser Leu Ser Thr Ser
1 5

<210> 1441
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1441
Asp Leu Pro Asn Lys Lys Thr
1 5

<210> 1442
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1442
Asp Leu Thr Ala Ala Arg Leu
1 5

<210> 1443
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1443
Glu Pro His Gln Phe Asn Tyr
1 5

<210> 1444
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1444
Glu Pro Gln Ser Asn His Thr
1 5

<210> 1445
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1445
Met Ser Ser Trp Pro Ser Gln
1 5

<210> 1446
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1446
Asn Pro Lys His Asn Ala Thr
1   5

<210> 1447
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1447
Pro Asp Gly Met Arg Thr Thr
1   5

<210> 1448
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1448
Pro Asn Asn Asn Lys Thr Thr
1   5

<210> 1449
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1449
Gln Ser Thr Thr His Asp Ser
1   5

<210> 1450
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1450
Thr Gly Ser Lys Gln Lys Gln
1   5

<210> 1451
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<400> 1451
Ser Leu Lys His Gln Ala Leu
1   5

<210> 1452
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1452
Ser Pro Ile Asp Gly Glu Gln
1   5

<210> 1453
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1453
Trp Ile Phe Pro Trp Ile Gln Leu
1 5

<210> 1454
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1454
Cys Asp Cys Arg Gly Asp Cys Phe Cys
1 5

<210> 1455
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1455
Cys Asn Gly Arg Cys
1 5

<210> 1456
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1456
Cys Pro Arg Glu Cys Glu Ser
1 5

<210> 1457
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1457
Cys Thr Thr His Trp Gly Phe Thr Leu Cys
1 5 10

<210> 1458
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1458
Cys Gly Arg Arg Ala Gly Gly Ser Cys
1 5

<210> 1459
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1459
Cys Lys Gly Gly Arg Ala Lys Asp Cys

1 5

<210> 1460
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<400> 1460
Cys Val Pro Glu Leu Gly His Glu Cys
1 5

<210> 1461
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1461
Cys Arg Arg Glu Thr Ala Trp Ala Lys
1 5

<210> 1462
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1462
Val Ser Trp Phe Ser His Arg Tyr Ser Pro Phe Ala Val Ser
1 5 10

<210> 1463
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1463
Gly Tyr Arg Asp Gly Tyr Ala Gly Pro Ile Leu Tyr Asn
1 5 10

<210> 1464
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
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<222> (1)..(3)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (5)..(7)
<223> Any naturally occurring amino acid

<400> 1464
Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5

<210> 1465
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
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<222> (2)..(2)
<223> /replace="Met"

<220>
<221> MISC_FEATURE
<222> (1)..(4)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 1465
Tyr Glu Asn Trp
1

<210> 1466
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1466
Arg Pro Leu Pro Pro Leu Pro
1 5

<210> 1467
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1467
Ala Pro Pro Leu Pro Pro Arg
1 5

<210> 1468
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1468
Asp Val Phe Tyr Pro Tyr Pro Tyr Ala Ser Gly Ser
1   5   10

<210> 1469
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1469
Met Tyr Trp Tyr Pro Tyr
1   5

<210> 1470
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1470
Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
1   5   10

<210> 1471
<211> 8
<212> PRT
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Leu"

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 1471
Cys Trp Asp Asp Gly Trp Leu Cys
1 5

<210> 1472
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1472
Glu Trp Cys Glu Tyr Leu Gly Gly Tyr Leu Arg Cys Tyr Ala
1 5 10

<210> 1473
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
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<222> (2)..(2)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (4)..(5)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (8)..(8)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Any naturally occurring amino acid

<400> 1473
Tyr Xaa Cys Xaa Xaa Gly Pro Xaa Thr Trp Xaa Cys Xaa Pro
1   5   10

<210> 1474
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1474
Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1   5   10

<210> 1475
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> MOD_RES
<222> (3)..(4)
<223> Any naturally occurring amino acid

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Trp" or "Phe" or "His"

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 1475
Leu Trp Xaa Xaa Tyr
1 5

<210> 1476
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
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<222> (1)..(1)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (3)..(4)
<223> Any naturally occurring amino acid

<400> 1476
Xaa Phe Xaa Xaa Tyr Leu Trp
1 5

<210> 1477
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1477
Ser Ser Ile Ile Ser His Phe Arg Trp Gly Leu Cys Asp
1 5 10

<210> 1478
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1478
Met Ser Arg Pro Ala Cys Pro Pro Asn Asp Lys Tyr Glu
1 5 10

<210> 1479
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1479
Cys Leu Arg Ser Gly Arg Gly Cys
1 5

<210> 1480
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1480
Cys His Trp Met Phe Ser Pro Trp Cys
1 5

<210> 1481
<211> 4
<212> PRT
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<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> MOD_RES
<222> (2)..(3)
<223> Any naturally occurring amino acid

<400> 1481
Trp Xaa Xaa Phe
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<210> 1482
<211> 8
<212> PRT
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1482
Cys Ser Ser Arg Leu Asp Ala Cys
1 5

<210> 1483
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1483
Cys Leu Pro Val Ala Ser Cys
1 5

<210> 1484
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1484
Cys Gly Phe Glu Cys Val Arg Gln Cys Pro Glu Arg Cys
1 5 10

<210> 1485
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1485
Cys Val Ala Leu Cys Arg Glu Ala Cys Gly Glu Gly Cys
1 5 10

<210> 1486
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1486
Ser Trp Cys Glu Pro Gly Trp Cys Arg
1 5

<210> 1487
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1487
Tyr Ser Gly Lys Trp Gly Trp
1 5

<210> 1488
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1488
Gly Leu Ser Gly Gly Arg Ser
1 5

<210> 1489
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1489
Leu Met Leu Pro Arg Ala Asp
1 5

<210> 1490
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1490
Cys Ser Cys Phe Arg Asp Val Cys Cys
1 5

<210> 1491
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1491
Cys Arg Asp Val Val Ser Val Ile Cys
1 5

<210> 1492
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1492
Met Ala Arg Ser Gly Leu
1 5

<210> 1493
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1493
Met Ala Arg Ala Lys Glu
1 5

<210> 1494
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1494
Met Ser Arg Thr Met Ser
1 5

<210> 1495
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1495
Lys Cys Cys Tyr Ser Leu
1 5

<210> 1496
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1496
Met Tyr Trp Gly Asp Ser His Trp Leu Gln Tyr Trp Tyr Glu
1 5 10

<210> 1497
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1497
Met Gln Leu Pro Leu Ala Thr
1 5

<210> 1498
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1498
Glu Trp Leu Ser
1

<210> 1499
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1499
Ser Asn Glu Trp
1

<210> 1500
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1500
Thr Asn Tyr Leu
1

<210> 1501
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1501
Trp Asp Leu Ala Trp Met Phe Arg Leu Pro Val Gly

1 5 10

<210> 1502
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1502
Cys Thr Val Ala Leu Pro Gly Gly Tyr Val Arg Val Cys
1 5 10

<210> 1503
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1503
Cys Val Ala Tyr Cys Ile Glu His His Cys Trp Thr Cys
1 5 10

<210> 1504
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1504
Cys Val Phe Ala His Asn Tyr Asp Tyr Leu Val Cys
1 5 10

<210> 1505
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1505
Cys Val Phe Thr Ser Asn Tyr Ala Phe Cys
1 5 10

<210> 1506
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1506
Val His Ser Pro Asn Lys Lys
1 5

<210> 1507
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1507
Cys Arg Gly Asp Gly Trp Cys
1 5

<210> 1508
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any naturally occurring amino acid

<220>
<221> MOD_RES
<222> (6)..(6)
<223> Any naturally occurring amino acid

<400> 1508
Xaa Arg Gly Cys Asp Xaa
1   5

<210> 1509
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> MOD_RES
<222> (2)..(4)
<223> Any naturally occurring amino acid

<400> 1509
Pro Xaa Xaa Xaa
1

<210> 1510
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1510
Ser Gly Lys Gly Pro Arg Gln Ile Thr Ala Leu
1   5   10

<210> 1511

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
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<222> (10)..(10)
<223> /replace="Gln"

<220>
<221> VARIANT
<222> (11)..(11)
<223> /replace="Ala"

<220>
<221> VARIANT
<222> (12)..(12)
<223> /replace="Tyr"

<220>
<221> VARIANT
<222> (13)..(13)
<223> /replace="Val" or "Met" or "Arg"

<220>
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<222> (14)..(14)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 1511
Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Asn Leu Thr Xaa
1 5 10

<210> 1512
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1512
Val Tyr Met Ser Pro Phe
1   5

<210> 1513
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1513
Ala Thr Trp Leu Pro Pro Arg
1   5

<210> 1514
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1514
His Thr Met Tyr Tyr His His Tyr Gln His His Leu
1   5   10

<210> 1515
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1515
Ser Glu Val Gly Cys Arg Ala Gly Pro Leu Gln Trp Leu Cys Glu Lys

1 5 10 15

Tyr Phe Gly

<210> 1516
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1516
Cys Gly Leu Leu Pro Val Gly Arg Pro Asp Arg Asn Val Trp Arg Trp
1 5 10 15

Leu Cys

<210> 1517
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1517
Cys Lys Gly Gln Cys Asp Arg Phe Lys Gly Leu Pro Trp Glu Cys
1 5 10 15

<210> 1518
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1518

Ser Gly Arg Ser Ala
1 5

<210> 1519
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1519
Trp Gly Phe Pro
1

<210> 1520
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1520
Ala Glu Pro Met Pro His Ser Leu Asn Phe Ser Gln Tyr Leu Trp Tyr
1 5 10 15

Thr

<210> 1521
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> VARIANT
<222> (4)..(4)

<223> /replace="Phe"

<220>
<221> MISC_FEATURE
<222> (1)..(6)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 1521
Trp Ala Tyr Trp Ser Pro
1 5

<210> 1522
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1522
Ile Glu Leu Leu Gln Ala Arg
1 5

<210> 1523
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1523
Ala Tyr Thr Lys Cys Ser Arg Gln Trp Arg Thr Cys Met Thr Thr His
1 5 10 15

<210> 1524
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 1524
Pro Gln Asn Ser Lys Ile Pro Gly Pro Thr Phe Leu Asp Pro His
1 5 10 15

<210> 1525
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1525
Ser Met Glu Pro Ala Leu Pro Asp Trp Trp Trp Lys Met Phe Lys
1 5 10 15

<210> 1526
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1526
Ala Asn Thr Pro Cys Gly Pro Tyr Thr His Asp Cys Pro Val Lys Arg
1 5 10 15

<210> 1527
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1527
Thr Ala Cys His Gln His Val Arg Met Val Arg Pro
1 5 10

<210> 1528
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1528
Val Pro Trp Met Glu Pro Ala Tyr Gln Arg Phe Leu
1 5 10

<210> 1529
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1529
Asp Pro Arg Ala Thr Pro Gly Ser
1 5

<210> 1530
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1530
Phe Arg Pro Asn Arg Ala Gln Asp Tyr Asn Thr Asn
1 5 10

<210> 1531
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1531
Cys Thr Lys Asn Ser Tyr Leu Met Cys
1   5

<210> 1532
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> VARIANT
<222> (2)..(2)
<223> /replace="Arg"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Arg"

<220>
<221> VARIANT
<222> (5)..(5)
<223> /replace="Asn"

<220>
<221> VARIANT
<222> (6)..(7)
<223> Any amino acid

<220>
<221> VARIANT
<222> (9)..(9)
<223> /replace="Val"

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<400> 1532

Cys Gln Leu Thr Gly Xaa Xaa Gly Ala Gly Cys
1   5   10

<210> 1533
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1533
Cys Pro Ile Glu Asp Arg Pro Met Cys
1   5

<210> 1534
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1534
His Glu Trp Ser Tyr Leu Ala Pro Tyr Pro Trp Phe
1   5   10

<210> 1535
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1535
Met Cys Pro Lys His Pro Leu Gly Cys
1   5

<210> 1536
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1536
Arg Met Trp Pro Ser Ser Thr Val Asn Leu Ser Ala Gly Arg Arg
1 5 10 15

<210> 1537
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1537
Ser Ala Lys Thr Ala Val Ser Gln Arg Val Trp Leu Pro Ser His Arg
1 5 10 15

Gly Gly Glu Pro
20

<210> 1538
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1538
Lys Ser Arg Glu His Val Asn Asn Ser Ala Cys Pro Ser Lys Arg Ile
1 5 10 15

Thr Ala Ala Leu
20

<210> 1539
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1539
Glu Gly Phe Arg
1

<210> 1540
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1540
Ala Gly Leu Gly Val Arg
1 5

<210> 1541
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1541
Gly Thr Arg Gln Gly His Thr Met Arg Leu Gly Val Ser Asp Gly
1 5 10 15

<210> 1542
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1542
Ile Ala Gly Leu Ala Thr Pro Gly Trp Ser His Trp Leu Ala Leu
1   5   10   15

<210> 1543
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1543
Ser Met Ser Ile Ala Arg Leu
1   5

<210> 1544
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1544
His Thr Phe Glu Pro Gly Val
1   5

<210> 1545
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1545
Asn Thr Ser Leu Lys Arg Ile Ser Asn Lys Arg Ile Arg Arg Lys
1   5   10   15

<210> 1546

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1546
Leu Arg Ile Lys Arg Lys Arg Arg Lys Arg Lys Lys Thr Arg Lys
1 5 10 15

<210> 1547
<211> 21
<212> DNA
<213> Adeno-associated virus 2

<400> 1547
agcvvmdcag garscascaa c 21

<210> 1548
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1548
Ser Asp Ser Gly Ala Ser Asn
1 5

<210> 1549
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1549
Ser Pro Ser Gly Ala Ser Asn
1 5

<210> 1550
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1550
Ser His Ser Gly Ala Ser Asn
1 5

<210> 1551
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1551
Ser Arg Ser Gly Ala Ser Asn
1 5

<210> 1552
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1552
Ser Lys Ser Gly Ala Ser Asn
1 5

<210> 1553
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1553
Ser Asn Ser Gly Ala Ser Asn
1   5

<210> 1554
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1554
Ser Gly Ser Gly Ala Ser Asn
1   5

<210> 1555
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1555
Ser Ala Ser Gly Ala Ser Asn
1   5

<210> 1556
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1556
Ser Glu Ser Gly Thr Ser Asn
1   5

<210> 1557
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1557
Ser Thr Thr Gly Gly Ser Asn
1 5

<210> 1558
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1558
Ser Ser Ala Gly Ser Thr Asn
1 5

<210> 1559
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1559
Asn Asn Asp Ser Gln Ala
1 5

<210> 1560
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1560
Asn Asn Arg Asn Gln Ala
1   5

<210> 1561
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1561
Asn Asn Asn Lys Gln Ala
1   5

<210> 1562
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1562
Asn Ala Lys Arg Gln Ala
1   5

<210> 1563
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1563
Asn Asp Glu His Gln Ala

1 5

<210> 1564
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1564
Asn Thr Ser Gln Lys Ala
1 5

<210> 1565
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1565
Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Asp Thr Gln Ser
1 5 10 15

Arg Leu Val Phe Ser Gln Ala Gly Ala
20 25

<210> 1566
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1566
Tyr Tyr Leu Ser Arg Thr Asn Thr Asp Ser Gly Thr Glu Thr Gln Ser
1 5 10 15

Gly Leu Asp Phe Ser Gln Ala Gly Ala
            20   25

<210> 1567
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1567
Tyr Tyr Leu Ser Arg Thr Asn Thr Glu Ser Gly Thr Pro Thr Gln Ser
1   5   10   15

Ala Leu Glu Phe Ser Gln Ala Gly Ala
            20   25

<210> 1568
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1568
Tyr Tyr Leu Ser Arg Thr Asn Thr His Ser Gly Thr His Thr Gln Ser
1   5   10   15

Pro Leu His Phe Ser Gln Ala Gly Ala
            20   25

<210> 1569
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1569
Tyr Tyr Leu Ser Arg Thr Asn Thr Ser Ser Gly Thr Ile Thr Ile Ser
1   5   10   15

His Leu Ile Phe Ser Gln Ala Gly Ala
            20   25

<210> 1570
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1570
Tyr Tyr Leu Ser Arg Thr Asn Thr Arg Ser Gly Ile Met Thr Lys Ser
1   5   10   15

Ser Leu Met Phe Ser Gln Ala Gly Ala
            20   25

<210> 1571
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1571
Tyr Tyr Leu Ser Arg Thr Asn Thr Lys Ser Gly Arg Lys Thr Leu Ser
1   5   10   15

Asn Leu Ser Phe Ser Gln Ala Gly Ala
            20   25

<210> 1572
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1572
Tyr Tyr Leu Ser Arg Thr Asn Asp Gly Ser Gly Pro Val Thr Pro Ser
1   5   10   15

Lys Leu Arg Phe Ser Gln Arg Gly Ala
            20   25

<210> 1573
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1573
Tyr Tyr Leu Ser Arg Thr Asn Ala Ala Ser Gly His Ala Thr His Ser
1   5   10   15

Asp Leu Lys Phe Ser Gln Pro Gly Ala
            20   25

<210> 1574
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1574
Tyr Tyr Leu Ser Arg Thr Asn Gly Gln Ala Gly Ser Leu Thr Met Ser
1   5   10   15

Glu Leu Gly Phe Ser Gln Val Gly Ala
            20   25

<210> 1575
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1575
Tyr Tyr Leu Ser Arg Thr Asn Ser Thr Gly Gly Asn Gln Thr Thr Ser
1 5 10 15

Gln Leu Leu Phe Ser Gln Leu Ser Ala
20 25

<210> 1576
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1576
Tyr Phe Leu Ser Arg Thr Asn Asn Asn Thr Gly Leu Asn Thr Asn Ser
1 5 10 15

Thr Leu Asn Phe Ser Gln Gly Arg Ala
20 25

<210> 1577
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1577
Ser Lys Thr Gly Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1578
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1578
Ser Lys Thr Asp Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1579
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1579
Ser Lys Thr Glu Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1580
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1580
Ser Lys Thr Pro Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1581
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1581
Ser Lys Thr His Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1582
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1582
Ser Lys Thr Gln Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1583
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1583
Ser Lys Thr Ile Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1584
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1584
Ser Lys Thr Met Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1585
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1585
Ser Lys Thr Arg Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1586
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1586
Ser Lys Thr Asn Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1587
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1587
Ser Lys Thr Val Gly Arg Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1588
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1588
Ser Lys Thr Ala Asp Arg Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1589
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1589
Ser Lys Lys Leu Ser Gln Asn Asn Asn Ser Lys Tyr Ser Trp Gln Gly
1 5 10 15

<210> 1590
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1590
Ser Lys Pro Thr Thr Gly Asn Asn Asn Ser Asp Tyr Ser Trp Pro Gly
1 5 10 15

<210> 1591
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1591
Ser Thr Gln Lys Asn Glu Asn Asn Asn Ser Asn Tyr Ser Trp Pro Gly

1 5 10 15

<210> 1592
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1592
His Lys Asp Asp Glu Gly Lys Phe
1 5

<210> 1593
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1593
His Lys Asp Asp Asn Arg Lys Phe
1 5

<210> 1594
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1594
His Lys Asp Asp Thr Asn Lys Phe
1 5

<210> 1595
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1595
His Glu Asp Ser Asp Lys Asn Phe
1   5

<210> 1596
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1596
His Arg Asp Gly Ala Asp Ser Phe
1   5

<210> 1597
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1597
His Gly Asp Asn Lys Ser Arg Phe
1   5

<210> 1598
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1598

Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Phe Glu Glu Val
1   5   10

<210> 1599
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1599
Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ser Glu Glu Val
1   5   10

<210> 1600
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1600
Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Val Glu Glu Val
1   5   10

<210> 1601
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1601
Lys Gln Gly Ser Asp Lys Thr Asn Val Asp Asp Ala Gly Val
1   5   10

<210> 1602
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1602
Lys Gln Gly Ser Ser Lys Thr Asn Val Asp Pro Arg Glu Val
1   5   10

<210> 1603
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1603
Lys Gln Gly Ser Arg Lys Thr Asn Val Asp His Lys Gln Val
1   5   10

<210> 1604
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1604
Lys Gln Gly Ser Lys Gly Gly Asn Val Asp Thr Asn Arg Val
1   5   10

<210> 1605
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1605
Lys Gln Gly Ser Gly Glu Ala Asn Val Asp Asn Gly Asp Val
1   5   10

<210> 1606
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1606
Lys Gln Asp Ala Ala Ala Asp Asn Ile Asp Tyr Asp His Val
1   5   10

<210> 1607
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1607
Lys Gln Ser Gly Thr Arg Ser Asn Ala Ala Ala Ser Ser Val
1   5   10

<210> 1608
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1608
Lys Glu Asn Thr Asn Thr Asn Asp Thr Glu Leu Thr Asn Val
1   5   10

<210> 1609
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1609
Gln Arg Gly Asn Asn Val Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 1610
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1610
Gln Arg Gly Asn Asn Glu Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 1611
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1611
Gln Arg Gly Asn Asn Pro Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 1612
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1612
Gln Arg Gly Asn Asn His Ala Ala Thr Ala Asp Val Asn Thr
1   5   10

<210> 1613
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1613
Gln Glu Glu Asn Asn Ile Ala Ala Thr Pro Gly Val Asn Thr
1   5   10

<210> 1614
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1614
Gln Pro Pro Asn Asn Met Ala Ala Thr His Glu Val Asn Thr
1   5   10

<210> 1615
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1615
Gln His His Asn Asn Ser Ala Ala Thr Thr Ile Val Asn Thr
1   5   10

<210> 1616

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1616
Gln Thr Thr Asn Asn Arg Ala Ala Phe Asn Met Val Glu Thr
1 5 10

<210> 1617
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1617
Gln Lys Lys Asn Asn Asn Ala Ala Ser Lys Lys Val Ala Thr
1 5 10

<210> 1618
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1618
Gln Gly Gly Asn Asn Lys Ala Ala Asp Asp Ala Val Lys Thr
1 5 10

<210> 1619
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 1619
Gln Ala Ala Lys Gly Gly Ala Ala Asp Asp Ala Val Lys Thr
1 5 10

<210> 1620
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1620
Gln Asp Asp Arg Ala Ala Ala Ala Asn Glu Ser Val Asp Thr
1 5 10

<210> 1621
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1621
Gln Gln Gln His Asp Asp Ala Ala Tyr Gln Arg Val His Thr
1 5 10

<210> 1622
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1622
Gln Ser Ser Ser Ser Leu Ala Ala Val Ser Thr Val Gln Thr
1 5 10

<210> 1623
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1623
Gln Asn Asn Gln Thr Thr Ala Ala Ile Arg Asn Val Thr Thr
1 5 10

<210> 1624
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1624
Asn Tyr Asn Lys Lys Ser Asp Asn Val Asp Phe Thr
1 5 10

<210> 1625
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1625
Asn Tyr Asn Lys Lys Ser Glu Asn Val Asp Phe Thr
1 5 10

<210> 1626
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1626
Asn Tyr Asn Lys Lys Ser Leu Asn Val Asp Phe Thr
1 5 10

<210> 1627
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1627
Asn Tyr Asn Lys Lys Ser Pro Asn Val Asp Phe Thr
1 5 10

<210> 1628
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1628
Asn Tyr Ser Lys Lys Ser His Cys Val Asp Phe Thr
1 5 10

<210> 1629
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1629
Asn Tyr Arg Lys Thr Ile Tyr Val Asp Phe Thr
1 5 10

<210> 1630
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1630
Asn Tyr Lys Glu Lys Lys Asp Val His Phe Thr
1 5 10

<210> 1631
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1631
Asn Tyr Gly His Arg Ala Ile Val Gln Phe Thr
1 5 10

<210> 1632
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1632
Asn Tyr Ala Asn His Gln Phe Val Val Cys Thr
1 5 10

<210> 1633
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1633
Asn Tyr Asp Asp Asp Pro Thr Gly Val Leu Leu Thr
1 5 10

<210> 1634
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1634
Asn Tyr Asp Asp Pro Thr Gly Val Leu Leu Thr
1 5 10

<210> 1635
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1635
Asn Phe Glu Gln Gln Asn Ser Val Glu Trp Thr
1 5 10

<210> 1636
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1636
Ser Gln Ser Gly Ala Ser Asn
1 5

<210> 1637
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1637
Asn Asn Gly Ser Gln Ala
1 5

<210> 1638
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1638
Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Trp Ser
1 5 10 15

Arg Leu Gln Phe Ser Gln Ala Gly Ala
20 25

<210> 1639
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1639
Ser Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly
1 5 10 15

<210> 1640

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1640
His Lys Asp Asp Glu Glu Lys Phe
1 5

<210> 1641
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1641
Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Glu Val
1 5 10

<210> 1642
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1642
Gln Arg Gly Asn Asn Gln Ala Ala Thr Ala Asp Val Asn Thr
1 5 10

<210> 1643
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 1643
Asn Tyr Asn Lys Lys Ser Val Asn Val Asp Phe Thr
1   5   10

<210> 1644
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1644
Ser Gln Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1   5   10   15

Gln Ser Arg Leu Gln Phe Ser Thr Ser Ala Asp Asn Asn Asn Ser Glu
            20   25   30

Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His
        35   40

<210> 1645
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1645
Ser Ala Ser Gly Ala Ser Asn Phe Asn Ser Glu Gly Gly Ser Leu Thr
1   5   10   15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
            20   25   30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
        35   40

<210> 1646
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1646
Ser Gln Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1 5 10 15

Gln Ser Arg Leu Gln Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 1647
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1647
Ser Ala Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1 5 10 15

Gln Ser Arg Leu Gln Phe Ser Thr Ser Ala Asp Asn Asn Asn Ser Glu
20 25 30

Phe Ser Trp Pro Gly Ala Thr Thr Tyr His
35 40

<210> 1648
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1648
Ser Gln Ser Gly Ala Ser Asn Phe Asn Ser Glu Gly Gly Ser Leu Thr
1 5 10 15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 1649
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1649
Ser Ala Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Ser Leu Thr
1 5 10 15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 1650
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1650

Ser Gln Ser Gly Ala Ser Asn Tyr Asn Thr Pro Ser Gly Thr Thr Thr
1 5 10 15

Gln Ser Arg Leu Gln Phe Ser Thr Ser Ala Asp Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 1651
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1651
Ser Gly Ala Gly Ala Ser Asn Phe Asn Ser Glu Gly Gly Ser Leu Thr
1 5 10 15

Gln Ser Ser Leu Gly Phe Ser Thr Asp Gly Glu Asn Asn Asn Ser Asp
20 25 30

Phe Ser Trp Thr Gly Ala Thr Lys Tyr His
35 40

<210> 1652
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1652
Ser Gly Ala Gly Ala Ser Asn
1 5

<210> 1653
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1653
Asn Ser Glu Gly Gly Ser Leu Thr Gln Ser Ser Leu Gly Phe Ser
1 5 10 15

<210> 1654
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1654
Thr Asp Gly Glu Asn Asn Asn Ser Asp Phe Ser
1 5 10

<210> 1655
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1655
Ser Glu Phe Ser Trp Pro Gly Ala Thr Thr
1 5 10

<210> 1656
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1656
Thr Ser Ala Asp Asn Asn Asn Ser Asp Phe Ser Trp Thr
1 5 10

<210> 1657
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1657
Ser Gln Ser Gly Ala Ser Asn Tyr
1 5

<210> 1658
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1658
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
1 5 10 15

<210> 1659
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1659
Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr
1 5 10 15

Lys Tyr His

<210> 1660
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1660
Ser Ala Ser Gly Ala Ser Asn Phe
1 5

<210> 1661
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1661
Thr Asp Gly Glu Asn Asn Asn Ser Asp Phe Ser Trp Thr Gly Ala Thr
1 5 10 15

Lys Tyr His

<210> 1662
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1662
Ser Ala Ser Gly Ala Ser Asn Tyr
1 5

<210> 1663
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1663
Thr Ser Ala Asp Asn Asn Asn Ser Glu Phe Ser Trp Pro Gly Ala Thr
1 5 10 15

Thr Tyr His

<210> 1664
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1664
Asn Thr Pro Ser Gly Ser Leu Thr Gln Ser Ser Leu Gly Phe Ser
1 5 10 15

<210> 1665
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1665
Thr Ser Ala Asp Asn Asn Asn Ser Asp Phe Ser Trp Thr Gly Ala Thr
1 5 10 15

Lys Tyr His

<210> 1666
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1666
Ser Gly Ala Gly Ala Ser Asn Phe
1 5

<210> 1667
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (20)..(20)
<223> a, c, g, or t

<220>
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<222> (35)..(35)
<223> a, c, g, or t

<400> 1667
ctccagvvsv vsmrsrvcvn sgcagctdhc vvsrnsgtcv msacacaa 48

<210> 1668
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1668

ctccagagag gcaacagaca agcagctacc gcagatgtca acacacaa 48

<210> 1669
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1669
Ser Ala Ala Gly Ala Ser Asn
1 5

<210> 1670
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1670
Tyr Phe Leu Ser Arg Thr Asn Thr Glu Ser Gly Ser Thr Thr Gln Ser
1 5 10 15

Thr Leu Arg Phe Ser Gln Ala Gly
20

<210> 1671
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1671
Ser Lys Thr Ser Ala Asp Asn Asn Asn Ser Asp Phe Ser
1 5 10

<210> 1672
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1672
Lys Gln Gly Ser Glu Lys Thr Asp Val Asp Ile Asp Lys Val
1 5 10

<210> 1673
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1673
Ser Thr Ala Gly Ala Ser Asn
1 5

<210> 1674
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1674
Tyr Phe Leu Ser Arg Thr Asn Thr Thr Ser Gly Ile Glu Thr Gln Ser
1 5 10 15

Thr Leu Arg Phe Ser Gln Ala Gly
20

<210> 1675
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1675
Ser Lys Thr Asp Gly Glu Asn Asn Asn Ser Asp Phe Ser
1 5 10

<210> 1676
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1676
Lys Gln Gly Ala Ala Ala Asp Asp Val Glu Ile Asp Gly Val
1 5 10

<210> 1677
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1677
Ser Glu Ala Gly Ala Ser Asn
1 5

<210> 1678
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1678
Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser
1   5   10   15

Arg Leu Gln Phe Ser Gln Ala Gly
            20

<210> 1679
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1679
Ser Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser
1   5   10

<210> 1680
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1680
Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val
1   5   10

<210> 1681
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1681
Tyr Phe Leu Ser Arg Thr Asn Asp Ala Ser Gly Ser Asp Thr Lys Ser
1   5   10   15

Thr Leu Leu Phe Ser Gln Ala Gly
            20

<210> 1682
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1682
Ser Thr Thr Pro Ser Glu Asn Asn Asn Ser Glu Tyr Ser
1   5   10

<210> 1683
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1683
Ser Ala Ala Gly Ala Thr Asn
1   5

<210> 1684
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 1684
Tyr Phe Leu Ser Arg Thr Asn Gly Glu Ala Gly Ser Ala Thr Leu Ser
1   5   10   15

Glu Leu Arg Phe Ser Gln Ala Gly

<210> 1685
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1685
His Gly Asp Asp Ala Asp Arg Phe
1 5

<210> 1686
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1686
Lys Gln Gly Ala Glu Lys Ser Asp Val Glu Val Asp Arg Val
1 5 10

<210> 1687
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1687
Lys Gln Asp Ser Gly Gly Asp Asn Ile Asp Ile Asp Gln Val
1 5 10

<210> 1688
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1688
Ser Asp Ala Gly Ala Ser Asn
1 5

<210> 1689
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1689
Tyr Phe Leu Ser Arg Thr Asn Thr Glu Gly Gly His Asp Thr Gln Ser
1 5 10 15

Thr Leu Arg Phe Ser Gln Ala Gly
20

<210> 1690
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1690
Lys Glu Asp Gly Gly Gly Ser Asp Val Ala Ile Asp Glu Val
1 5 10

<210> 1691
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1691
Ser Asn Ala Gly Ala Ser Asn
1 5

<210> 1692
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1692
Tyr Phe Leu Ser Arg Thr Asn Gly Glu Ala Gly Ser Ala Thr Leu Ser
1 5 10 15

Glu Leu Arg Phe Ser Gln Pro Gly
20

<210> 1693
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1693
agcvvmdcag garscascaa c 21

<210> 1694
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1694

aacracrrsm rsmaggca 18

<210> 1695
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1695
cacrrggacr rcrmsrrsar sttt 24

<210> 1696
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (35)..(35)
<223> a, c, g, or t

<400> 1696
tatttcttga gcagaacaaa crvcvvsrsc ggamncvhsa cgmhstcavv scttvdsttt 60

tctcagsbcr gsgcg 75

<210> 1697
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base

<222> (11)..(11)
<223> a, c, g, or t

<400> 1697
tcaamammav nsrvcsrsaa caacaacagt rasttctcgt ggmmagga 48

<210> 1698
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (31)..(31)
<223> a, c, g, or t

<400> 1698
aagsaarrcr scrvsrvarv cratrycgms nhcrvmvrsg tc 42

<210> 1699
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<220>
<221> modified_base
<222> (17)..(17)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (32)..(32)
<223> a, c, g, or t

<400> 1699
cagvvsvvsm rsrvcvnsgc agctdhcvvs rnsgtcvmsa ca 42

<210> 1700
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1700
aactwcrvsv asmvsvhsdd tgtgswstks act 33

<210> 1701
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1701
ttgttgaaca tcaccacgtg acgcacgttc 30

<210> 1702
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1702
tccccgtggt tctactacat aatgtggccg 30

<210> 1703
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1703
ttccacactc cgttttggat aatgttgaac 30

<210> 1704
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1704
agggacatcc ccagctccat gctgtggtcg 30

<210> 1705
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1705
agggacaacc cctccgactc gccctaatcc 30

<210> 1706
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1706
tcctagtaga agacaccctc tcactgcccg 30

<210> 1707
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1707
agtaccatgt acacccactc tcccagtgcc 30

<210> 1708
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1708
atatggacgt tcatgctgat caccataccg 30

<210> 1709
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1709
agcaggagct ccttggcctc agcgtgcgag 30

<210> 1710
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1710
acaagcagct tcactatgac aaccactgac 30

<210> 1711
<211> 284

<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> modified_base
<222> (59)..(59)
<223> a, c, g, or t

<220>
<221> modified_base
<222> (244)..(244)
<223> a, c, g, or t

<400> 1711
cagcctagga actggcttcc tggaccctgt taccgccagc agagagtctc aamammavns 60

rvcsrsaaca acaacagtra sttctcctgg mmaggagcta ccaagtacca cctcaatggc 120

agagactctc tggtgaatcc cggaccagct atggcaagcc acrrggacrr crmsrrsars 180

ttttttcctc agagcggggt tctcatcttt gggaagsaar rcrscrvsrv arvcratryc 240

gmsnhcrvmv rsgtcatgat tacagacgaa gaggagatct ggac 284

<210> 1712
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1712
tgggacaatg gcggtcgtct ctcagagttk tkkt 34

<210> 1713
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1713
agaggacckk tcctcgatgg ttcatggtgg agtta 35

<210> 1714
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1714
ccacttaggg cctggtcgat accgttcggt g 31

<210> 1715
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1715
tctcgcccca agagtagaaa cccttcstty yg 32

<210> 1716
<211> 735
<212> PRT
<213> Adeno-associated virus 2

<400> 1716
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

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Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255
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Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
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Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670
```

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Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210> 1717
<211> 736
<212> PRT
<213> Adeno-associated virus 9

<400> 1717
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
```

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        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

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                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
```

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    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 1718

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1718
Gly Ser Thr Pro Pro Pro Met
1 5

<210> 1719
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1719
Gly Glu Thr Arg Ala Pro Leu
1 5

<210> 1720
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 1720
Ser Pro Ala Lys Phe Ala
1 5

<210> 1721
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 1721
Asn Lys Asp Lys Leu Asn
1 5

<210> 1722
<211> 18
<212> PRT
<213> Homo sapiens

<400> 1722
Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
1 5 10 15

Gln Ala

<210> 1723
<211> 44
<212> PRT
<213> Homo sapiens

<400> 1723
Met Ser Ser Gly Ala Ser Arg Lys Ser Trp Asp Pro Gly Asn Pro Trp
1 5 10 15

Pro Pro Asp Trp Pro Ile Thr Gly Arg Lys Met Lys Val Leu Trp Ala
20 25 30

Ala Leu Leu Val Thr Phe Leu Ala Gly Cys Gln Ala
35 40

<210> 1724
<211> 317
<212> PRT
<213> Homo sapiens

<400> 1724
Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
1 5 10 15

Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu
20 25 30

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Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu
        35                  40                  45

Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln
    50                  55                  60

Val Gln Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala
65                  70                  75                  80

Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu
                85                  90                  95

Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser
            100                 105                 110

Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp
        115                 120                 125

Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu
    130                 135                 140

Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg
145                 150                 155                 160

Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg
                165                 170                 175

Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu
            180                 185                 190

Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val
        195                 200                 205

Arg Ala Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg
    210                 215                 220

Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly
225                 230                 235                 240
```

Ser Arg Thr Arg Asp Arg Leu Asp Glu Val Lys Glu Gln Val Ala Glu
245 250 255

Val Arg Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala
260 265 270

Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu
275 280 285

Asp Met Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala
290 295 300

Val Gly Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His
305 310 315

<210> 1725
<211> 299
<212> PRT
<213> Homo sapiens

<400> 1725
Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln
1 5 10 15

Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg
20 25 30

Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln
35 40 45

Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met
50 55 60

Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu
65 70 75 80

Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu
85 90 95

Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys

100 105 110

Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln
115 120 125

Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu
130 135 140

Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala
145 150 155 160

Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala
165 170 175

Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val Arg Ala
180 185 190

Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg Ala Gln
195 200 205

Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly Ser Arg
210 215 220

Thr Arg Asp Arg Leu Asp Glu Val Lys Glu Gln Val Ala Glu Val Arg
225 230 235 240

Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala Glu Ala
245 250 255

Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu Asp Met
260 265 270

Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala Val Gly
275 280 285

Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His
290 295

<210> 1726

<211> 216
<212> PRT
<213> Homo sapiens

<400> 1726

```
Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
1               5                  10                  15

Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu
            20                  25                  30

Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu
        35                  40                  45

Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln
    50                  55                  60

Val Gln Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala
65                  70                  75                  80

Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu
                85                  90                  95

Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser
            100                 105                 110

Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp
        115                 120                 125

Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu
    130                 135                 140

Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg
145                 150                 155                 160

Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg
                165                 170                 175

Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu
            180                 185                 190
```

```
Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val
        195                 200                 205


Arg Ala Ala Thr Val Gly Ser Leu
    210                 215


<210> 1727
<211> 198
<212> PRT
<213> Homo sapiens

<400> 1727
Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln
1               5                   10                  15


Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg
            20                  25                  30


Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln
        35                  40                  45


Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met
    50                  55                  60


Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu
65                  70                  75                  80


Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu
                85                  90                  95


Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys
            100                 105                 110


Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln
        115                 120                 125


Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu
    130                 135                 140


Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala
```

145 150 155 160

Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala
165 170 175

Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val Arg Ala
180 185 190

Ala Thr Val Gly Ser Leu
195

<210> 1728
<211> 269
<212> PRT
<213> Homo sapiens

<400> 1728
Met Ser Ser Gly Ala Ser Arg Lys Ser Trp Asp Pro Gly Asn Pro Trp
1 5 10 15

Pro Pro Asp Trp Pro Ile Thr Gly Arg Lys Met Lys Val Leu Trp Ala
20 25 30

Ala Leu Leu Val Thr Phe Leu Ala Gly Cys Gln Ala Lys Val Glu Gln
35 40 45

Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln Gln Thr Glu Trp
50 55 60

Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg Phe Trp Asp Tyr
65 70 75 80

Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln Glu Glu Leu Leu
85 90 95

Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met Asp Glu Thr Met
100 105 110

Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu Gln Leu Thr Pro
115 120 125

```
Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu Leu Gln Ala Ala
    130                 135                 140


Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys Gly Arg Leu Val
145                 150                 155                 160


Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln Ser Thr Glu Glu
                165                 170                 175


Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu Arg Lys Arg Leu
            180                 185                 190


Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala Val Tyr Gln Ala
        195                 200                 205


Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala Ile Arg Glu Arg
    210                 215                 220


Leu Gly Pro Leu Val Glu Gln Gly Arg Val Arg Ala Ala Thr Val Gly
225                 230                 235                 240


Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg Ala Gln Ala Trp Gly Glu
                245                 250                 255


Arg Leu Arg Ala Arg Met Glu Glu Met Gly Ser Arg Thr
            260                 265


<210> 1729
<211> 225
<212> PRT
<213> Homo sapiens

<400> 1729
Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln
1               5                   10                  15


Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg
            20                  25                  30


Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln
```

35 40 45

Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met
50 55 60

Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu
65 70 75 80

Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu
85 90 95

Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys
100 105 110

Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln
115 120 125

Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu
130 135 140

Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala
145 150 155 160

Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala
165 170 175

Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val Arg Ala
180 185 190

Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg Ala Gln
195 200 205

Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly Ser Arg
210 215 220

Thr
225

<210> 1730

<211> 219
<212> PRT
<213> Homo sapiens

<400> 1730

```
Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys
1               5                  10                  15

Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu
            20                  25                  30

Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu
        35                  40                  45

Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln
    50                  55                  60

Val Gln Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala
65                  70                  75                  80

Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu
                85                  90                  95

Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser
            100                 105                 110

Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp
        115                 120                 125

Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu
    130                 135                 140

Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg
145                 150                 155                 160

Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg
                165                 170                 175

Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu
            180                 185                 190
```

```
Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val
        195                 200                 205


Arg Ala Ala Thr Val Gly Ser Leu Ala Gly Gln
    210                 215


<210> 1731
<211> 201
<212> PRT
<213> Homo sapiens

<400> 1731
Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln
1               5                   10                  15


Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg
            20                  25                  30


Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln
        35                  40                  45


Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met
    50                  55                  60


Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu
65                  70                  75                  80


Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu
                85                  90                  95


Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys
            100                 105                 110


Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln
        115                 120                 125


Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu
    130                 135                 140


Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala
```

145 150 155 160

Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala
165 170 175

Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val Arg Ala
180 185 190

Ala Thr Val Gly Ser Leu Ala Gly Gln
195 200

<210> 1732
<211> 343
<212> PRT
<213> Homo sapiens

<400> 1732
Met Ser Ser Gly Ala Ser Arg Lys Ser Trp Asp Pro Gly Asn Pro Trp
1 5 10 15

Pro Pro Asp Trp Pro Ile Thr Gly Arg Lys Met Lys Val Leu Trp Ala
20 25 30

Ala Leu Leu Val Thr Phe Leu Ala Gly Cys Gln Ala Lys Val Glu Gln
35 40 45

Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln Gln Thr Glu Trp
50 55 60

Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg Phe Trp Asp Tyr
65 70 75 80

Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln Glu Glu Leu Leu
85 90 95

Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met Asp Glu Thr Met
100 105 110

Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu Gln Leu Thr Pro
115 120 125

```
Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu Leu Gln Ala Ala
    130                 135                 140

Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys Gly Arg Leu Val
145                 150                 155                 160

Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln Ser Thr Glu Glu
                165                 170                 175

Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu Arg Lys Arg Leu
            180                 185                 190

Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala Val Tyr Gln Ala
        195                 200                 205

Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala Ile Arg Glu Arg
    210                 215                 220

Leu Gly Pro Leu Val Glu Gln Gly Arg Val Arg Ala Ala Thr Val Gly
225                 230                 235                 240

Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg Ala Gln Ala Trp Gly Glu
                245                 250                 255

Arg Leu Arg Ala Arg Met Glu Glu Met Gly Ser Arg Thr Arg Asp Arg
            260                 265                 270

Leu Asp Glu Val Lys Glu Gln Val Ala Glu Val Arg Ala Lys Leu Glu
        275                 280                 285

Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala Glu Ala Phe Gln Ala Arg
    290                 295                 300

Leu Lys Ser Trp Phe Glu Pro Leu Val Glu Asp Met Gln Arg Gln Trp
305                 310                 315                 320

Ala Gly Leu Val Glu Lys Val Gln Ala Ala Val Gly Thr Ser Ala Ala
                325                 330                 335
```

```
Pro Val Pro Ser Asp Asn His
            340


<210> 1733
<211> 299
<212> PRT
<213> Homo sapiens

<400> 1733
Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu Arg Gln
1               5                   10                  15


Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu Gly Arg
            20                  25                  30


Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln Val Gln
        35                  40                  45


Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala Leu Met
    50                  55                  60


Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu Glu Glu
65                  70                  75                  80


Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu
                85                  90                  95


Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp Val Cys
            100                 105                 110


Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln
        115                 120                 125


Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu
    130                 135                 140


Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg Leu Ala
145                 150                 155                 160


Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu Ser Ala
```

165 170 175

Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val Arg Ala
180 185 190

Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg Ala Gln
195 200 205

Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly Ser Arg
210 215 220

Thr Arg Asp Arg Leu Asp Glu Val Lys Glu Gln Val Ala Glu Val Arg
225 230 235 240

Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala Glu Ala
245 250 255

Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu Asp Met
260 265 270

Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala Val Gly
275 280 285

Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His
290 295

<210> 1734
<211> 1208
<212> DNA
<213> Homo sapiens

<400> 1734
agggggagcc ctataattgg acaagtctgg gatccttgag tcctactcag ccccagcgga 60

ggtgaaggac gtccttcccc aggagccgac tggccaatca caggcaggaa gatgaaggtt 120

ctgtgggctg cgttgctggt cacattcctg gcaggatgcc aggccaaggt ggagcaagcg 180

gtggagacag agccggagcc cgagctgcgc cagcagaccg agtggcagag cggccagcgc 240

tgggaactgg cactgggtcg cttttgggat tacctgcgct gggtgcagac actgtctgag 300

caggtgcagg aggagctgct cagctcccag gtcacccagg aactgagggc gctgatggac 360

gagaccatga aggagttgaa ggcctacaaa tcggaactgg aggaacaact gaccccggtg 420

gcggaggaga cgcgggcacg gctgtccaag gagctgcagg cggcgcaggc ccggctgggc 480

gcggacatgg aggacgtgtg cggccgcctg gtgcagtacc gcggcgaggt gcaggccatg 540

ctcggccaga gcaccgagga gctgcgggtg cgcctcgcct cccacctgcg caagctgcgt 600

aagcggctcc tccgcgatgc cgatgacctg cagaagcgcc tggcagtgta ccaggccggg 660

gcccgcgagg gcgccgagcg cggcctcagc gccatccgcg agcgcctggg gcccctggtg 720

gaacagggcc gcgtgcgggc cgccactgtg ggctccctgg ccggccagcc gctacaggag 780

cgggcccagg cctggggcga gcggctgcgc gcgcggatgg aggagatggg cagccggacc 840

cgcgaccgcc tggacgaggt gaaggagcag gtggcggagg tgcgcgccaa gctggaggag 900

caggcccagc agatacgcct gcaggccgag gccttccagg cccgcctcaa gagctggttc 960

gagcccctgg tggaagacat gcagcgccag tgggccgggc tggtggagaa ggtgcaggct 1020

gccgtgggca ccagcgccgc ccctgtgccc agcgacaatc actgaacgcc gaagcctgca 1080

gccatgcgac cccacgccac cccgtgcctc ctgcctccgc gcagcctgca gcgggagacc 1140

ctgtccccgc cccagccgtc ctcctggggt ggaccctagt ttaataaaga ttcaccaagt 1200

ttcacgca 1208

<210> 1735
<211> 954
<212> DNA
<213> Homo sapiens

<400> 1735
atgaaggttc tgtgggctgc gttgctggtc acattcctgg caggatgcca ggccaaggtg 60

gagcaagcgg tggagacaga gccggagccc gagctgcgcc agcagaccga gtggcagagc 120

ggccagcgct gggaactggc actgggtcgc ttttgggatt acctgcgctg ggtgcagaca 180

ctgtctgagc aggtgcagga ggagctgctc agctcccagg tcacccagga actgagggcg 240

ctgatggacg agaccatgaa ggagttgaag gcctacaaat cggaactgga ggaacaactg 300

accccggtgg cggaggagac gcgggcacgg ctgtccaagg agctgcaggc ggcgcaggcc 360

cggctgggcg cggacatgga ggacgtgtgc ggccgcctgg tgcagtaccg cggcgaggtg 420

caggccatgc tcggccagag caccgaggag ctgcgggtgc gcctcgcctc ccacctgcgc 480

aagctgcgta agcggctcct ccgcgatgcc gatgacctgc agaagcgcct ggcagtgtac 540

caggccgggg cccgcgaggg cgccgagcgc ggcctcagcg ccatccgcga gcgcctgggg 600

cccctggtgg aacagggccg cgtgcgggcc gccactgtgg gctccctggc cggccagccg 660

ctacaggagc gggcccaggc ctggggcgag cggctgcgcg cgcggatgga ggagatgggc 720

agccggaccc gcgaccgcct ggacgaggtg aaggagcagg tggcggaggt gcgcgccaag 780

ctggaggagc aggcccagca gatacgcctg caggccgagg ccttccaggc ccgcctcaag 840

agctggttcg agcccctggt ggaagacatg cagcgccagt gggccgggct ggtggagaag 900

gtgcaggctg ccgtgggcac cagcgccgcc cctgtgccca gcgacaatca ctga 954

<210> 1736
<211> 737
<212> DNA
<213> Homo sapiens

<400> 1736
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cattcctggc aggatgccag gccaaggtgg agcaagcggt ggagacagag ccggagcccg 180

agctgcgcca gcagaccgag tggcagagcg gccagcgctg ggaactggca ctgggtcgct 240

tttgggatta cctgcgctgg gtgcagacac tgtctgagca ggtgcaggag gagctgctca 300

gctcccaggt cacccaggaa ctgagggcgc tgatggacga gaccatgaag gagttgaagg 360

cctacaaatc ggaactggag gaacaactga ccccggtggc ggaggagacg cgggcacggc 420

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atgacctgca gaagcgcctg gcagtgtacc aggccggggc ccgcgagggc gccgagcgcg 660

gcctcagcgc catccgcgag cgcctggggc ccctggtgga acagggccgc gtgcgggccg 720

ccactgtggg ctccctg 737

<210> 1737
<211> 771
<212> DNA
<213> Homo sapiens

<400> 1737
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gcggggcttg ctcggttccc cccgctcctc cccctctcat cctcacctca acctcctggc 180

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aacagcgatt tgacgctctc tgggcctcgg tttcccccat ccttgagata ggagttagaa 300

gttgttttgt tgttgttgtt tgttgttgtt gttttgtttt tttgagatga agtctcgctc 360

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tacaggcgtg agccaccgca cctggctggg agttagaggt ttctaatgca ttgcaggcag 660

atagtgaata ccagacacgg ggcagctgtg atctttattc tccatcaccc ccacacagcc 720

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<210> 1738
<211> 864
<212> DNA
<213> Homo sapiens

<400> 1738
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atcacaggca ggaagatgaa ggttctgtgg gctgcgttgc tggtcacatt cctggcagga 180

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cgctgggtgc agacactgtc tgagcaggtg caggaggagc tgctcagctc ccaggtcacc 360

caggaactga gggcgctgat ggacgagacc atgaaggagt tgaaggccta caaatcggaa 420

ctggaggaac aactgacccc ggtggcggag gagacgcggg cacggctgtc caaggagctg 480

caggcggcgc aggcccggct gggcgcggac atggaggacg tgtgcggccg cctggtgcag 540

taccgcggcg aggtgcaggc catgctcggc cagagcaccg aggagctgcg ggtgcgcctc 600

gcctcccacc tgcgcaagct gcgtaagcgg ctcctccgcg atgccgatga cctgcagaag 660

cgcctggcag tgtaccaggc cggggcccgc gagggcgccg agcgcggcct cagcgccatc 720

cgcgagcgcc tggggccccct ggtggaacag ggccgcgtgc gggccgccac tgtgggctcc 780

ctggccggcc agccgctaca ggagcgggcc caggcctggg gcgagcggct gcgcgcgcgg 840

atggaggaga tgggcagccg gacc 864

<210> 1739
<211> 923
<212> DNA
<213> Homo sapiens

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gaccaggagg gagttaaata gggaatgggt tgggggcggc ttggtaaatg tgctgggatt 120

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ccaggtcacc caggaactga gggcgctgat ggacgagacc atgaaggagt tgaaggccta 540

caaatcggaa ctggaggaac aactgacccc ggtggcggag gagacgcggg cacggctgtc 600

caaggagctg caggcggcgc aggcccggct gggcgcggac atggaggacg tgtgcggccg 660

cctggtgcag taccgcggcg aggtgcaggc catgctcggc cagagcaccg aggagctgcg 720

ggtgcgcctc gcctcccacc tgcgcaagct gcgtaagcgg ctcctccgcg atgccgatga 780

cctgcagaag cgcctggcag tgtaccaggc cggggcccgc gagggcgccg agcgcggcct 840

cagcgccatc cgcgagcgcc tggggcccct ggtggaacag ggccgcgtgc gggccgccac 900

tgtgggctcc ctggccggcc agc 923

<210> 1740
<211> 1234
<212> DNA
<213> Homo sapiens

<400> 1740
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aggttctgtg ggctgcgttg ctggtcacat tcctggcagg atgccaggcc aaggtggagc 180

aagcggtgga gacagagccg gagcccgagc tgcgccagca gaccgagtgg cagagcggcc 240

agcgctggga actggcactg ggtcgctttt gggattacct gcgctgggtg cagacactgt 300

ctgagcaggt gcaggaggag ctgctcagct cccaggtcac ccaggaactg agggcgctga 360

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cggtggcgga ggagacgcgg gcacggctgt ccaaggagct gcaggcggcg caggcccggc 480

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caagtttcac gcatcaaaaa aaaaaaaaaa aaaa 1234

<210> 1741
<211> 1165
<212> DNA
<213> Homo sapiens

<400> 1741
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agacagagcc ggagcccgag ctgcgccagc agaccgagtg gcagagcggc cagcgctggg 180

aactggcact gggtcgcttt tgggattacc tgcgctgggt gcagacactg tctgagcagg 240

tgcaggagga gctgctcagc tcccaggtca cccaggaact gagggcgctg atggacgaga 300

ccatgaagga gttgaaggcc tacaaatcgg aactggagga acaactgacc ccggtggcgg 360

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ccctggtgga agacatgcag cgccagtggg ccgggctggt ggagaaggtg caggctgccg 960

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tgcgacccca cgccaccccg tgcctcctgc ctccgcgcag cctgcagcgg gagaccctgt 1080

ccccgcccca gccgtcctcc tggggtggac cctagtttaa taaagattca ccaagtttca 1140

cgcatcaaaa aaaaaaaaaa aaaaa 1165

<210> 1742
<211> 1265
<212> DNA

<213> Homo sapiens

<400> 1742
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tggtaaatgt gctgggatta ggctgttgca gataatgcaa caaggcttgg aaggctaacc 120

tgggactggc caatcacagg caggaagatg aaggttctgt gggctgcgtt gctggtcaca 180

ttcctggcag gatgccaggc caaggtggag caagcggtgg agacagagcc ggagcccgag 240

ctgcgccagc agaccgagtg gcagagcggc cagcgctggg aactggcact gggtcgcttt 300

tgggattacc tgcgctgggt gcagacactg tctgagcagg tgcaggagga gctgctcagc 360

tcccaggtca cccaggaact gagggcgctg atggacgaga ccatgaagga gttgaaggcc 420

tacaaatcgg aactggagga acaactgacc ccggtggcgg aggagacgcg ggcacggctg 480

tccaaggagc tgcaggcggc gcaggcccgg ctgggcgcgg acatggagga cgtgtgcggc 540

cgcctggtgc agtaccgcgg cgaggtgcag gccatgctcg gccagagcac cgaggagctg 600

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tgcctcctgc ctccgcgcag cctgcagcgg gagaccctgt ccccgcccca gccgtcctcc 1200

tggggtggac cctagtttaa taaagattca ccaagtttca cgcatcaaaa aaaaaaaaaa 1260

aaaaa 1265

<210> 1743
<211> 1249
<212> DNA
<213> Homo sapiens

<400> 1743
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caggcaggaa gatgaaggtt ctgtgggctg cgttgctggt cacattcctg gcaggatgcc 180

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aggaacaact gaccccggtg gcggaggaga cgcgggcacg gctgtccaag gagctgcagg 480

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agcgcctggg gcccctggtg gaacagggcc gcgtgcgggc cgccactgtg ggctccctgg 780

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<210> 1744
<211> 1316
<212> DNA
<213> Homo sapiens

<400> 1744
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ctgcaggcgg cgcaggcccg gctgggcgcg gacatggagg acgtgtgcgg ccgcctggtg 600

cagtaccgcg gcgaggtgca ggccatgctc ggccagagca ccgaggagct gcgggtgcgc 660

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ccctagttta ataaagattc accaagtttc acgcatcaaa aaaaaaaaaa aaaaaa 1316

<210> 1745
<211> 210
<212> PRT
<213> Homo sapiens

<400> 1745
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1 5 10 15

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Ser Pro Ala Gln Ala Gln Thr Leu Thr Arg Val Pro Arg Pro Ala Glu
            20                  25                  30

Leu Ala Pro Leu Cys Gly Arg Arg Gly Leu Arg Thr Asp Ile Asp Ala
        35                  40                  45

Thr Cys Thr Pro Arg Arg Ala Ser Ser Asn Gln Arg Gly Leu Asn Gln
    50                  55                  60

Ile Trp Asn Val Lys Lys Gln Ser Val Tyr Leu Met Asn Leu Arg Lys
65                  70                  75                  80

Ser Gly Thr Leu Gly His Pro Gly Ser Leu Asp Glu Thr Thr Tyr Glu
                85                  90                  95

Arg Leu Ala Glu Glu Thr Leu Asp Ser Leu Ala Glu Phe Phe Glu Asp
            100                 105                 110

Leu Ala Asp Lys Pro Tyr Thr Phe Glu Asp Tyr Asp Val Ser Phe Gly
        115                 120                 125

Ser Gly Val Leu Thr Val Lys Leu Gly Gly Asp Leu Gly Thr Tyr Val
    130                 135                 140

Ile Asn Lys Gln Thr Pro Asn Lys Gln Ile Trp Leu Ser Ser Pro Ser
145                 150                 155                 160

Ser Gly Pro Lys Arg Tyr Asp Trp Thr Gly Lys Asn Trp Val Tyr Ser
                165                 170                 175

His Asp Gly Val Ser Leu His Glu Leu Leu Ala Ala Glu Leu Thr Lys
            180                 185                 190

Ala Leu Lys Thr Lys Leu Asp Leu Ser Ser Leu Ala Tyr Ser Gly Lys
        195                 200                 205

Asp Ala
    210
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<210> 1746
<211> 196
<212> PRT
<213> Homo sapiens

<400> 1746
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Ser Pro Ala Gln Ala Gln Thr Leu Thr Arg Val Pro Arg Pro Ala Glu
            20   25   30

Leu Ala Pro Leu Cys Gly Arg Arg Gly Leu Arg Thr Asp Ile Asp Ala
        35   40   45

Thr Cys Thr Pro Arg Arg Ala Ser Ser Asn Gln Arg Gly Leu Asn Gln
    50   55   60

Ile Trp Asn Val Lys Lys Gln Ser Val Tyr Leu Met Asn Leu Arg Lys
65   70   75   80

Ser Gly Thr Leu Gly His Pro Gly Ser Leu Asp Glu Thr Thr Tyr Glu
                85   90   95

Arg Leu Ala Glu Glu Thr Leu Asp Ser Leu Ala Glu Phe Phe Glu Asp
            100   105   110

Leu Ala Asp Lys Pro Tyr Thr Phe Glu Asp Tyr Asp Val Ser Phe Gly
        115   120   125

Ser Gly Val Leu Thr Val Lys Leu Gly Gly Asp Leu Gly Thr Tyr Val
    130   135   140

Ile Asn Lys Gln Thr Pro Asn Lys Gln Ile Trp Leu Ser Ser Pro Ser
145   150   155   160

Arg Tyr Val Val Asp Leu Ser Val Met Thr Gly Leu Gly Lys Thr Gly
                165   170   175

```
Cys Thr Pro Thr Thr Ala Cys Pro Ser Met Ser Cys Trp Pro Gln Ser
            180                 185                 190


Ser Leu Lys Pro
        195


<210> 1747
<211> 171
<212> PRT
<213> Homo sapiens

<400> 1747
Met Trp Thr Leu Gly Arg Arg Ala Val Ala Gly Leu Leu Ala Ser Pro
1               5                  10                  15


Ser Pro Ala Gln Ala Gln Thr Leu Thr Arg Val Pro Arg Pro Ala Glu
            20                  25                  30


Leu Ala Pro Leu Cys Gly Arg Arg Gly Leu Arg Thr Asp Ile Asp Ala
        35                  40                  45


Thr Cys Thr Pro Arg Arg Ala Ser Ser Asn Gln Arg Gly Leu Asn Gln
    50                  55                  60


Ile Trp Asn Val Lys Lys Gln Ser Val Tyr Leu Met Asn Leu Arg Lys
65                  70                  75                  80


Ser Gly Thr Leu Gly His Pro Gly Ser Leu Asp Glu Thr Thr Tyr Glu
                85                  90                  95


Arg Leu Ala Glu Glu Thr Leu Asp Ser Leu Ala Glu Phe Phe Glu Asp
            100                 105                 110


Leu Ala Asp Lys Pro Tyr Thr Phe Glu Asp Tyr Asp Val Ser Phe Gly
        115                 120                 125


Ser Gly Val Leu Thr Val Lys Leu Gly Gly Asp Leu Gly Thr Tyr Val
    130                 135                 140


Ile Asn Lys Gln Thr Pro Asn Lys Gln Ile Trp Leu Ser Ser Pro Ser
145                 150                 155                 160
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Arg Leu Thr Trp Leu Leu Trp Leu Phe His Pro
165 170

<210> 1748
<211> 7168
<212> DNA
<213> Homo sapiens

<400> 1748
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atttttgtta aatgcacgaa tagtgctaag ctgggaagtt cttcctgagg tctaacctct 120

agctgctccc ccacagaaga gtgcctgcgg ccagtggcca ccaggggtcg ccgcagcacc 180

cagcgctgga gggcggagcg ggcggcagac ccggagcagc atgtggactc tcgggcgccg 240

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gcagacgcca aacaagcaaa tctggctatc ttctccatcc agtggaccta agcgttatga 720

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cagcttcatt atgcagctga ggtctgtttt ttgttgttgt tgttgtttat ttttttatt 960

cctgcttttg aggacagttg ggctatgtgt cacagctctg tagaaagaat gtgttgcctc 1020

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Ala Ile Gly Cys Ile Gly Phe Ser Trp Ala Ala Ser Pro Ala Cys Thr

100 105 110

Glu Leu Glu Thr Val Met Met Asp Trp Leu Gly Lys Met Leu Glu Leu
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Pro Lys Ala Phe Leu Asn Glu Lys Ala Gly Glu Gly Gly Gly Val Ile
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Gln Gly Ser Ala Ser Glu Ala Thr Leu Val Ala Leu Leu Ala Ala Arg
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Thr Lys Val Ile His Arg Leu Gln Ala Ala Ser Pro Glu Leu Thr Gln
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Ile Pro Ser Asp Gly Asn Phe Ala Met Arg Ala Ser Ala Leu Gln Glu
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Ala Leu Glu Arg Asp Lys Ala Ala Gly Leu Ile Pro Phe Phe Met Val
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Ala Thr Leu Gly Thr Thr Thr Cys Cys Ser Phe Asp Asn Leu Leu Glu
245 250 255

Val Gly Pro Ile Cys Asn Lys Glu Asp Ile Trp Leu His Val Asp Ala
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Asn Gly Val Glu Phe Ala Asp Ser Phe Asn Phe Asn Pro His Lys Trp
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Leu Leu Val Asn Phe Asp Cys Ser Ala Met Trp Val Lys Lys Arg Thr

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Asp Leu Thr Gly Ala Phe Arg Leu Asp Pro Thr Tyr Leu Lys His Ser
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His Gln Asp Ser Gly Leu Ile Thr Asp Tyr Arg His Trp Gln Ile Pro
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Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg Met
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Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln Leu
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Ser His Glu Phe Glu Ser Leu Val Arg Gln Asp Pro Arg Phe Glu Ile
385 390 395 400

Cys Val Glu Val Ile Leu Gly Leu Val Cys Phe Arg Leu Lys Gly Ser
405 410 415

Asn Lys Val Asn Glu Ala Leu Leu Gln Arg Ile Asn Ser Ala Lys Lys
420 425 430

Ile His Leu Val Pro Cys His Leu Arg Asp Lys Phe Val Leu Arg Phe
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<212> PRT
<213> Homo sapiens

<400> 1755
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            20   25   30

Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Pro
        35   40   45

Pro Pro Pro Gln Leu Pro Gln Pro Pro Pro Gln Ala Gln Pro Leu Leu
    50   55   60

Pro Gln Pro Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Pro
65   70   75   80

Ala Val Ala Glu Glu Pro Leu His Arg Pro Lys Lys Glu Leu Ser Ala
                85   90   95

Thr Lys Lys Asp Arg Val Asn His Cys Leu Thr Ile Cys Glu Asn Ile
            100   105   110

Val Ala Gln Ser Val Arg Asn Ser Pro Glu Phe Gln Lys Leu Leu Gly
        115   120   125

Ile Ala Met Glu Leu Phe Leu Leu Cys Ser Asp Asp Ala Glu Ser Asp
    130   135   140

Val Arg Met Val Ala Asp Glu Cys Leu Asn Lys Val Ile Lys Ala Leu
145   150   155   160

Met Asp Ser Asn Leu Pro Arg Leu Gln Leu Glu Leu Tyr Lys Glu Ile
                165   170   175

Lys Lys Asn Gly Ala Pro Arg Ser Leu Arg Ala Ala Leu Trp Arg Phe
            180   185   190

Ala Glu Leu Ala His Leu Val Arg Pro Gln Lys Cys Arg Pro Tyr Leu
        195   200   205

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Val Asn Leu Leu Pro Cys Leu Thr Arg Thr Ser Lys Arg Pro Glu Glu
    210                 215                 220

Ser Val Gln Glu Thr Leu Ala Ala Ala Val Pro Lys Ile Met Ala Ser
225                 230                 235                 240

Phe Gly Asn Phe Ala Asn Asp Asn Glu Ile Lys Val Leu Leu Lys Ala
                245                 250                 255

Phe Ile Ala Asn Leu Lys Ser Ser Ser Pro Thr Ile Arg Arg Thr Ala
            260                 265                 270

Ala Gly Ser Ala Val Ser Ile Cys Gln His Ser Arg Arg Thr Gln Tyr
        275                 280                 285

Phe Tyr Ser Trp Leu Leu Asn Val Leu Leu Gly Leu Leu Val Pro Val
    290                 295                 300

Glu Asp Glu His Ser Thr Leu Leu Ile Leu Gly Val Leu Leu Thr Leu
305                 310                 315                 320

Arg Tyr Leu Val Pro Leu Leu Gln Gln Gln Val Lys Thr Ser Leu Lys
                325                 330                 335

Gly Ser Phe Gly Val Thr Arg Lys Glu Met Glu Val Ser Pro Ser Ala
            340                 345                 350

Glu Gln Leu Val Gln Val Tyr Glu Leu Thr Leu His His Thr Gln His
        355                 360                 365

Gln Asp His Asn Val Val Thr Gly Ala Leu Glu Leu Leu Gln Gln Leu
    370                 375                 380

Phe Arg Thr Pro Pro Pro Glu Leu Leu Gln Thr Leu Thr Ala Val Gly
385                 390                 395                 400

Gly Ile Gly Gln Leu Thr Ala Ala Lys Glu Glu Ser Gly Gly Arg Ser
                405                 410                 415
```

```
Arg Ser Gly Ser Ile Val Glu Leu Ile Ala Gly Gly Gly Ser Ser Cys
            420                 425                 430

Ser Pro Val Leu Ser Arg Lys Gln Lys Gly Lys Val Leu Leu Gly Glu
        435                 440                 445

Glu Glu Ala Leu Glu Asp Asp Ser Glu Ser Arg Ser Asp Val Ser Ser
    450                 455                 460

Ser Ala Leu Thr Ala Ser Val Lys Asp Glu Ile Ser Gly Glu Leu Ala
465                 470                 475                 480

Ala Ser Ser Gly Val Ser Thr Pro Gly Ser Ala Gly His Asp Ile Ile
                485                 490                 495

Thr Glu Gln Pro Arg Ser Gln His Thr Leu Gln Ala Asp Ser Val Asp
            500                 505                 510

Leu Ala Ser Cys Asp Leu Thr Ser Ser Ala Thr Asp Gly Asp Glu Glu
        515                 520                 525

Asp Ile Leu Ser His Ser Ser Ser Gln Val Ser Ala Val Pro Ser Asp
    530                 535                 540

Pro Ala Met Asp Leu Asn Asp Gly Thr Gln Ala Ser Ser Pro Ile Ser
545                 550                 555                 560

Asp Ser Ser Gln Thr Thr Thr Glu Gly Pro Asp Ser Ala Val Thr Pro
                565                 570                 575

Ser Asp Ser Ser Glu Ile Val Leu Asp Gly Thr Asp Asn Gln Tyr Leu
            580                 585                 590

Gly Leu Gln Ile Gly Gln Pro Gln Asp Glu Asp Glu Glu Ala Thr Gly
        595                 600                 605

Ile Leu Pro Asp Glu Ala Ser Glu Ala Phe Arg Asn Ser Ser Met Ala
    610                 615                 620
```

```
Leu Gln Gln Ala His Leu Leu Lys Asn Met Ser His Cys Arg Gln Pro
625                 630                 635                 640

Ser Asp Ser Ser Val Asp Lys Phe Val Leu Arg Asp Glu Ala Thr Glu
                645                 650                 655

Pro Gly Asp Gln Glu Asn Lys Pro Cys Arg Ile Lys Gly Asp Ile Gly
            660                 665                 670

Gln Ser Thr Asp Asp Asp Ser Ala Pro Leu Val His Cys Val Arg Leu
        675                 680                 685

Leu Ser Ala Ser Phe Leu Leu Thr Gly Gly Lys Asn Val Leu Val Pro
    690                 695                 700

Asp Arg Asp Val Arg Val Ser Val Lys Ala Leu Ala Leu Ser Cys Val
705                 710                 715                 720

Gly Ala Ala Val Ala Leu His Pro Glu Ser Phe Phe Ser Lys Leu Tyr
                725                 730                 735

Lys Val Pro Leu Thr Thr Glu Tyr Pro Glu Glu Gln Tyr Val Ser Asp
            740                 745                 750

Ile Leu Asn Tyr Ile Asp His Gly Asp Pro Gln Val Arg Gly Ala Thr
        755                 760                 765

Ala Ile Leu Cys Gly Thr Leu Ile Cys Ser Ile Leu Ser Arg Ser Arg
    770                 775                 780

Phe His Val Gly Asp Trp Met Gly Thr Ile Arg Thr Leu Thr Gly Asn
785                 790                 795                 800

Thr Phe Ser Leu Ala Asp Cys Ile Pro Leu Leu Arg Lys Thr Leu Lys
                805                 810                 815

Asp Glu Ser Ser Val Thr Cys Lys Leu Ala Cys Thr Ala Val Arg Asn
            820                 825                 830
```

```
Cys Val Met Ser Leu Cys Ser Ser Ser Tyr Ser Glu Leu Gly Leu Gln
        835                 840                 845

Leu Ile Ile Asp Val Leu Thr Leu Arg Asn Ser Ser Tyr Trp Leu Val
    850                 855                 860

Arg Thr Glu Leu Leu Glu Thr Leu Ala Glu Ile Asp Phe Arg Leu Val
865                 870                 875                 880

Ser Phe Leu Glu Ala Lys Ala Glu Asn Leu His Arg Gly Ala His His
                885                 890                 895

Tyr Thr Gly Leu Leu Lys Leu Gln Glu Arg Val Leu Asn Asn Val Val
            900                 905                 910

Ile His Leu Leu Gly Asp Glu Asp Pro Arg Val Arg His Val Ala Ala
        915                 920                 925

Ala Ser Leu Ile Arg Leu Val Pro Lys Leu Phe Tyr Lys Cys Asp Gln
    930                 935                 940

Gly Gln Ala Asp Pro Val Val Ala Val Ala Arg Asp Gln Ser Ser Val
945                 950                 955                 960

Tyr Leu Lys Leu Leu Met His Glu Thr Gln Pro Pro Ser His Phe Ser
                965                 970                 975

Val Ser Thr Ile Thr Arg Ile Tyr Arg Gly Tyr Asn Leu Leu Pro Ser
            980                 985                 990

Ile Thr Asp Val Thr Met Glu Asn  Asn Leu Ser Arg Val  Ile Ala Ala
        995                 1000                1005

Val Ser  His Glu Leu Ile Thr  Ser Thr Thr Arg Ala  Leu Thr Phe
    1010                1015                1020

Gly Cys  Cys Glu Ala Leu Cys  Leu Leu Ser Thr Ala  Phe Pro Val
    1025                1030                1035
```

```
Cys Ile  Trp Ser Leu Gly Trp  His Cys Gly Val Pro  Pro Leu Ser
    1040                1045                1050

Ala Ser  Asp Glu Ser Arg Lys  Ser Cys Thr Val Gly  Met Ala Thr
    1055                1060                1065

Met Ile  Leu Thr Leu Leu Ser  Ser Ala Trp Phe Pro  Leu Asp Leu
    1070                1075                1080

Ser Ala  His Gln Asp Ala Leu  Ile Leu Ala Gly Asn  Leu Leu Ala
    1085                1090                1095

Ala Ser  Ala Pro Lys Ser Leu  Arg Ser Ser Trp Ala  Ser Glu Glu
    1100                1105                1110

Glu Ala  Asn Pro Ala Ala Thr  Lys Gln Glu Glu Val  Trp Pro Ala
    1115                1120                1125

Leu Gly  Asp Arg Ala Leu Val  Pro Met Val Glu Gln  Leu Phe Ser
    1130                1135                1140

His Leu  Leu Lys Val Ile Asn  Ile Cys Ala His Val  Leu Asp Asp
    1145                1150                1155

Val Ala  Pro Gly Pro Ala Ile  Lys Ala Ala Leu Pro  Ser Leu Thr
    1160                1165                1170

Asn Pro  Pro Ser Leu Ser Pro  Ile Arg Arg Lys Gly  Lys Glu Lys
    1175                1180                1185

Glu Pro  Gly Glu Gln Ala Ser  Val Pro Leu Ser Pro  Lys Lys Gly
    1190                1195                1200

Ser Glu  Ala Ser Ala Ala Ser  Arg Gln Ser Thr Ser  Gly Pro Val
    1205                1210                1215

Thr Thr  Ser Lys Ser Ser Ser  Leu Gly Ser Phe Tyr  His Leu Pro
    1220                1225                1230
```

```
Ser Tyr  Leu Lys Leu His Asp  Val Leu Lys Ala Thr  His Ala Asn
    1235                1240                1245

Tyr Lys  Val Thr Leu Asp Leu  Gln Asn Ser Thr Glu  Lys Phe Gly
    1250                1255                1260

Gly Phe  Leu Arg Ser Ala Leu  Asp Val Leu Ser Gln  Ile Leu Glu
    1265                1270                1275

Leu Ala  Thr Leu Gln Asp Ile  Gly Lys Cys Val Glu  Glu Ile Leu
    1280                1285                1290

Gly Tyr  Leu Lys Ser Cys Phe  Ser Arg Glu Pro Met  Met Ala Thr
    1295                1300                1305

Val Cys  Val Gln Gln Leu Leu  Lys Thr Leu Phe Gly  Thr Asn Leu
    1310                1315                1320

Ala Ser  Gln Phe Asp Gly Leu  Ser Ser Asn Pro Ser  Lys Ser Gln
    1325                1330                1335

Gly Arg  Ala Gln Arg Leu Gly  Ser Ser Ser Val Arg  Pro Gly Leu
    1340                1345                1350

Tyr His  Tyr Cys Phe Met Ala  Pro Tyr Thr His Phe  Thr Gln Ala
    1355                1360                1365

Leu Ala  Asp Ala Ser Leu Arg  Asn Met Val Gln Ala  Glu Gln Glu
    1370                1375                1380

Asn Thr  Ser Gly Trp Phe Asp  Val Leu Gln Lys Val  Ser Thr Gln
    1385                1390                1395

Leu Lys  Thr Asn Leu Thr Ser  Val Thr Lys Asn Arg  Ala Asp Lys
    1400                1405                1410

Asn Ala  Ile His Asn His Ile  Arg Leu Phe Glu Pro  Leu Val Ile
    1415                1420                1425
```

```
Lys Ala  Leu Lys Gln Tyr Thr  Thr Thr Thr Cys Val  Gln Leu Gln
    1430                1435                1440

Lys Gln  Val Leu Asp Leu Leu  Ala Gln Leu Val Gln  Leu Arg Val
    1445                1450                1455

Asn Tyr  Cys Leu Leu Asp Ser  Asp Gln Val Phe Ile  Gly Phe Val
    1460                1465                1470

Leu Lys  Gln Phe Glu Tyr Ile  Glu Val Gly Gln Phe  Arg Glu Ser
    1475                1480                1485

Glu Ala  Ile Ile Pro Asn Ile  Phe Phe Phe Leu Val  Leu Leu Ser
    1490                1495                1500

Tyr Glu  Arg Tyr His Ser Lys  Gln Ile Ile Gly Ile  Pro Lys Ile
    1505                1510                1515

Ile Gln  Leu Cys Asp Gly Ile  Met Ala Ser Gly Arg  Lys Ala Val
    1520                1525                1530

Thr His  Ala Ile Pro Ala Leu  Gln Pro Ile Val His  Asp Leu Phe
    1535                1540                1545

Val Leu  Arg Gly Thr Asn Lys  Ala Asp Ala Gly Lys  Glu Leu Glu
    1550                1555                1560

Thr Gln  Lys Glu Val Val Val  Ser Met Leu Leu Arg  Leu Ile Gln
    1565                1570                1575

Tyr His  Gln Val Leu Glu Met  Phe Ile Leu Val Leu  Gln Gln Cys
    1580                1585                1590

His Lys  Glu Asn Glu Asp Lys  Trp Lys Arg Leu Ser  Arg Gln Ile
    1595                1600                1605

Ala Asp  Ile Ile Leu Pro Met  Leu Ala Lys Gln Gln  Met His Ile
    1610                1615                1620
```

```
Asp Ser  His Glu Ala Leu Gly  Val Leu Asn Thr Leu  Phe Glu Ile
    1625                1630                1635

Leu Ala  Pro Ser Ser Leu Arg  Pro Val Asp Met Leu  Leu Arg Ser
    1640                1645                1650

Met Phe  Val Thr Pro Asn Thr  Met Ala Ser Val Ser  Thr Val Gln
    1655                1660                1665

Leu Trp  Ile Ser Gly Ile Leu  Ala Ile Leu Arg Val  Leu Ile Ser
    1670                1675                1680

Gln Ser  Thr Glu Asp Ile Val  Leu Ser Arg Ile Gln  Glu Leu Ser
    1685                1690                1695

Phe Ser  Pro Tyr Leu Ile Ser  Cys Thr Val Ile Asn  Arg Leu Arg
    1700                1705                1710

Asp Gly  Asp Ser Thr Ser Thr  Leu Glu Glu His Ser  Glu Gly Lys
    1715                1720                1725

Gln Ile  Lys Asn Leu Pro Glu  Glu Thr Phe Ser Arg  Phe Leu Leu
    1730                1735                1740

Gln Leu  Val Gly Ile Leu Leu  Glu Asp Ile Val Thr  Lys Gln Leu
    1745                1750                1755

Lys Val  Glu Met Ser Glu Gln  Gln His Thr Phe Tyr  Cys Gln Glu
    1760                1765                1770

Leu Gly  Thr Leu Leu Met Cys  Leu Ile His Ile Phe  Lys Ser Gly
    1775                1780                1785

Met Phe  Arg Arg Ile Thr Ala  Ala Ala Thr Arg Leu  Phe Arg Ser
    1790                1795                1800

Asp Gly  Cys Gly Gly Ser Phe  Tyr Thr Leu Asp Ser  Leu Asn Leu
    1805                1810                1815
```

```
Arg Ala  Arg Ser Met Ile Thr  Thr His Pro Ala Leu  Val Leu Leu
    1820                 1825                 1830

Trp Cys  Gln Ile Leu Leu Leu  Val Asn His Thr Asp  Tyr Arg Trp
    1835                 1840                 1845

Trp Ala  Glu Val Gln Gln Thr  Pro Lys Arg His Ser  Leu Ser Ser
    1850                 1855                 1860

Thr Lys  Leu Leu Ser Pro Gln  Met Ser Gly Glu Glu  Glu Asp Ser
    1865                 1870                 1875

Asp Leu  Ala Ala Lys Leu Gly  Met Cys Asn Arg Glu  Ile Val Arg
    1880                 1885                 1890

Arg Gly  Ala Leu Ile Leu Phe  Cys Asp Tyr Val Cys  Gln Asn Leu
    1895                 1900                 1905

His Asp  Ser Glu His Leu Thr  Trp Leu Ile Val Asn  His Ile Gln
    1910                 1915                 1920

Asp Leu  Ile Ser Leu Ser His  Glu Pro Pro Val Gln  Asp Phe Ile
    1925                 1930                 1935

Ser Ala  Val His Arg Asn Ser  Ala Ala Ser Gly Leu  Phe Ile Gln
    1940                 1945                 1950

Ala Ile  Gln Ser Arg Cys Glu  Asn Leu Ser Thr Pro  Thr Met Leu
    1955                 1960                 1965

Lys Lys  Thr Leu Gln Cys Leu  Glu Gly Ile His Leu  Ser Gln Ser
    1970                 1975                 1980

Gly Ala  Val Leu Thr Leu Tyr  Val Asp Arg Leu Leu  Cys Thr Pro
    1985                 1990                 1995

Phe Arg  Val Leu Ala Arg Met  Val Asp Ile Leu Ala  Cys Arg Arg
    2000                 2005                 2010
```

```
Val Glu  Met Leu Leu Ala Ala  Asn Leu Gln Ser Ser  Met Ala Gln
    2015                 2020                 2025

Leu Pro  Met Glu Glu Leu Asn  Arg Ile Gln Glu Tyr  Leu Gln Ser
    2030                 2035                 2040

Ser Gly  Leu Ala Gln Arg His  Gln Arg Leu Tyr Ser  Leu Leu Asp
    2045                 2050                 2055

Arg Phe  Arg Leu Ser Thr Met  Gln Asp Ser Leu Ser  Pro Ser Pro
    2060                 2065                 2070

Pro Val  Ser Ser His Pro Leu  Asp Gly Asp Gly His  Val Ser Leu
    2075                 2080                 2085

Glu Thr  Val Ser Pro Asp Lys  Asp Trp Tyr Val His  Leu Val Lys
    2090                 2095                 2100

Ser Gln  Cys Trp Thr Arg Ser  Asp Ser Ala Leu Leu  Glu Gly Ala
    2105                 2110                 2115

Glu Leu  Val Asn Arg Ile Pro  Ala Glu Asp Met Asn  Ala Phe Met
    2120                 2125                 2130

Met Asn  Ser Glu Phe Asn Leu  Ser Leu Leu Ala Pro  Cys Leu Ser
    2135                 2140                 2145

Leu Gly  Met Ser Glu Ile Ser  Gly Gly Gln Lys Ser  Ala Leu Phe
    2150                 2155                 2160

Glu Ala  Ala Arg Glu Val Thr  Leu Ala Arg Val Ser  Gly Thr Val
    2165                 2170                 2175

Gln Gln  Leu Pro Ala Val His  His Val Phe Gln Pro  Glu Leu Pro
    2180                 2185                 2190

Ala Glu  Pro Ala Ala Tyr Trp  Ser Lys Leu Asn Asp  Leu Phe Gly
    2195                 2200                 2205
```

```
Asp Ala  Ala Leu Tyr Gln Ser  Leu Pro Thr Leu Ala  Arg Ala Leu
    2210                 2215                 2220

Ala Gln  Tyr Leu Val Val Val  Ser Lys Leu Pro Ser  His Leu His
    2225                 2230                 2235

Leu Pro  Pro Glu Lys Glu Lys  Asp Ile Val Lys Phe  Val Val Ala
    2240                 2245                 2250

Thr Leu  Glu Ala Leu Ser Trp  His Leu Ile His Glu  Gln Ile Pro
    2255                 2260                 2265

Leu Ser  Leu Asp Leu Gln Ala  Gly Leu Asp Cys Cys  Cys Leu Ala
    2270                 2275                 2280

Leu Gln  Leu Pro Gly Leu Trp  Ser Val Val Ser Ser  Thr Glu Phe
    2285                 2290                 2295

Val Thr  His Ala Cys Ser Leu  Ile Tyr Cys Val His  Phe Ile Leu
    2300                 2305                 2310

Glu Ala  Val Ala Val Gln Pro  Gly Glu Gln Leu Leu  Ser Pro Glu
    2315                 2320                 2325

Arg Arg  Thr Asn Thr Pro Lys  Ala Ile Ser Glu Glu  Glu Glu Glu
    2330                 2335                 2340

Val Asp  Pro Asn Thr Gln Asn  Pro Lys Tyr Ile Thr  Ala Ala Cys
    2345                 2350                 2355

Glu Met  Val Ala Glu Met Val  Glu Ser Leu Gln Ser  Val Leu Ala
    2360                 2365                 2370

Leu Gly  His Lys Arg Asn Ser  Gly Val Pro Ala Phe  Leu Thr Pro
    2375                 2380                 2385

Leu Leu  Arg Asn Ile Ile Ile  Ser Leu Ala Arg Leu  Pro Leu Val
    2390                 2395                 2400
```

```
Asn Ser  Tyr Thr Arg Val Pro  Pro Leu Val Trp Lys  Leu Gly Trp
    2405                 2410                 2415

Ser Pro  Lys Pro Gly Gly Asp  Phe Gly Thr Ala Phe  Pro Glu Ile
    2420                 2425                 2430

Pro Val  Glu Phe Leu Gln Glu  Lys Glu Val Phe Lys  Glu Phe Ile
    2435                 2440                 2445

Tyr Arg  Ile Asn Thr Leu Gly  Trp Thr Ser Arg Thr  Gln Phe Glu
    2450                 2455                 2460

Glu Thr  Trp Ala Thr Leu Leu  Gly Val Leu Val Thr  Gln Pro Leu
    2465                 2470                 2475

Val Met  Glu Gln Glu Glu Ser  Pro Pro Glu Glu Thr  Glu Arg Thr
    2480                 2485                 2490

Gln Ile  Asn Val Leu Ala Val  Gln Ala Ile Thr Ser  Leu Val Leu
    2495                 2500                 2505

Ser Ala  Met Thr Val Pro Val  Ala Gly Asn Pro Ala  Val Ser Cys
    2510                 2515                 2520

Leu Glu  Gln Gln Pro Arg Asn  Lys Pro Leu Lys Ala  Leu Thr Arg
    2525                 2530                 2535

Phe Gly  Arg Lys Leu Ser Ile  Ile Arg Gly Ile Val  Glu Gln Glu
    2540                 2545                 2550

Ile Gln  Ala Met Val Ser Lys  Arg Glu Asn Ile Ala  Thr His His
    2555                 2560                 2565

Leu Tyr  Gln Ala Trp Asp Pro  Val Pro Ser Leu Ser  Pro Ala Thr
    2570                 2575                 2580

Thr Gly  Ala Leu Ile Ser His  Glu Lys Leu Leu Leu  Gln Ile Asn
    2585                 2590                 2595
```

```
Pro Glu  Arg Glu Leu Gly Ser  Met Ser Tyr Lys Leu  Gly Gln Val
    2600                 2605                 2610

Ser Ile  His Ser Val Trp Leu  Gly Asn Ser Ile Thr  Pro Leu Arg
    2615                 2620                 2625

Glu Glu  Glu Trp Asp Glu Glu  Glu Glu Glu Glu Ala  Asp Ala Pro
    2630                 2635                 2640

Ala Pro  Ser Ser Pro Pro Thr  Ser Pro Val Asn Ser  Arg Lys His
    2645                 2650                 2655

Arg Ala  Gly Val Asp Ile His  Ser Cys Ser Gln Phe  Leu Leu Glu
    2660                 2665                 2670

Leu Tyr  Ser Arg Trp Ile Leu  Pro Ser Ser Ser Ala  Arg Arg Thr
    2675                 2680                 2685

Pro Ala  Ile Leu Ile Ser Glu  Val Val Arg Ser Leu  Leu Val Val
    2690                 2695                 2700

Ser Asp  Leu Phe Thr Glu Arg  Asn Gln Phe Glu Leu  Met Tyr Val
    2705                 2710                 2715

Thr Leu  Thr Glu Leu Arg Arg  Val His Pro Ser Glu  Asp Glu Ile
    2720                 2725                 2730

Leu Ala  Gln Tyr Leu Val Pro  Ala Thr Cys Lys Ala  Ala Ala Val
    2735                 2740                 2745

Leu Gly  Met Asp Lys Ala Val  Ala Glu Pro Val Ser  Arg Leu Leu
    2750                 2755                 2760

Glu Ser  Thr Leu Arg Ser Ser  His Leu Pro Ser Arg  Val Gly Ala
    2765                 2770                 2775

Leu His  Gly Val Leu Tyr Val  Leu Glu Cys Asp Leu  Leu Asp Thr
    2780                 2785                 2790
```

```
Ala Lys  Gln Leu Ile Pro Val  Ile Ser Asp Tyr Leu  Leu Ser Asn
    2795                 2800                 2805

Leu Lys  Gly Ile Ala His Cys  Val Asn Ile His Ser  Gln Gln His
    2810                 2815                 2820

Val Leu  Val Met Cys Ala Thr  Ala Phe Tyr Leu Ile  Glu Asn Tyr
    2825                 2830                 2835

Pro Leu  Asp Val Gly Pro Glu  Phe Ser Ala Ser Ile  Ile Gln Met
    2840                 2845                 2850

Cys Gly  Val Met Leu Ser Gly  Ser Glu Glu Ser Thr  Pro Ser Ile
    2855                 2860                 2865

Ile Tyr  His Cys Ala Leu Arg  Gly Leu Glu Arg Leu  Leu Leu Ser
    2870                 2875                 2880

Glu Gln  Leu Ser Arg Leu Asp  Ala Glu Ser Leu Val  Lys Leu Ser
    2885                 2890                 2895

Val Asp  Arg Val Asn Val His  Ser Pro His Arg Ala  Met Ala Ala
    2900                 2905                 2910

Leu Gly  Leu Met Leu Thr Cys  Met Tyr Thr Gly Lys  Glu Lys Val
    2915                 2920                 2925

Ser Pro  Gly Arg Thr Ser Asp  Pro Asn Pro Ala Ala  Pro Asp Ser
    2930                 2935                 2940

Glu Ser  Val Ile Val Ala Met  Glu Arg Val Ser Val  Leu Phe Asp
    2945                 2950                 2955

Arg Ile  Arg Lys Gly Phe Pro  Cys Glu Ala Arg Val  Val Ala Arg
    2960                 2965                 2970

Ile Leu  Pro Gln Phe Leu Asp  Asp Phe Phe Pro Pro  Gln Asp Ile
    2975                 2980                 2985
```

```
Met Asn  Lys Val Ile Gly Glu  Phe Leu Ser Asn Gln  Gln Pro Tyr
    2990                 2995                 3000

Pro Gln  Phe Met Ala Thr Val  Val Tyr Lys Val Phe  Gln Thr Leu
    3005                 3010                 3015

His Ser  Thr Gly Gln Ser Ser  Met Val Arg Asp Trp  Val Met Leu
    3020                 3025                 3030

Ser Leu  Ser Asn Phe Thr Gln  Arg Ala Pro Val Ala  Met Ala Thr
    3035                 3040                 3045

Trp Ser  Leu Ser Cys Phe Phe  Val Ser Ala Ser Thr  Ser Pro Trp
    3050                 3055                 3060

Val Ala  Ala Ile Leu Pro His  Val Ile Ser Arg Met  Gly Lys Leu
    3065                 3070                 3075

Glu Gln  Val Asp Val Asn Leu  Phe Cys Leu Val Ala  Thr Asp Phe
    3080                 3085                 3090

Tyr Arg  His Gln Ile Glu Glu  Glu Leu Asp Arg Arg  Ala Phe Gln
    3095                 3100                 3105

Ser Val  Leu Glu Val Val Ala  Ala Pro Gly Ser Pro  Tyr His Arg
    3110                 3115                 3120

Leu Leu  Thr Cys Leu Arg Asn  Val His Lys Val Thr  Thr Cys
    3125                 3130                 3135


<210> 1756
<211> 758
<212> PRT
<213> Homo sapiens

<400> 1756
Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1               5                  10                  15
```

```
Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65                  70                  75                  80

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
                85                  90                  95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
            100                 105                 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Glu Pro Glu Ser
        115                 120                 125

Gly Lys Val Val Gln Glu Gly Phe Leu Arg Glu Pro Gly Pro Pro Gly
    130                 135                 140

Leu Ser His Gln Leu Met Ser Gly Met Pro Gly Ala Pro Leu Leu Pro
145                 150                 155                 160

Glu Gly Pro Arg Glu Ala Thr Arg Gln Pro Ser Gly Thr Gly Pro Glu
                165                 170                 175

Asp Thr Glu Gly Gly Arg His Ala Pro Glu Leu Leu Lys His Gln Leu
            180                 185                 190

Leu Gly Asp Leu His Gln Glu Gly Pro Pro Leu Lys Gly Ala Gly Gly
        195                 200                 205

Lys Glu Arg Pro Gly Ser Lys Glu Glu Val Asp Glu Asp Arg Asp Val
    210                 215                 220
```

```
Asp Glu Ser Ser Pro Gln Asp Ser Pro Pro Ser Lys Ala Ser Pro Ala
225                 230                 235                 240


Gln Asp Gly Arg Pro Pro Gln Thr Ala Ala Arg Glu Ala Thr Ser Ile
                245                 250                 255


Pro Gly Phe Pro Ala Glu Gly Ala Ile Pro Leu Pro Val Asp Phe Leu
            260                 265                 270


Ser Lys Val Ser Thr Glu Ile Pro Ala Ser Glu Pro Asp Gly Pro Ser
        275                 280                 285


Val Gly Arg Ala Lys Gly Gln Asp Ala Pro Leu Glu Phe Thr Phe His
    290                 295                 300


Val Glu Ile Thr Pro Asn Val Gln Lys Glu Gln Ala His Ser Glu Glu
305                 310                 315                 320


His Leu Gly Arg Ala Ala Phe Pro Gly Ala Pro Gly Glu Gly Pro Glu
                325                 330                 335


Ala Arg Gly Pro Ser Leu Gly Glu Asp Thr Lys Glu Ala Asp Leu Pro
            340                 345                 350


Glu Pro Ser Glu Lys Gln Pro Ala Ala Ala Pro Arg Gly Lys Pro Val
        355                 360                 365


Ser Arg Val Pro Gln Leu Lys Ala Arg Met Val Ser Lys Ser Lys Asp
    370                 375                 380


Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Thr Ser Thr Arg Ser Ser
385                 390                 395                 400


Ala Lys Thr Leu Lys Asn Arg Pro Cys Leu Ser Pro Lys His Pro Thr
                405                 410                 415


Pro Gly Ser Ser Asp Pro Leu Ile Gln Pro Ser Ser Pro Ala Val Cys
            420                 425                 430
```

```
Pro Glu Pro Pro Ser Ser Pro Lys Tyr Val Ser Ser Val Thr Ser Arg
        435                 440                 445

Thr Gly Ser Ser Gly Ala Lys Glu Met Lys Leu Lys Gly Ala Asp Gly
    450                 455                 460

Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys
465                 470                 475                 480

Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro
                485                 490                 495

Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly Asp Arg Ser
            500                 505                 510

Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser Arg Ser Arg
        515                 520                 525

Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys Lys Val Ala
    530                 535                 540

Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser Arg Leu
545                 550                 555                 560

Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys Ser Lys
                565                 570                 575

Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly Lys Val
            580                 585                 590

Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser Lys Cys
        595                 600                 605

Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser Val Gln
    610                 615                 620

Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys Cys Gly
625                 630                 635                 640
```

Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val Glu Val
645 650 655

Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys Ile Gly
660 665 670

Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys Lys Ile
675 680 685

Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp
690 695 700

His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser Gly Asp Thr
705 710 715 720

Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile Asp Met
725 730 735

Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val Ser Ala Ser
740 745 750

Leu Ala Lys Gln Gly Leu
755

<210> 1757
<211> 441
<212> PRT
<213> Homo sapiens

<400> 1757
Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1 5 10 15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
20 25 30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
35 40 45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
50 55 60

```
Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65                  70                  75                  80

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
                85                  90                  95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
            100                 105                 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
        115                 120                 125

Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
    130                 135                 140

Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145                 150                 155                 160

Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
                165                 170                 175

Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
            180                 185                 190

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
        195                 200                 205

Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
    210                 215                 220

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225                 230                 235                 240

Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
                245                 250                 255

Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
            260                 265                 270
```

```
Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
        275                 280                 285

Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
    290                 295                 300

Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
305                 310                 315                 320

Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln
                325                 330                 335

Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
            340                 345                 350

Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn
        355                 360                 365

Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala
    370                 375                 380

Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
385                 390                 395                 400

Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser
                405                 410                 415

Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val
            420                 425                 430

Ser Ala Ser Leu Ala Lys Gln Gly Leu
        435                 440
```

<210> 1758
<211> 383
<212> PRT
<213> Homo sapiens

<400> 1758

```
Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1               5                  10                  15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Ala Glu Glu Ala
        35                  40                  45

Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val
    50                  55                  60

Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp
65                  70                  75                  80

Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro
                85                  90                  95

Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg
            100                 105                 110

Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly
        115                 120                 125

Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser
    130                 135                 140

Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro
145                 150                 155                 160

Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys
                165                 170                 175

Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met
            180                 185                 190

Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu
        195                 200                 205
```

```
Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu
    210                 215                 220

Asp Leu Ser Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys
225                 230                 235                 240

His Val Pro Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val Asp
                245                 250                 255

Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His
            260                 265                 270

Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe
        275                 280                 285

Lys Asp Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His
    290                 295                 300

Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe
305                 310                 315                 320

Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr
                325                 330                 335

Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn
            340                 345                 350

Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala
        355                 360                 365

Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
    370                 375                 380


<210> 1759
<211> 352
<212> PRT
<213> Homo sapiens

<400> 1759
Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1               5                   10                  15
```

```
Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Ala Glu Glu Ala
        35                  40                  45

Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val
    50                  55                  60

Thr Gln Ala Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp
65                  70                  75                  80

Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro
                85                  90                  95

Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg
            100                 105                 110

Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly
        115                 120                 125

Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser
    130                 135                 140

Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro
145                 150                 155                 160

Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys
                165                 170                 175

Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met
            180                 185                 190

Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu
        195                 200                 205

Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Val Tyr Lys Pro Val
    210                 215                 220
```

```
Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His
225                 230                 235                 240


His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp
                245                 250                 255


Phe Lys Asp Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr
            260                 265                 270


His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr
        275                 280                 285


Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val
    290                 295                 300


Tyr Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser
305                 310                 315                 320


Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu
                325                 330                 335


Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
            340                 345                 350


<210> 1760
<211> 412
<212> PRT
<213> Homo sapiens

<400> 1760
Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1               5                   10                  15


Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30


Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45
```

```
Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Ala Glu Glu Ala Gly Ile Gly
65                  70                  75                  80

Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala
                85                  90                  95

Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys
            100                 105                 110

Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala
        115                 120                 125

Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala
    130                 135                 140

Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro
145                 150                 155                 160

Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr
                165                 170                 175

Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg
            180                 185                 190

Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser
        195                 200                 205

Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu
    210                 215                 220

Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln
225                 230                 235                 240

Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser
                245                 250                 255
```

```
Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro
            260                 265                 270

Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys
        275                 280                 285

Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly
    290                 295                 300

Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg
305                 310                 315                 320

Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly
                325                 330                 335

Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn
            340                 345                 350

Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro
        355                 360                 365

Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser
    370                 375                 380

Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala
385                 390                 395                 400

Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
                405                 410


<210> 1761
<211> 776
<212> PRT
<213> Homo sapiens

<400> 1761
Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1               5                   10                  15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30
```

```
Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65                  70                  75                  80

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
                85                  90                  95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
            100                 105                 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Glu Pro Glu Ser
        115                 120                 125

Gly Lys Val Val Gln Glu Gly Phe Leu Arg Glu Pro Gly Pro Pro Gly
    130                 135                 140

Leu Ser His Gln Leu Met Ser Gly Met Pro Gly Ala Pro Leu Leu Pro
145                 150                 155                 160

Glu Gly Pro Arg Glu Ala Thr Arg Gln Pro Ser Gly Thr Gly Pro Glu
                165                 170                 175

Asp Thr Glu Gly Gly Arg His Ala Pro Glu Leu Leu Lys His Gln Leu
            180                 185                 190

Leu Gly Asp Leu His Gln Glu Gly Pro Pro Leu Lys Gly Ala Gly Gly
        195                 200                 205

Lys Glu Arg Pro Gly Ser Lys Glu Glu Val Asp Glu Asp Arg Asp Val
    210                 215                 220

Asp Glu Ser Ser Pro Gln Asp Ser Pro Pro Ser Lys Ala Ser Pro Ala
225                 230                 235                 240
```

```
Gln Asp Gly Arg Pro Pro Gln Thr Ala Ala Arg Glu Ala Thr Ser Ile
                245                 250                 255

Pro Gly Phe Pro Ala Glu Gly Ala Ile Pro Leu Pro Val Asp Phe Leu
            260                 265                 270

Ser Lys Val Ser Thr Glu Ile Pro Ala Ser Glu Pro Asp Gly Pro Ser
        275                 280                 285

Val Gly Arg Ala Lys Gly Gln Asp Ala Pro Leu Glu Phe Thr Phe His
    290                 295                 300

Val Glu Ile Thr Pro Asn Val Gln Lys Glu Gln Ala His Ser Glu Glu
305                 310                 315                 320

His Leu Gly Arg Ala Ala Phe Pro Gly Ala Pro Gly Glu Gly Pro Glu
                325                 330                 335

Ala Arg Gly Pro Ser Leu Gly Glu Asp Thr Lys Glu Ala Asp Leu Pro
            340                 345                 350

Glu Pro Ser Glu Lys Gln Pro Ala Ala Ala Pro Arg Gly Lys Pro Val
        355                 360                 365

Ser Arg Val Pro Gln Leu Lys Ala Arg Met Val Ser Lys Ser Lys Asp
    370                 375                 380

Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Thr Ser Thr Arg Ser Ser
385                 390                 395                 400

Ala Lys Thr Leu Lys Asn Arg Pro Cys Leu Ser Pro Lys His Pro Thr
                405                 410                 415

Pro Gly Ser Ser Asp Pro Leu Ile Gln Pro Ser Ser Pro Ala Val Cys
            420                 425                 430

Pro Glu Pro Pro Ser Ser Pro Lys Tyr Val Ser Ser Val Thr Ser Arg
        435                 440                 445
```

```
Thr Gly Ser Ser Gly Ala Lys Glu Met Lys Leu Lys Gly Ala Asp Gly
    450                 455                 460

Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys
465                 470                 475                 480

Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro
                485                 490                 495

Lys Thr Pro Pro Ser Ser Ala Thr Lys Gln Val Gln Arg Arg Pro Pro
            500                 505                 510

Pro Ala Gly Pro Arg Ser Glu Arg Gly Glu Pro Pro Lys Ser Gly Asp
        515                 520                 525

Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser Arg
    530                 535                 540

Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys Lys
545                 550                 555                 560

Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser
                565                 570                 575

Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys
            580                 585                 590

Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly
        595                 600                 605

Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser
    610                 615                 620

Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser
625                 630                 635                 640

Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys
                645                 650                 655
```

```
Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val
            660                 665                 670

Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys
        675                 680                 685

Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys
    690                 695                 700

Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys
705                 710                 715                 720

Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser Gly
                725                 730                 735

Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile
            740                 745                 750

Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val Ser
        755                 760                 765

Ala Ser Leu Ala Lys Gln Gly Leu
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<212> PRT
<213> Homo sapiens

<400> 1762
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Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45
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Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Ala Glu Glu Ala Gly Ile Gly
65                  70                  75                  80

Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala
                85                  90                  95

Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys
            100                 105                 110

Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala
        115                 120                 125

Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala
    130                 135                 140

Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro
145                 150                 155                 160

Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr
                165                 170                 175

Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg
            180                 185                 190

Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser
        195                 200                 205

Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu
    210                 215                 220

Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln
225                 230                 235                 240

Pro Gly Gly Gly Lys Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser
                245                 250                 255
```

```
Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro
            260                 265                 270


Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp
        275                 280                 285


Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro
    290                 295                 300


Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu
305                 310                 315                 320


Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser
                325                 330                 335


Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser
            340                 345                 350


Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu
        355                 360                 365


Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
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<211> 410
<212> PRT
<213> Homo sapiens

<400> 1763
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Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30


Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45


Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60
```

```
Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65                  70                  75                  80

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
                85                  90                  95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
            100                 105                 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
        115                 120                 125

Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
    130                 135                 140

Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145                 150                 155                 160

Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
                165                 170                 175

Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
            180                 185                 190

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
        195                 200                 205

Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
    210                 215                 220

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225                 230                 235                 240

Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
                245                 250                 255

Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
            260                 265                 270
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```
Gly Lys Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr
        275                 280                 285

Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly
    290                 295                 300

Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln
305                 310                 315                 320

Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly
                325                 330                 335

Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys
            340                 345                 350

Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val
        355                 360                 365

Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly
    370                 375                 380

Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu
385                 390                 395                 400

Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
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<212> DNA
<213> Homo sapiens

<400> 1764

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<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

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gggcaccagu cagcuacccu ggugggaauc uggguagcc 99

<210> 1796
<211> 54
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1796
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<210> 1797
<211> 35
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1797
cugaggagcg ccuugacagc agccauggga gggcc 35

<210> 1798
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 1798
cugcggagcg ccuugacagc agccauggga gggccgcccc cuaccucagu ga 52

<210> 1799
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 1799

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aggggttcct tgtagttaat gattaacccg ccatgctact tatctaccag ggtaatgggg 180

atcctctaga actatagcta gtcgacattg attattgact agttattaat agtaatcaat 240

tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 300

tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 360

tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta 420

aactgcccac ttggcagtac atcaagtgta tcatatgcca agtacgcccc ctattgacgt 480

caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 540

tacttggcag tacatctacg tattagtcat cgctattacc atgtcgaggc cacgttctgc 600

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ttattttgtg cagcgatggg ggcgggggg gggggcgcgc gccaggcggg gcggggcggg 720

gcgaggggcg gggcggggcg aggcggagag gtgcggcggc agccaatcag agcggcgcgc 780

tccgaaagtt tccttttatg gcgaggcggc ggcggcggcg gccctataaa aagcgaagcg 840

cgcggcgggc gggagcaagc tttattgcgg tagtttatca cagttaaatt gctaacgcag 900

tcagtgcttc tgacacaaca gtctcgaact taagctgcag aagttggtcg tgaggcactg 960

ggcaggtaag tatcaaggtt acaagacagg tttaaggaga ccaatagaaa ctgggcttgt 1020

cgagacagag aagactcttg cgtttctgat aggcacctat tggtcttact gacatccact 1080

ttgcctttct ctccacaggt gtccactccc agttcaatta cagctcttaa ggctagagta 1140

cttaatacga ctcactatag gctagtaata cgactcacta tagatggtga gcaagggcga 1200

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gttcatctgc accaccggca agctgcccgt gccctggccc accctcgtga ccaccctgac 1380

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gtccgccatg cccgaaggct acgtccagga gcgcaccatc ttcttcaagg acgacggcaa 1500

ctacaagacc cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc gcatcgagct 1560

gaagggcatc gacttcaagg aggacggcaa catcctgggg cacaagctgg agtacaacta 1620

caacagccac aacgtctata tcatggccga caagcagaag aacggcatca aggtgaactt 1680

caagatccgc cacaacatcg aggacggcag cgtgcagctc gccgaccact accagcagaa 1740

cacccccatc ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcacccagtc 1800

cgccctgagc aaagacccca acgagaagcg cgatcacatg gtcctgctgg agttcgtgac 1860

cgccgccggg atcactctcg gcatggacga gctgtacaag taaagcggcc ctagcgttta 1920

aacgggccct ctagactcga ggacggggtg aactacgcct gaggatccga tctttttccc 1980

tctgccaaaa attatgggga catcatgaag ccccttgagc atctgacttc tggctaataa 2040

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tggcgggtta atcattaact acaaggaacc cctagtgatg gagttggcca ctccctctct 2220

gcgcgctcgc tcgctcactg aggccgggcg accaaaggtc gcccgacgcc cgggctttgc 2280

ccgggcggcc tcagtgagcg agcgagcgcg cag 2313

<210> 1800
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

cagcagctca aggccggaga caacccgtac ctcaagtaca accacgccga cgccgagttc 300

caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctgggggа cagagtcatc 720

accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatc 780

tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

acggtccagg tcttcacgga ctcagactat cagctcccgt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg 1140

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ttaatttttg gcaaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata 1680

accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg 1740

gccacaaacc accagagtga tgggactttg gcggtgcctt ttaaggcaca ggcgcagacc 1800

ggctgggttc aaaaccaagg aatacttccg ggtatggttt ggcaggacag agatgtgtac 1860

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gtacctgcgg atcctccaac ggccttcaac aaggacaagc tgaactcttt catcacccag 2040

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cgctggaacc cggagatcca gtacacttcc aactattaca agtctaataa tgttgaattt 2160

gctgttaata ctgaaggtgt atatagtgaa ccccgcccca ttggcaccag atacctgact 2220

cgtaatctgt aa 2232

<210> 1801
<211> 1984
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1801
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aagatcaatt caattcacgc gtcgacattg attattgact agttattaat agtaatcaat 180

tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240

tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 300

tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta 360

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caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 480

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cgcggcgggc gggagcaagc ttgaactgaa aaaccagaaa gttaactggt aagtttagtc 840

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tctctcactc ggcctaggta gataagtagc atggcgggtt aatcattaac tacaaggaac 1860

ccctagtgat ggagttggcc actccctctc tgcgcgctcg ctcgctcact gaggccgggc 1920

gaccaaaggt cgcccgacgc ccgggctttg cccgggcggc ctcagtgagc gagcgagcgc 1980

gcag 1984

<210> 1802
<211> 2911
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1802

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ttacggggtc attagttcat agcccatata tggagttccg cgttacataa cttacggtaa 300

atggcccgcc tggctgaccg cccaacgacc cccgcccatt gacgtcaata atgacgtatg 360

ttcccatagt aacgccaata gggactttcc attgacgtca atgggtggag tatttacggt 420

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gacaagccat acacctttga ggactatgat gtttcctttg ggagtggtgt cttaactgtt 1860

aaactgggtg gagatctagg aacctacgtg atcaacaagc agacgccaaa caagcaaatc 1920

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tattcccacg acggcgtttc cctccatgag ctgctgggcg cagagctcac taaagcctta 2040

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gtgagcgagc gagcgcgcag ctgcctgcag g 2911

<210> 1803
<211> 997
<212> PRT
<213> Homo sapiens

<400> 1803
Met Glu Asn Ala His Thr Lys Thr Val Glu Glu Val Leu Gly His Phe
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Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys Leu
            20   25   30

Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr
        35   40   45

Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile
    50   55   60

Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
65   70   75   80

Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu
                85   90   95

Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
            100   105   110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
        115   120   125

Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp
    130   135   140

Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro
145   150   155   160

Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp
                165   170   175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp
            180   185   190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
        195   200   205

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Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val
    210                 215                 220

Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val
225                 230                 235                 240

Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe
                245                 250                 255

Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp
            260                 265                 270

Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp
        275                 280                 285

Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val
    290                 295                 300

Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala
305                 310                 315                 320

Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu
                325                 330                 335

Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys
            340                 345                 350

Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile
        355                 360                 365

Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr Ile
    370                 375                 380

Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys
385                 390                 395                 400

Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile
                405                 410                 415
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Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys Gly
            420                 425                 430

Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu
        435                 440                 445

Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys
    450                 455                 460

Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met Lys
465                 470                 475                 480

Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val
                485                 490                 495

Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met Phe
            500                 505                 510

Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile Arg
        515                 520                 525

Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys Ile
    530                 535                 540

Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg Cys
545                 550                 555                 560

Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met His
                565                 570                 575

Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr Phe
            580                 585                 590

Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala Ser
        595                 600                 605

Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile Thr
    610                 615                 620
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Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly Ile
625                 630                 635                 640

Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu
                645                 650                 655

Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn Ala
            660                 665                 670

Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu
        675                 680                 685

Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val
    690                 695                 700

Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly
705                 710                 715                 720

Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp
                725                 730                 735

Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile
            740                 745                 750

Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val
        755                 760                 765

Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu
    770                 775                 780

Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly
785                 790                 795                 800

Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met
                805                 810                 815

Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu
            820                 825                 830
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Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val
        835                 840                 845

Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val
    850                 855                 860

Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro
865                 870                 875                 880

Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met
                885                 890                 895

Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu
            900                 905                 910

Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu
        915                 920                 925

Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe
    930                 935                 940

Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro
945                 950                 955                 960

Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val
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Pro Ala Ile Leu Glu
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Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr
        35                  40                  45

Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile
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Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
65                  70                  75                  80

Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu
                85                  90                  95

Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
            100                 105                 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
        115                 120                 125

Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp
    130                 135                 140

Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro
145                 150                 155                 160

Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp
                165                 170                 175

Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp
            180                 185                 190

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
        195                 200                 205
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Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val
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Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val
225                 230                 235                 240

Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe
                245                 250                 255

Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp
            260                 265                 270

Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp
        275                 280                 285

Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val
    290                 295                 300

Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala
305                 310                 315                 320

Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu
                325                 330                 335

Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys
            340                 345                 350

Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile
        355                 360                 365

Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr Ile
    370                 375                 380

Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys
385                 390                 395                 400

Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile
                405                 410                 415
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Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys Gly
            420                 425                 430

Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu
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Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys
    450                 455                 460

Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met Lys
465                 470                 475                 480

Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val
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Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met Phe
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Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile Arg
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Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys Ile
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Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg Cys
545                 550                 555                 560

Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met His
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Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr Phe
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Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala Ser
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Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile Thr
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Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu
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Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn Ala
            660                 665                 670


Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu
        675                 680                 685


Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val
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Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly
705                 710                 715                 720


Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp
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Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile
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Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val
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Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu
    770                 775                 780


Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly
785                 790                 795                 800


Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met
                805                 810                 815


Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu
            820                 825                 830
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Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val
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Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val
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Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro
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Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met
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Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu
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Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu
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Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe
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Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro
945                 950                 955                 960

Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val
                965                 970                 975

Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu Glu
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Pro Gly Lys Glu Cys Val Gln Pro  Ala Thr Lys Ser Cys  Ser Phe Ser
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Ala Cys  Thr Asp Gly Ile Ser  Trp Pro Phe Val Leu  Leu Ile Met
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gtagccagat ccctctccag tgacattgga acatgctact ttttaattgg ccctgtacag 7980

tttgcttatt tataaattca ttaaaaacac tacaggtgtt gaatggttaa aatgtaggcc 8040

tccagttcat tttcagttat tttctgagtg tgcagacagc tatttcgcac tgtattaaat 8100

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<210> 1807
<211> 94
<212> PRT
<213> Homo sapiens

<400> 1807
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His Ala His Ser Gly Lys Glu Gly Asp Lys Tyr Lys Leu Ser Lys Lys
20 25 30

Glu Leu Lys Glu Leu Leu Gln Thr Glu Leu Ser Gly Phe Leu Asp Ala
35 40 45

Gln Lys Asp Val Asp Ala Val Asp Lys Val Met Lys Glu Leu Asp Glu
50 55 60

Asn Gly Asp Gly Glu Val Asp Phe Gln Glu Tyr Val Val Leu Val Ala
65 70 75 80

Ala Leu Thr Val Ala Cys Asn Asn Phe Phe Trp Glu Asn Ser
85 90

<210> 1808
<211> 607
<212> DNA
<213> Homo sapiens

<400> 1808
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ctgagctgga gacggcgatg gagaccctca tcaacgtgtt ccacgcccac tcgggcaaag 180

aggggacaa gtacaagctg agcaagaagg agctgaaaga gctgctgcag acggagctct 240

ctggcttcct ggatgcccag aaggatgtgg atgctgtgga caaggtgatg aaggagctag 300

acgagaatgg agacggggag gtggacttcc aggagtatgt ggtgcttgtg gctgctctca 360

cagtggcctg taacaatttc ttctgggaga acagttgagc agacagccac attgggcagc 420

gcccttcctc tccaccctcc cagacctgcc tcttcccct gcttccacct caccccactt 480

atccctctcc ataaccccac ccttgcccac cccaccccca cccccaccaa gggcgcaaga 540

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aaaaaaa 607

<210> 1809
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1809
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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tccaacagca catctggagg atcttcaaat gacaacgcct acttcggcta cagcaccccc 840

tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900

ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960

caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020

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cgctggaacc cggagatcca gtacacttcc aactattaca agtctaataa tgttgaattt 2160

gctgttaata ctgaaggtgt atatagtgaa ccccgcccca ttggcaccag atacctgact 2220

cgtaatctgt aa 2232

<210> 1810
<211> 2232
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1810
atggctgccg atggttatct tccagattgg ctcgaggaca accttagtga aggaattcgc 60

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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac 180

aaggggggagc cggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240

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caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360

gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420

ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggtattggc 480

aaatcgggtg cacagcccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag 540

tcagtcccag accctcaacc aatcggagaa cctcccgcag ccccctcagg tgtgggatct 600

cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga 660

gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcatc 720

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cgctggaacc cggagatcca gtacacttcc aactattaca agtctaataa tgttgaattt 2160

gctgttaata ctgaaggtgt atatagtgaa ccccgcccca ttggcaccag atacctgact 2220

cgtaatctgt aa 2232

<210> 1811
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1811
agaaagaggc ga 12

<210> 1812
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1812
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<210> 1813
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1813
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ggccct 66

<210> 1814
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1814

atgggatgga gctggatctt tctctttctc ctgtcaggaa ctacaggtgt cctctctgag 60

gtccagctgc aacagtctgg acctgagctg gtgaagcctg gggcttcagt gaagatatcc 120

tgcaagactt ctggatacac attcactgaa tacaccatac actgggtgaa gcagagccat 180

ggagagagcc ttgagtggat tggaggtatt aatccaaacg atggtggtac tatttacaac 240

cagaagttca agggcaaggc cacattgact gtagacaagt cctccaaaac agcctacatg 300

gagctccgca gcctgacatc tgaggattct gcagtctttt actgtgcaag agggccctcc 360

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gcccacccgg ccagcagcac caaggtggac aagaaaattg tgcccaggga ttgtggttgt 720

aagccttgca tatgtacagt cccagaagta tcatctgtct tcatcttccc cccaaagccc 780

aaggatgtgc tcaccattac tctgactcct aaggtcacgt gtgttgtggt agacatcagc 840

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<210> 1815

<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1815
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gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc 120

atctcttgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 180

ttgttacaga ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac 240

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cggacgttcg gtggaggcac caagctggaa atcaaacggg ctgatgctgc accaactgta 420

tccatcttcc caccatccag tgagcagtta acatctggag gtgcctcagt cgtgtgcttc 480

ttgaacaact tctaccccaa agacatcaat gtcaagtgga agattgatgg cagtgaacga 540

caaaatggcg tcctgaacag ttggactgat caggacagca aagacagcac ctacagcatg 600

agcagcaccc tcacgttgac caaggacgag tatgaacgac ataacagcta tacctgtgag 660

gccactcaca agacatcaac ttcacccatt gtcaagagct tcaacaggaa tgagtgt 717

<210> 1816
<211> 2174
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1816
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tcctctctga ggtccagctg caacagtctg gacctgagct ggtgaagcct ggggcttcag 120

tgaagatatc ctgcaagact tctggataca cattcactga atacaccata cactgggtga 180

agcagagcca tggagagagc cttgagtgga ttggaggtat taatccaaac gatggtggta 240

ctatttacaa ccagaagttc aagggcaagg ccacattgac tgtagacaag tcctccaaaa 300

cagcctacat ggagctccgc agcctgacat ctgaggattc tgcagtcttt tactgtgcaa 360

gagggccctc cgccaggttt ccttactggg gccaagggac tctggtcact gtctctgcag 420

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gcacctacag catgagcagc accctcacgt tgaccaagga cgagtatgaa cgacataaca 2100

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<210> 1817
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1817
gaggagccac c 11

<210> 1818
<211> 2174
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1818
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aaccagcctc catctcttgc aagtcaagtc agagcctctt agatagtgat ggaaagacat 180

atttgaattg gttgttacag aggccaggcc agtctccaaa gcgcctaatc tatctggtgt 240

ctaaactgga ctctggagtc cctgacagat tcactggcag tggatcaggg acagatttca 300

cactgaaaat tagcagagtg gaggctgagg atttgggagt ttattattgc tggcaaggta 360

cacattttcc tcggacgttc ggtggaggca ccaagctgga aatcaaacgg gctgatgctg 420

caccaactgt atccatcttc ccaccatcca gtgagcagtt aacatctgga ggtgcctcag 480

tcgtgtgctt cttgaacaac ttctacccca aagacatcaa tgtcaagtgg aagattgatg 540

gcagtgaacg acaaaatggc gtcctgaaca gttggactga tcaggacagc aaagacagca 600

cctacagcat gagcagcacc ctcacgttga ccaaggacga gtatgaacga cataacagct 660

atacctgtga ggccactcac aagacatcaa cttcacccat tgtcaagagc ttcaacagga 720

atgagtgtag aaagaggcga gagggcagag gaagtcttct aacatgcggt gacgtggagg 780

agaatcccgg ccctatggga tggagctgga tctttctctt tctcctgtca ggaactacag 840

gtgtcctctc tgaggtccag ctgcaacagt ctggacctga gctggtgaag cctggggctt 900

cagtgaagat atcctgcaag acttctggat acacattcac tgaatacacc atacactggg 960

tgaagcagag ccatggagag agccttgagt ggattggagg tattaatcca aacgatggtg 1020

gtactattta caaccagaag ttcaagggca aggccacatt gactgtagac aagtcctcca 1080

aaacagccta catggagctc cgcagcctga catctgagga ttctgcagtc ttttactgtg 1140

caagagggcc ctccgccagg tttccttact ggggccaagg gactctggtc actgtctctg 1200

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cgaaggctcc acaggtgtac accattccac ctcccaagga gcagatggcc aaggataaag 1920

tcagtctgac ctgcatgata acagacttct tccctgaaga cattactgtg gagtggcagt 1980

ggaatgggca gccagcggag aactacaaga acactcagcc catcatggac acagatggct 2040

cttacttcgt ctacagcaag ctcaatgtgc agaagagcaa ctgggaggca ggaaatactt 2100

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<210> 1819
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1819
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tcttgcaagt caagtcagag cctcttagat agtgatggaa agacatattt gaattggttg 180

ttacagaggc caggccagtc tccaaagcgc ctaatctatc tggtgtctaa actggactct 240

ggagtccctg acagattcac tggcagtgga tcagggacag atttcacact gaaaattagc 300

agagtggagg ctgaggattt gggagtttat tattgctggc aaggtacaca ttttcctcgg 360

acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgt 714

<210> 1820
<211> 2171
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1820
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tgaagatatc ctgcaagact tctggataca cattcactga atacaccata cactgggtga 180

agcagagcca tggagagagc cttgagtgga ttggaggtat taatccaaac gatggtggta 240

ctatttacaa ccagaagttc aagggcaagg ccacattgac tgtagacaag tcctccaaaa 300

cagcctacat ggagctccgc agcctgacat ctgaggattc tgcagtcttt tactgtgcaa 360

gagggccctc cgccaggttt ccttactggg gccaagggac tctggtcact gtctctgcag 420

ccaaaacgac acccccatct gtctatccac tggcccctgg atctgctgcc caaactaact 480

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cacattttcc tcggacgttc ggtggaggca ccaagctgga aatcaaacgg gctgatgctg 1860

caccaactgt atccatcttc ccaccatcca gtgagcagtt aacatctgga ggtgcctcag 1920

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gcagtgaacg acaaaatggc gtcctgaaca gttggactga tcaggacagc aaagacagca 2040

cctacagcat gagcagcacc ctcacgttga ccaaggacga gtatgaacga cataacagct 2100

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atgagtgtta g 2171

<210> 1821
<211> 2171
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1821
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ccaacggtga tgttgtgatg acccagactc cactcacttt gtcggttacc attggacaac 120

cagcctccat ctcttgcaag tcaagtcaga gcctcttaga tagtgatgga aagacatatt 180

tgaattggtt gttacagagg ccaggccagt ctccaaagcg cctaatctat ctggtgtcta 240

aactggactc tggagtccct gacagattca ctggcagtgg atcagggaca gatttcacac 300

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acagcatgag cagcaccctc acgttgacca aggacgagta tgaacgacat aacagctata 660

cctgtgaggc cactcacaag acatcaactt cacccattgt caagagcttc aacaggaatg 720

agtgtagaaa gaggcgagag ggcagaggaa gtcttctaac atgcggtgac gtggaggaga 780

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cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc ctctcccact 2160

ctcctggtta g 2171